Algae and Innovations

“이 발표논문집은 2017년도 정부재원(과학기술진흥기금 및 복권기금)으로 한국과학기술단체총연합회의 지원을 받아 발간되었음”

사단법인 한국조류학회
THE KOREAN SOCIETY OF PHYCOLOGY

제31회 학술발표대회 및 정기총회

조류, 새로운 도약의 기회

2017. 11

사단법인 한국조류학회

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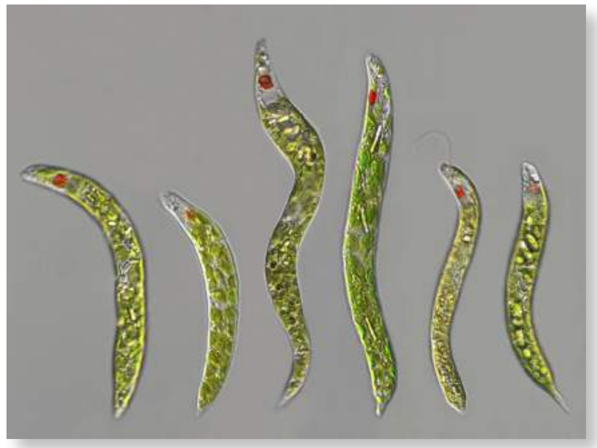
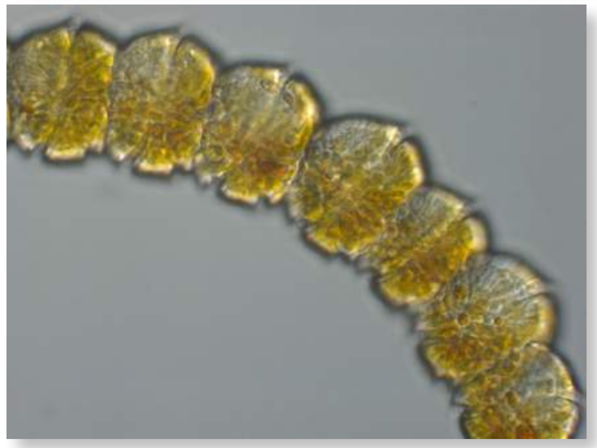
조류, 새로운 도약의 기회!

Algae and Innovations

날짜 : 2017. 11.2~3
장소 : 경상대학교 통영캠퍼스





주최 사단법인 한국조류학회 THE KOREAN SOCIETY OF PHYCOLOGY　주관 사단법인 한국조류학회 THE KOREAN SOCIETY OF PHYCOLOGY　FIRA 한국수산자원관리공단 KOREA FISHERIES RESOURCES AGENCY

후원: 한국과학기술단체총연합회 / 한국물학술단체연합회 / 21세기해양개발(주) / 동성해양개발(주) / 국립해양생물자원관 / 상록엔비텍(주) / (주)테코

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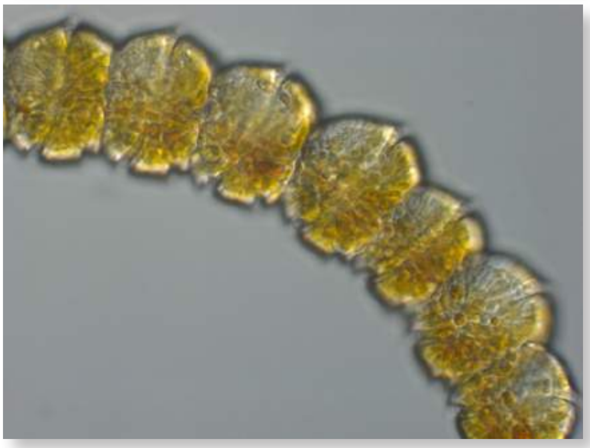

주최 사단법인 한국조류학회 THE KOREAN SOCIETY OF PHYCOLOGY
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목 차

전체일정

장소 : 경상대(통영) 해양생물교육연구센터

11. 02(목)					
시간		총시간	해양생물교육센터 4층 (대회의실, 1917홀)	해양생물교육센터 1층 (해양생물실험실)	수산관 합동강의실 (005-102호)
12:30	13:00	30'	등록		
13:00	13:30	30'	"개회식 및 축사 (김형근회장, 정영훈이사장, 김정균학장)"		
13:30	14:10	40'	"기조 강연 Ⅰ 겐트대학교 한태준 교수"		
14:10	14:25	15'	Break Time		
14:25	15:40	75'		학생구두 Ⅰ (분류 및 형태)	학생구두 Ⅲ (생리, 생태, 응용)
15:40	15:50	10'	Break Time		
15:50	16:50	60'		학생구두 Ⅱ (분류 및 형태)	학생구두 Ⅳ (생리, 생태, 응용)
16:50	17:00	10'	Break Time		
17:00	18:00	60'		일반구두발표 Ⅰ	일반구두발표 Ⅱ
18:00	18:30	30'	만찬장소 이동		
18:30	20:30	120'	기념만찬		

11. 03(금)					
시간		총시간	해양생물교육센터 4층 (대회의실, 1917홀)	해양생물교육센터 1층 (해양생물실험실)	수산관 합동강의실 (005-102호)
8:30	9:00	30'	등록		
9:00	9:40	40'	"기조 강연 Ⅱ 생명공학연구원 오희목 박사"		
9:40	9:50	10'	Break Time		
9:50	10:50	60'	신진연구자발표		
10:50	11:00	10'	Break Time		
11:00	12:25	85'	"특별세션 (바다숲의 가치와 복원)"		
12:25	14:00	95'	점심	평의원회	
14:00	15:00	60'	포스터 발표		
15:00	15:10	10'	Break Time		
15:10	16:00	50'	총회		

발표일정(Program)

11. 2(목)

기조강연

대회의실 4층(1917홀)
좌장 : 김광용 교수

13:30~14:10	PL Ⅰ.	해조류 연구지식의 가치화(valorization)에 대한 고찰 한태준

학생구두발표 Ⅰ
SO-1. 분류 및 형태

해양생물센터(1층)
좌장 : 신웅기, 박명길 교수

14:25~14:40	SO-01	Genome sequencing and population genomic analyses provide insights into the adaptation to new environments of *Undaria pinnatifida* Louis Graf1, Youn Hee Shin1, Ji Hyun Yang1, JunMo Lee1, Sung Min Boo2, Hwan Su Yoon1
14:40~14:55	SO-02	Oxidative burst mediated by respiratory burst oxidase homologue in *Pyropia tenera* with pathogen attacks Da Jeong Lee, Tatyana A. Klochkova, Gwang Hoon Kim
15:55~15:10	SO-03	The organelle inheritance and genome rearrangement in the brown algae with different types of fertilization. Ji Won Choi1, Louis Graf1, Koki Nishitsuji2, Asuka Arimoto2, Eiichi Shoguchi2, Hwan Su Yoon1
15:10~15:25	SO-04	Phylogeography of intertidal red algae, *Gloiopeltis,* (Gigartinales) reveals species complex in the North-Pacific Mi Yeon Yang1, Eun Chan Yang2, Gary W. Saunders3 and Myung Sook Kim1*
15:25~15:40	SO-05	Ultra-morphology and phylogeny of the genus *Phymatolithon* (Hapalidiales, Rhodophyta) with assessment of the features about a novel genus So Young Jeong, Boo Yeon Won, Tae Oh Cho

학생구두발표 Ⅱ
SO-2. 분류 및 형태

해양생물센터(1층)
좌장 : 황일기, 김희식 박사

15:50~16:05	SO-06	Somatic cell fusion in a red alga *Griffithsia* monilis is mediated by two different signaling molecules 문종석, 김광훈
16:05~16:20	SO-07	Plastid genome evolution of genus *Porphyridium* Eun Jeung Kim, JunMo Lee, Hwan Su Yoon
16:20~16:35	SO-08	DNA barcoding for identification of hidden diversity in *Pyropia* (Bangiophyceae, Rhodophyta) from Korea Young Ho Koh, Myung Sook Kim
16:35~16:50	SO-09	Insights into the evolutionary history of the photosynthetic Stramenopiles using novel plastid genomes from four classes, Pinguiophyceae, Dictyochophyceae, Synchromophyceae, and Pelagophyceae (Stramenopiles) Kwiyoung Han1, Louis Graf1, Robert A. Andersen2, Hwan Su Yoon1

학생구두발표 Ⅲ

SO-3. 생리, 생태, 응용

수산관 강의실(102호)
좌장 : 최창근, 김장균 교수

14:25~14:40	SO-10	Effects of stocking density in productivity and nutrient removal of *Gracilaria vermiculophylla* in biofloc effluent Sookkyung Shin1, Su-Kyoung Kim2, Jun-Hwan Kim2 and Jang K. Kim1
14:40~14:55	SO-11	The new reports on life cycle of *Heterosigma akashiwo* (Raphidophyceae) Joo-Hwan Kim, Jin Ho Kim, Pengbin Wang, Bum Soo Park and Myung-Soo Han
15:55~15:10	SO-12	Phenology of *Z. caespitosa* in Tongyeong, Southern coast of Korea 윤준식, 김남길
15:10~15:25	SO-13	Phosphatidylinositol-3-phosphate are involved in host cell entry of an oomycete pathogen *Olpidiopsis pyropiae* 정승진, 김광훈
15:25~15:40	SO-14	Assessment of marine ecological health using diatoms Soyeon Choi1, Jihae Park2, Hojun Lee1, Ju-hyung Lee3, Min-ju Kim3, Hye-jin Kil3, Young-Tae Oh3, Ki-in Bang3, Sung-Mo Lee3, Taejun Han1,2,*

학생구두발표 Ⅳ

SO-4. 생리, 생태, 응용

수산관 강의실(102호)
좌장 : 김장균, 최창근 교수

15:50~16:05	SO-15	A silicon transporter PyLsi plays a critical role in stress tolerance in marine red alga *Pyropia yezoensis* Bao Le1, Man-Gu Kang2, Mawra Nadeem1, Seung Hwan Yang1, Kirill S. Golokhvast3, Sang-Mi Sun1*
16:05~16:20	SO-16	Development of a PCR-free marine biodiversity assessment methodology Jihoon Jo1,3, Hyun-Gwan Lee2,3, Keunyong Kim2,3, Juhee Min2,3, Jingyo Lee2,3, Kwang Young Kim2,3 and Chungoo Park1,3*
16:20~16:35	SO-17	방사무늬김(*Pyropia yezoensis*)의 살리실산 매개 질병 저항성 정서경, 김광훈
16:35~16:50	SO-18	Optimization for protoplast isolation from the gametophytes of *Undaria pinnatifida* using response surface methodology Jose Avila, Boo Yeon Won, Tae Oh Cho

일반구두발표 Ⅰ

해양생물센터(1층)
좌장 : 윤호성, 박명길 교수

17:00~17:20	OO-01	Pathogen-specific gene regulation in the red alga *Pyropia tenera* against the three most common diseases in sea farms Gwang Hoon Kim, Soo Hyun Im, Da Jeoung Lee and Tatyana A. Klochkova
17:20~17:40	OO-02	Revealing the distinct habitat ranges and hybrid zone of genetic sub-populations within *Pseudo-nitzschia pungens* (Bacillariophyceae) in the West Pacific area Jin Ho Kim, Pengbin Wang, Bum Soo Park, Joo-Hwan Kim, Shailesh Kumar Patidar, Myung-Soo Han
17:40~18:00	OO-03	Improved Pigment Content of Microalgae by Use of CRISPR-CAS9 Technology Kwangryul Baek1, Sangsu Bae2 and EonSeon Jin1

일반구두발표 Ⅱ

수산관 강의실(102호)
좌장 : 김명숙, 김영식 교수

17:00~17:20	OO-04	*Learn from the Assembling Red Algal Tree of Life (RedToL)* Hwan Su Yoon, and the RedToL research team
17:20~17:40	OO-05	Integrated Multi-Trophic Aquaculture for Korea Waters Jang Kyun Kim1, Hailong Wu1, Miseon Park2, Youngdae Kim2, Yonghyun Do2, Taejun Han1,3 and Charles Yarish4
17:40~18:00	OO-06	Development of methods for evaluation of natural seaweed beds in Korea Chang Geun Choi1*, Ok-in Choi2 and Mi Kyung Choe2

11. 3(목)

기조강연

대회의실 4층(1917홀)
좌장 : 진언선 교수

9:00~9:40	PL II	Ambivalence of Algae: *Microcystis* aeruginosa vs. Ettlia sp. Hee-Mock Oh

신진연구자발표

대회의실 4층(1917홀)
좌장 : 조태오, 최한길 교수

9:50~10:10	AO-01	What is the real species tree? JunMo Lee1, Suzanne Fredericq2, Wendy A. Nelson3, Tae Oh Cho4, Han-Gu Choi5, Hwan Su Yoon1
10:10~10:30	AO-02	The study of endophytic green algae (Ulvophyceae) from Korea Chansong Kim1, Young Sik Kim1*, Han Gil Choi2, Ki Wan Nam3
10:30~10:50	AO-03	상주 공검지 퇴적층의 연대별 돌말류 분석을 통한 고대 환경 변화 연구 이상득, 윤석민, 조표연

특별세션

대회의실 4층(1917홀)
좌장 : 최미경 박사

11:00~11:10	SC Ⅰ-01	한국의 바다숲 복원 및 관리방향 김정하
11:10~11:25	SC Ⅰ-02	Manipulation of sea urchin density and application of metapopulation concept for recovery and maintenance of kelp forest in barren grounds Jeong Ha Kim, Young Wook Ko, Kwon Mo Yang, Ji Young Hwang
11:25~11:40	SC Ⅰ-03	Growth and Maturation of Sargassum macrocarpum in Cheongsan-Do Island in Southwestern coast of Korea Nam-Gil Kim, Joon-Sik Yoon, Min-Jeong Lee and Min-Ju Kim
11:40~11:55	SC Ⅰ-04	A Study on the Selection of Suitable Sites for Sea-forest Enhancement Tae-Geon Oh, Dong-Hyeon Im, and Sang-Ho Baek
11:55~12:10	SC Ⅰ-05	Effects of the artificial spawning area with seaweed plate and reef on local sailfin sandfish species *Arctoscopus japonicas* in the East Coast of Korea Ji-Huyn Lee*1, Yong-Woo Choi2, Wan-Ki Kim1, Jong-Kuk Youn1, Eungyu Han1, Jung-Mi Ahn1
12:10~12:25	SC Ⅰ-06	2016년 바다숲의 생태적 · 경제적 가치평가 강석규

포스터발표		대회의실 4층 로비
PA. 분류 및 형태		좌장 : 박명길 교수, 황일기 박사
14:00~15:00	PA-01	Description and application of a marine microalga Auxenochlorella protothecoides isolated from Ulleung-do Hyeong Seok Jang1, Nam Seon Kang2, Kyeong Mi Kim1, Byung Hee Jeon1, Joon Sang Park1, and Ji Won Hong1
	PA-02	Species diversity of phytoplankton in Cheonjin lake, North-East South Korea Hyo Seong Jeong, Han Soon Kim
	PA-03	Evolutionary Dynamics of Cryptophyte Plastid Genomes Jong Im Kim1, Christa E. Moore2, John M. Archibald2, Debashish Bhattacharya3, Gangman Yi4, Hwan Su Yoon5*, & Woongghi Shin1*
	PA-04	Complete mitochondrial genomes of two Sargassum species, *S. nigrifolium* and *S. yezoense* (Fucales, Phaeophyceae) Kyeong Mi Kim, Hyeong Seok Jang, and Ji Won Hong
	PA-05	Taxonomy and description of freshwater microalga Mirye Park, Seung Won Nam, Chang Soo Lee, Hyun-Jin Kwon, Kyung June Yim, Eun Sun Joo
	PA-06	New records of diatoms (Bacillariophyceae) and floristic survey in Korea Suk Min Yun, Sang Deuk Lee, Hye-Won Yang, Oe Jung Kim, Pyo Yun Cho
	PA-07	*Surirella nnibria* sp. nov. in freshwater, South Korea Suk Min Yun1, Sang Deuk Lee1, Han Soon Kim2
	PA-08	Morphological Characteristics of Sand-Dwelling Benthic Dinoflagellates as Newly Recorded Species to Korean Waters Su-Min Kang, Gyu-Beom Kim and Joon-Baek Lee
	PA-09	Complete organelle genome and “flip-flop” structure of chloroplast genome of *Capsosiphon fulvescens* (Ulotrichales, Ulvophyceae) Dong Seok Kim, Ji Won Choi, Jun Mo Lee, Hwan Su Yoon
	PA-10	Morphological observations and phylogenetic position of the parasitoid nanoflagellate *Pseudopirsonia* sp. (Cercozoa) infecting the marine diatom *Coscinodiscus wailesii* (acillariophyta) 김선주1, 전창범2, 박명길2
	PA-11	Three Antarctic *Asterochloris species* (Trebouxiophyceae) from King George island, Antarctica Yongjun Kim 1, Jong Im Kim 1, Jae Eun So 2,3, Soon Gyu Hong 2,3, Han-Gu Choi2, Woongghi Shin1
	PA-12	New candidate species of endophytic green algae *Bolbocoleon minus* sp. nov. (Ulvophyceae) from Korea. Chansong Kim1, Young Sik Kim1*, Hyeon Jeong Lee1, Ki Wan Nam2
	PA-13	경상남도 산지습지에서의 규조류 군집분포 박솔이1, 김진희2, 이재학1, 리지아시우1, 진덕현1, 김한순1
	PA-14	Comparative genomics of plastid and mitochondria in *Minerva aenigmata* and *Pyropia pulchra* (Rhodophyta) Seung In Park1, Jun Mo Lee1, Hwan Su Yoon1 Wendy A.Nelson2 , Kathy A. Miller3
	PA-15	곰피(*Ecklonia stolonifera*)의 양식과 품종 구분을 위한 형질분석 옥정현, 이상래, 황일기1, 김승오1, 황미숙1
	PA-16	홍조식물 *Griffithsia monilis*의 형태 발생에 대한 DNA-methylation 저해제 5-azacytidine의 영향 윤지호, 김광훈
	PA-17	A new report of two marine *Mallomonas* (Synurophyceae) from Korea Minseock Jeong, Jong Im Kim, Woongghi Shin
	PA-18	Diatoms (Bacillariophyta) from a tidal sandflat of the western coast, with emphasis on the richness and diversity of epibenthic species 조경제
	PA-19	Isolation and computational characterization of glutathione peroxidase gene from *Pyropia yezoensis* Mawra Nadeem1, Bao Le1, Man-Gu Kang2, Seung Hwan Yang1, Kirill S. Golokhvast3, Sang-Mi Sun1
	PA-20	The crustose coralline alga, two new *Phymatolithon* species (Hapalidiales, Rhodophyta) from Korea So Young Jeong, Boo Yeon Won, Tae Oh Cho*
	PA-21	A new record of epilithic coralline algae *Lithothamnion japonicum* (Hapalidiales, Rhodophyta) from Korea So Young Jeong, Boo Yeon Won, Tae Oh Cho*

PA-22	The ITS2 genetic polymorphisms within *Pseudo-nitzschia pungens* (Bacillariophyceae) resulted from the sexual reproduction Jin Ho Kim1, Joo-Hwan Kim1, Bum Soo Park1, Myung-Soo Han1, Penelope Ajani2, Shauna Murray2, Hong Chang Lim3, Po Teen Lim4
PA-23	한국산 돌말류 속 이상의 분류군의 국명화 연구 이진환
PA-24	Cloning of a novel Cyclophilin B gene in the red tide dinoflagellate *Cochlodinium polykrikoides*: molecular characterizations and transcription to environmental stresses Sofia Abassi, Hui Wang, Won-Ji Choi, Sathasivam Ramaraj, Jang-Seu Ki1
PA-25	Description of S. coreanum sp. nov. in the Korean coasts Il Ki Hwang1, Ga Youn Cho2, Martha S. Calderon3, Sung Min Boo3
PA-26	Revision of the genus *Streblocladia* (Rhodomelaceae) in New Zealand, with genetic evidence for a new species M.S. Kim1*, M.Y. Yang1, B. Kim1, R. D’ Archino2, W. Nelson2 and J. Sutherland2
PA-27	New auxiliary cell ampullae based on foliose red algae, *Nesoia* gen. nov. (Haleminiaceae, Rhodophyta) from Korea Hyung Woo Lee and Myung Sook Kim
PA-28	Molecular and morphological investigations of the genus *Scinaia* (Nemaliales, Rhodophyta) from the northern Pacific Jong Chul Lee1, 2, Hyung Woo Lee1, Kathy Ann Miller3, and Myung Sook Kim1
PA-29	Transfer four species of *Haraldiophyllum* (Delesseriaceae, Rhodophyta) to *Neoharaldiophyllum* gen. nov. based on cystocarp development and molecular data Jeong Chan Kang, Mi Yeon Yang and Myung Sook Kim
PA-30	Species boundary of *Scinaia johnstoniae* (Nemaliales, Rhodophyta) from the northern Pacific using molecular analysis Jong Chul Lee1, 2, Hyung Woo Lee1, Kathy Ann Miller3, and Myung Sook Kim1
PA-31	Cryptic species diversity of the genus *Herposiphonia* (Rhodomelaceae, Rhodophyta) from the south-eastern coast of Spain Young Ho Koh1, Ricardo Bermejo2, Myung Sook Kim1
PA-32	Taxonomy and Phylogeny of the genus *Phymatolithon* (Hapalidiaceae, Rhodophyta) So Young Jeong, Boo Yeon Won, Tae Oh Cho
PA-33	Protoplast regeneration from male and female gametophytes of *Undaria pinnatifida* José Avila, Boo Yeon Won, Tae Oh Cho
PA-34	New insights of the taxonomy of *Pyropia pseudolinearis* complex: Proposal a new cryptic species, *Pyropia donghaeensis* S.M. Kim et H.-S. Kim, from the east coast of Korea (Bangiaceae, Rhodophyta) Sun-Mi Kim1, Il-Ki Hwang2, Han Gu, Choi1, Mi Sook Hwang2*, and Hyung-Seop Kim3*
PA-35	New candidate species of endophytic green algae *Phlegma teres* gen. et sp. nov. (Ulvophyceae) from Korea Chansong Kim1, Young Sik Kim1*, Soung Yeon Choi1, Ki Wan Nam2
PA-36	Rediscovery of the Ochromonas type species, *Ochromonas triangulata* Wysotski, from sample of the type locality Louis Graf
PA-37	Multigene phylogeny reveals pattern of evolution of the multicellularity in the Heterokontophyta SI clade Louis Graf1, Robert A. Andersen2 & Hwan Su Yoon1
PA-38	Chromatophore genome of Paulinella longichromatophora: Changes during endosymbiotic organogenesis Duckhyun Lhee, Sunju Kim, Myung Gil Park, Debashish Bhattacharya, Hwan Su Yoon
PA-39	The genomic analysis of *Apophlaea lyallii* (Florideophyceae, Rhodophyta); the algal-fungal symbiosis Chung Hyun Cho1, Wendy Nelson2,3, Hwan Su Yoon1
PA-40	*Pleurostomum flabellatum* genomics; New paradigm to unveil the adaptation of extreme salinity Khaoula Ettahi1, Jong Soo Park2, Hwan Su Yoon
PA-41	A new endophytic green algal species: *Ulvella jejuensis* sp. nov. (Ulvellaceae, Chlorophyta) from Korea Chansong Kim1, Young Sik Kim1*, Han Gil Choi2, Ki Wan Nam3
PA-42	Nitrogen uptake and growth of thalli of *Pyropia yezoensis* under several culture conditions Soung Youn Choi1, Hyeon Jeong Lee1, Chansong Kim1, Jae Seong Kim2, Young Sik Kim1

포스터발표 대회의실 4층 로비

PB. 생태 좌장 : 윤호성 교수, 기장서 교수

14:00~15:00	PB–01	Short–term variations of the phytoplankton species composition and environmental parameters in Youngsan River estuary Arnold Jesfel Rejuso, Yongsik Sin*
	PB–02	Ecological Study in Macroalgal Assemblage of Ulleungdo on East Coast of Korea Gyu Jin Park1, Chang Geun Choi2
	PB–03	영산강 하구의 담수유입에 따른 생태적 영향 Inyeol Kim1, Jewoo Park1, Hayan Yoon2, Yongsik Shin1*
	PB–04	Seasonal growth and reproduction of *Gelidium coreanum* and *G. elegans* (Rhodophyta) from the east coast of Korea Juil Lee1, Changgeun Choi2, Ilki Hwang3, Kyusam Han4, Hyunggeun Kim4, Sungmin Boo1
	PB–05	목포해역 식물플랑크톤 Chlorophyll a의 계절별 크기구조 Sehee Kim1, Hwaeun Cha1, Hayan Yoon2, Yongsik Shin1
	PB–06	Holocene environmental changes from a diatom record in Korea (Reservoir Gonggeomji, Sangju City) Suk Min Yun, Sang Deuk Lee, Pyo Yun Cho
	PB–07	Akashiwo sanguinea 적조 발생 및 미 발생시의 환경변화 차이 강준수1,2, 김현정2, 한혜정2, 오석진1, 정승원2
	PB–08	Effects of salinity on growth and photosynthetic performance of *Ulva ohnoi* (Chlorophyta) 김나현, 문한비, 이숙연, 김주형
	PB–09	Surveys on high–temperature resistant natural populations of *Pyropia* species in Korea Ro Won Kim 1, Tatyana A. Klochkova 2, Min Seok Kwak 1, Gwang Hoon Kim 1
	PB–10	한국 연안에 서식하는 군소의 섭식생태 김민주, 김남길
	PB–11	갯벌에서 광량에 따른 저서미세조류의 영양염 흡수율 김소연1, 이숙연2, 김일남1, 김주형2
	PB–12	통영해역에서 출현하는 식물플랑크톤 변동 특성 1: 차세대 염기서열 및 현미경 분석을 통한 규조류의 변동 차이 김현정, 정승원
	PB–13	Abundance of three *Alexandrium* species in the South Sea, Korea during the summer 2017 Hye Mi Kim, Hyun–Gwan Lee, Kwang Young Kim
	PB–14	Quantification of inorganic carbon removal efficiency by *Pyropia* aquaculture bed 문한비, 김나현, 이숙연, 김주형
	PB–15	Effect of red algal blooms on trophic structure of macrobenthic food web in the southern coast of Korea revealed by C and N stable isotope analyses 박현제1, 곽정현2, 강창근3
	PB–16	춘계 제주도 연안의 유독 착생 와편모류 *Ostreopsis*의 분포와 분자계통학적 위치 서효정1, 김현정1, 김돈기1, 정영교1, 백승호2, 김선주1
	PB–17	한국산 방사무늬김(Pyropia yezoensis)의 건조 스트레스에 의한 붉은갯병(red rot disease) 감염률 비교 심준보, 하동수, 이순정
	PB–18	Practicality of mitochondrial marker for diatoms community monitoring of the west coast of Korea 양은찬, 안성민, 노재훈
	PB–19	Impact of ocean acidification and warming on chlorophyll a fluorescence and growth of the canopy forming alga *Sargassum horneri* 이숙연1, 민주희2, 김광용2, 김주형1
	PB–20	Mapping distribution of cysts of recent dinoflagellate and *Cochlodinium polykrikoides* using next–generation sequencing and morphological approaches in South Sea, Korea 정승원, 김현정
	PB–21	남, 동해 하천 하구역의 부착규조를 이용한 수생태계 건강성 평가 최재신, 채현식, 이재학, 김한순
	PB–22	통영 연안 해역에서 여름철 Chlorophyll a 연속 관측 및 식물플랑크톤 군집 변화 한혜정1, 강준수1,2 정승원1
	PB–23	와편모조류 *Oxyrrhis marina*의 섭식 과정 중 편모의 역할에 대한 초고속 촬영 분석 홍찬영, 김광훈

	PB-24	채취법에 따른 우뭇가사리 종조성 및 생물량 변화 양상 김현겸1, 이진호1, 양문호1, 한명일1, 한은규1, 이영돈2, 강정찬2
	PB-25	Benthic invertebrate community structure in natural and restored *Zostera marina* beds in Seosan, Korea Yejin Hyeon1 2, Mi-Kyung Choi1, Ok-In Choi1, Yong-Woo Choi1, Seok-Kyu Kang 3, Min-Ho Son4, Young-Chul Park5, Jae-Won Yoo6, Kun-Seop Lee 2*
	PB-26	Treatment of secondary wastewater effluent using High Rate Algal Ponds in New Zealand Jason Park *1, Rupert Craggs 1, Chris Tanner
	PB-27	Influence of salinity on growth, nutrient uptake and nutrient bioextraction capacity of seaweeds Sookkyung Shin1, Hailong Wu1, Miseon Park2, Youngdae Kim2, Yonghyun Do2 and Jang K. Kim
	PB-28	Seaweed Cultivation in Northeast America for Food, Feeds, Fertilizer, Ecosystem Services & Biofuels Jang K. Kim1,2, Charles Yarish2,3, Bren Smith4, & Simona Augyte2,4
	PB-29	Study of Community Structure and Algal Flora of Gageodo Island, West-southern Coast, Korea Seung Wook Jung1, Yoon Sik Oh2, Chang Geun Choi1
	PB-30	Study of Ecological Structure and Flora in Marine Macro algae on East Coast and Jeju Island, Korea Gyu Jin Park, Chang Geun Choi
	PB-31	Trophic structures of benthic microalgae to benthos in marine ecosystems of Korea using stable isotopes and food web analyses Donghoon Shin*1,2, Chang Geun Choi2, Chang-Keun Kang3
	PB-32	홍조류 진두발 야외개체군의 계절 및 조위에 따른 생장과생식변화 Cyr Abel Maranguy Ogandaga1, Lee Jung Rok1, Han Gil Choi *1, Jeong Ha Kim2, Young Sik Kim3, Ki Wan Nam4

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대회의실 4층 로비

PC.
생리 및 유전

좌장 : 김명숙 교수, 김희식 박사

14:00~15:00	PC-01	Overexpression of a S-Adenosylmethionine Synthetase gene from *Pyropia tenera* confers enhanced tolerance to salinity stress Hyun Dae Hong, Jin-Woo Han, Jong Won Han, Hyun-Ju Hwang
	PC-02	Biomass analysis of four domestic microalgae strains using wastewater treatment for different types of applications Jeong-Mi Do1, Seung-Woo Jo2, Ho Ra1, Ho-Sung Yoon1,2
	PC-03	RNA-seq analysis for the study of circadian gene expression in multicellular red algal *Gracilariopsis chorda* Ji Hyun Yang, JunMo Lee, Khaoula Ettahi, Hwan Su Yoon
	PC-04	Alteration of inorganic carbon acquisition on geniculate coralline alga *Corallina officinalis* under hypoxia and warming Juhee Min1, Hanbi Moon2, Nahyeon Kim2, Ju-Hyoung Kim2, Kwang Young Kim1
	PC-05	DNA methylation is involved in regeneration and differentiation of protoplasts in the *Bryopsis plumosa* Minseok Kwak 1, Tatyana A. Klochkova 2, Gwang Hoon Kim 1
	PC-06	Interactive effects of temperature and light properties (intensity and wavelength) on the photosynthesis and growth of red alga *Pyropia dentata* (Bangiales, Rhodophyta) in a conchocelis phase 김주형1, 이숙연1, 최성제2
	PC-07	해양 낭균에 감염된 홍조식물 엇가지풀의 전신획득저항성 문현영, 김광훈
	PC-08	Viral infection enhances resistance to oomycete pathogens in *Pyropia yezoensis* 박지혜, 이다정, 김광훈
	PC-09	홍조식물 *Bostrychia moritziana*의 성 특이적 importin alpha 유전자의 규명 심은영1, 심준보2, 김광훈1
	PC-10	*Labyrinthula zosterae* 감염에 의한 거머리말(*Zostera marina*)의 Mn-SOD 유전자 발현 심준보, 하동수, 이순정

	PC-11	양식 김 엽체의 기계적 절단에 의한 무성포자 방출 유도 이정은, 김광훈
	PC-12	녹조식물 해캄(*Spirogyra varians*)의 phototropin 분석 이지웅, 김광훈
	PC-13	세 가지 갯병에 대한 참김 (*Pyropia tenera*)의 특이적 면역 반응 분석 임수현, Tatyana A. Klochkova, 이다정, 김광훈
	PC-14	방사무늬김(*Pyropia yezoensis*) 6개 품종의 신안지역 적합성 확인을 위한 생장 비교 김지건, 모기호, 김영희, 이지은, 허진석, 박은정
	PC-15	방사무늬김 우량계통주 선발을 위한 저준위 감마선조사 김지건, 모기호, 김영희, 이지은, 허진석, 박은정
	PC-16	Diatom-Based Paleoenvironmental Reconstruction in Upo Wetland, South Korea Sang Deuk Lee, Suk Min Yun, Pyo Yun Cho
	PC-17	Combined effect of irradiance and temperature on egg discharge efficiency from female gametophytes of *Undaria peterseniana* (Phaeophyta) SM Mustafizur Rahman1,3, Jae Hong Pak2 and Hyung Geun Kim3
	PC-18	Protoplast isolation and regeneration from the filamentous brown alga, *Hecatonema terminale* (Ectocarpales, Chordariaceae) Jose Avila, Boo Yeon Won, Tae Oh Cho
	PC-19	바다숲 복원을 위한 지충이와 꼬시래기의 생리 · 생태 및 종묘생산 Jeong Rok Lee1, Nam-Gil Kim2, Han Gil Choi1
	PC-20	퇴적물의 양과 입자 크기가 갈조류 지충이 접합자의 부착률과 배아의 생존 및 생장에 미치는 영향 Gao Xu, Jeong Rok Lee, Seo Kyeong Park, Han Gil Choi
	PC-21	우리나라 양식종(방사무늬김, 모무늬돌김, 잇바디돌김)의 채묘 효율을 높이기 위한 최적 온도 및 조도조건 탐색 허진석, 박은정, 김영희, 하동수
	PC-22	유리배우체 채묘 효율 향상을 위한 최적 배우체 비율 및 고온자극이 아포체 형성에 미치는 영향 유현일, 김수홍, 이기현, 하동수
	PC-23	Physiological effects of copper on the freshwater algae *Closterium ehrenbergii* and its potential use in toxicity assessments Hui Wang, Hansol Kim, Sathasivam Ramaraj, Jang-Seu Ki
	PC-24	Feasibility study on seed production and aquaculture of *Saccharina japonica* (Phaeophyta) in the middle coast of East Sea, Korea Min Su Park, Suraiya Arzu, Su Min Ko, Jae Joong Jin, Hyung Geun Kim
	PC-25	Sexual maturity of male and female gametophytes of *Undaria peterseniana* (Phaeophyta) in Ulleungdo island Hyung Geun Kim1, SM Mustafizur Rahman1,3, Sung Jin Yoon2, Yun Bae Kim2, Chung Il Lee1
	PC-26	Outdoor cultivation of Korean domestic microalgae in large scale Ji Won Hong1, Oh Hong Kim1, Seung-Woo Jo2, Jeong-Mi Do3, Ho Na3, Ho-Sung Yoon1,2,3,*

포스터발표

PD.
응용조류 및 생명공학

좌장 : 최창근 교수, 김영식 교수

14:00~15:00	PD-01	Cryopreservation method of freshwater microalgae in Korea Chang Soo Lee, Mirye Park, Eun Sun Joo, Hyun-Jin Kwon, Seung Won Nam, Kyung June Yim, Jee-Hwan Kim
	PD-02	Possible Application of the Polychaete-Assisted Integrated Culture for IMTA Development Chang-Hoon Kim1, Dong Ju Kim1, War War Phoo1, Ye Pyae Naing1, Hong Jin Kim2
	PD-03	Effects of extracellular polymeric substances (EPS) components on the flocculation and adsorption behaviors of *Ettlia* sp. Chau Hai Thai Vu 1,2, Seong-Jun Chun 1,2, Seong-Hyun Seo 1,3, Hee-Mock Oh 1,2
	PD-04	A new strain development of *Saccharina japonica* for stable abalone feed industry in Korea Eun Kyoung Hwang1, Dong Soo Ha1, Chan Sun Park2
	PD-05	Development of molecule delivery system by using cell-penetrating peptides in red alga *Pyropia tenera* Hancheol Jeon, Hyun Dae Hong, Yong Tae Kim, Jin-Woo Han, Hyun-Ju Hwang, Jong Won Han

PD-06	Comparative transcriptomics of thermal responses in red-tide algae *Cochlodinium polykrikoides* Hyun-Hee Honga,c, Hyun-Gwan Leeb,c, Jihoon Joa,c, Sung-Gwon Leea,c, Hyewon Kimb,c, Kwang Young Kimb,c, Chungoo Parka,c*
PD-07	The discovery of novel stage-specific biomarkers for early detection of harmful marine organisms using transcriptome profiling analysis Jooseong Oh1,3, Hyun-Gwan Lee2,3, Juhee Min2,3, Hyemi Kim2,3, Keunyeong Kim2,3, Kwang Young Kim2,3, Chungoo Park1,3
PD-08	Loss of CpSRP components affected LHCP transport and assembly of thylakoid membranes in Chlamydomonas reinhardtii Jooyeon Jeong1, Kwangryul Baek1, Henning Kirst2, Nico Betterle2, Anastasios Melis2, EonSeon Jin1
PD-09	Study of the screening method of *H.pluvialis* mutants for enhancing the astaxanthin yield Lee Yu Kyong1, Sang A Lee1, Bit Na Lee1, Chang-Hee Hong2, Dae Geun Kim2
PD-10	The methods for increasing Astaxanthin and DHA contents from *Schizochytrium* SHG 104 Sang A Lee1, Yu Kyong Lee1, Bit Na Lee1, Chang-Hee Hong2, Dae Geun Kim2
PD-11	Isolation and Characterization of high temperature tolerant strain in *Pyropia yezoensis* Yoon Ju Shin, Da Yeon Kang, Jong-Min Lim, Won-Joong Jeong
PD-12	해양심층수를 활용한 스피룰리나 (Arthrospira platensis)의 광합성 색소와 항산화능 연구 김미성, 김용찬, 김영라, 김종현, 이정석, 한영석
PD-13	Development of Efficient Transformation and Selection Methods for Microalgae Min-Jeong Kim, Aryan Rahimi-Midani, Yelin Kim, Su-Hyun Kim, Anshuman Mishra, and Tae-Jin Choi
PD-14	신품종 심사를 위한 나문재의 특성조사요령 김승오, 김경환, 황일기, 이채길, 황미숙
PD-15	Rapid transformation of *Chlamydomonas reinhardtii* using Subtilisin (Alcalase) 김용태1, 황현주1, 강남선1, 김광훈2, 한종원1
PD-16	Effect of nutrient limitation on lipid production by *Chlamydomonas reinhardtii* 박서정, 최종일
PD-17	Anti-ulcer effect of polysaccharides from *Undaria* sp. 최종일, 박서정
PD-18	Optimized process for the sequential production of lipid and carotenoids from Ettlia sp. Nakyeong Lee 1, 2, So-Ra Ko 1, Chi-Yong Ahn 1, 2, Hee-Mock Oh 1, 2
PD-19	세포분열능이 우수한 *Haematococcus pluvialis* B0103의 Astaxanthin 생산 방식 개선에 관한 연구 이빛나1, 이유경1, 이상아1, 홍창희2, 김대근2*
PD-20	The anti-cancer compounds Saringosterol acetate from *Hizikia fusiforme* inhibit cancer cell growth and PIK3/AKT/mTORpathway on Hep3B and Du145 cancer cell lines. Hyo Geun Lee, You-Jin Jeon, WonWoo Lee*
PD-21	Functional expression and characterization of GlcNAc specific marine algal lectin 한진욱1, 황현주1, 김광훈2, 한종원1
PD-22	Inhibition of inflammatory responses elicited by urban fine dust particles in keratinocytes and macrophages by diphlorethohydroxy-carmalol isolated from a brown alga Ishige okamurae I. P. Shanura Fernando, Won-Woo Lee, Hyo Geun Lee, You-Jin Jeon*
PD-23	Anti-inflammatory effects of a sulfated polysaccharide isolated from an enzymatic digest of brown seaweed *Sargassum horneri* K.K.A Sanjeewa, Won-Woo Lee, Hyo Geun Lee, You-Jin Jeon
PD-24	Protective effect of a novel antioxidative peptide purified from a marine *Chlorella ellipsoidea* protein against oxidative stress induced by free radicals Lei Wang, Won-Woo Lee, Hyo Geun Lee, You-Jin Jeon
PD-25	Marine algal polyphenols stimulate muscle growth in C2C12 muscle cells through myogenesis pathways Seo-Young Kim, Won-Woo Lee, Hyo Geun Lee, You-Jin Jeon*
PD-26	Green TD- A New Environment-Friendly Algicidal Compound 김진원1, 백유민1, 조한설1, 이도훈1, 손형규2, 조훈2
PD-27	Seaweed beer: an application of seaweed biomass Sojin Jang, Seoyoon Kim, Hayeon Kim, Haram Jung and Jang K. Kim
PD-28	Identification and Characterization of an Isoform Antifreeze Protein from the Antarctic Marine Diatom, *Chaetoceros neogracile* and Suggestion of the Core Region Minjae Kim 1, Yunho Gwak 1, Woongsic Jung 2,* and EonSeon Jin 1,*
PD-29	Control of zooplankton populations using CO*2* asphyxiation: from laboratory cultures to a wastewater treatment High Rate Algal Pond Valerio Montemezzani a, , Ian C. Duggana, Ian D. Hogga, Rupert J. Craggsb.

인 사 말

안녕하십니까? 제 31회 (사)한국조류학회 학술발표대회 및 정기총회에 오신 내외빈 여러분, 그리고 한국조류학회 회원 여러분 모두 진심으로 환영합니다.

저는 이번 학술대회가 하늘과 땅, 바다와 섬이 맞닿아 있는 자연의 도시 통영, 이곳에서 개교 100년을 맞은 경상대학교 해양과학대학 캠퍼스에서 개최되는 것을 진심으로 감사하게 생각합니다. 아울러, 우리나라의 바다에 푸른 미래를 심어가고 있는 한국수산자원관리공단과 이번 대회를 공동으로 개최하게 되어 더욱 뜻 깊게 생각합니다.

우리 한국조류학회는 1986년에 창립되어 작년에 한 세대인 30년을 기념하였습니다. 창립 당시 93명으로 시작한 우리 학회가 어느덧 800명이 넘는 대규모의 학회로 성장하였고, SCIE급의 우수한 저널인 「ALGAE」를 발간하는 명실공히 세계적인 학회로 발전하였습니다. 지구의 탄생 이후 생명의 시작에는 조류가 함께 하였고, 지금도 자연의 일부로, 인간과 떼려야 뗄 수 없는 관계로 함께 하고 있습니다.

2017년 학술대회의 주제는 "조류, 새로운 도약의 기회! (Algae and Innovations!)로 정하였습니다. 우리 학회를 이루는 수 백 명의 회원들은 분류, 생태, 생리, 환경, 에너지, 생명공학 등 조류를 대상으로 하는 수많은 분야에서 활약하고 있고, 새롭게 자라는 후학 세대들은 더 큰 열정과 노력으로 새로운 분야에 도전해 가고 있습니다. 이 번 학술대회에서도 이러한 다양한 분야의 연구 성과들이 160여 편의 논문으로 발표되고 논의됨으로써 한국 조류학을 조금 더 발전시키는 기회가 될 것이라 믿습니다.

이번 대회를 공동으로 준비하고 후원해주신 한국수산자원관리공단 정영훈 이사장님 과 직원 여러분, 그리고 최고의 장소를 허락해 주신 경상대학교 해양과학대학 김정균 학장님과 김남길 교수님께 감사드립니다. 또한, 이번 대

회에서 기조강연을 해 주시는 겐트대학교 인천글로벌 캠퍼스의 한태준 부총장님, 한국생명공학연구원 오희목 박사님께 감사의 말씀 올립니다. 아울러, 본 학술대회를 준비하느라 며칠 밤잠을 설쳐가며 고생한 최한길 학술위원장을 비롯한 학술위원, 학회 임원진과 직원 여러분께 진심으로 고마움을 표합니다. 마지막으로 학술대회에 아낌없는 지원을 해 주신 국립해양생물자원관, 21세기해양개발(주, 동성해양개발(주), 상록엔비텍(주), 테코(주), 등 여러 후원기관 관계자 여러분께도 깊은 감사드립니다.

2017년 11월 2일
(사)한국조류학회 회장 김 형 근

인사말

제31회 한국조류학회 정기학술발표대회에 참석해주신 내외귀빈 여러분께 감사의 말씀을 드립니다.

한국수산자원관리공단 이사장 정영훈입니다.

이번 학술대회를 한국조류학회와 한국수산자원관리공단이 공동으로 개최하게 되어 영광으로 생각하며 바다의 땅, 통영에서 개최하게 된 것을 진심으로 축하드립니다.

또한 학술대회 개최를 위하여 수고를 아끼지 않으신 한국조류학회 김형근 회장님을 비롯한 학회 회장단과 사무국, 그리고 한국수산자원관리공단 실무자분들께 감사의 마음을 전합니다.

우리 공단은 수산자원을 체계적으로 조성관리하고 관련 기술을 개발하고 보급하는 전문기관으로서 지속가능한 어업생산 기반 구축과 어가소득 증대를 위해 풍요로운 어장을 조성하는 역할을 수행하고 있습니다.

하지만 우리나라 연근해 어업생산량은 남획, 기후변화, 환경오염 등의 복합적인 요인으로 연근해어업 생산량이 지속적으로 감소하여 지난해에는 1986년 173만톤의 절반인 93만톤 수준으로, 수산자원 회복이 절실한 실정입니다.

이에 따라 그 어느 때보다 우리공단의 역할에 대한 사명감과 책임감을 막중하게 느끼고 있습니다.

여러분들도 잘 아시는 바와 같이 해조류로 이루어진 바다숲은 해양생물이 태어나고 자라며 알을 낳고, 또 그 알들이 부화하고 다시금 자라는 산란장이자 서식처로서, 바로 생명의 안식처입니다.

우리공단은 이러한 해양생물의 터전인 바다숲이 매년 확산되고 있는 갯녹음으로 인하여 해조류가 감소되고 연안생태계가 점차 붕괴되어 가고 있는 것에 주목하였습니다.

수산자원의 회복을 위해서는 해양생물들의 삶의 터전인 바다숲, 연안생태계를 복원하는 것이 가장 필수적인 첫걸음이라 생각합니다.

이에 한국수산자원관리공단은 해양생물의 근간이 되는 연안생태계 건강성 제고를 위해 2030년까지 전 연안의 75%에 준하는 54,000ha의 바다숲 조성을 목표로 설정하고

지난 2016년 기준, 전국 연안 111개소에 총 12,208ha의 바다숲을 조성하였으며 체계적인 관리도 병행하고 있습니다.

특히, 해양생태계에 기반하여 해역별로 특화된 맞춤형으로 천연 해조장 보호·보전사업 등을 추진하고 어업인 소득 향상도 함께 도모하고 있습니다.

아울러 육상의 식목일을 통해 산림이 울창해졌듯이 세계최초로 매년 5월 10일을 바다식목일로 지정하고 전 국민과 함께 바다녹화운동을 펼쳐나가고 있습니다.

세계적 미래학자 앨빈 토플러는 해양수산 분야를 정보통신, 우주개발, 생명공학과 더불어 미래 4대 핵심 산업으로 분류한 바 있습니다.

이번 학술대회를 통해 해조류의 중요성과 무한한 미래 가치에 대한 다양한 분야의 학술 네트워크가 이루어지고 보다 과학적이고 체계적인 연구가 이어지길 바랍니다.

第31회 한국조류학회 정기 학술대회가 해양수산강국의 미래를 설계하는 소중한 기회가 되기를 기대하며 한국수산자원관리공단 역시 그 영광을 함께할 수 있도록 최선을 다하도록 하겠습니다.

감사합니다.

한국수산자원관리공단 이사장 정 영 훈

환 영 사

반갑습니다. 우리나라 조류관련기술분야의 발전을 위하여 앞장서서 이끌고 있는 한국조류학회 학술발표대회를 경상대학교 통영캠퍼스에서 개최하게 되어 영광스럽게 생각합니다.

저희 학교는 우리나라 수산관련학교의 효시로서, 1917년 4월에 개교하여 올해 100년이 되었습니다. 지난 4월 20일 100주년 개교기념식, 기념석설치, 1회 졸업생이 기부한 종각설치행사가 있었고, 다가오는 11월 24일에는 100주년 기념서 발간식과 타임캡슐 기념식을 가질 계획입니다. 학술행사로는 한국수산과학회, 한국어업기술학회, 한국과학교육학회가 성황리에 개최되었고, 오늘 개교 100주년 기념 마지막 학술대회를 한국조류학회가 장식하게 되어 매우 영광스럽습니다. 저희 학교에서 학술대회를 개최할 수 있도록 도와주신 김형근 회장님, 정영훈 이사장님과 김남길 교수님을 비롯한 임원진께 감사드립니다.

한국조류학회는 1986년 설립되어 31년의 역사를 가지고 있으며, 그 설립목적은 조류관련 학문발전, 조류관련 산업발전인 것으로 알고 있습니다.

학술대회는 학문적 가치 자체만으로도 그 의미가 크다고 할 수 있지만, 관련 산업과의 기술접목을 통한 새로운 산업적 가치를 창출할 수 있는 좋은 계기가 된다는 점에서 매우 중요하다고 생각합니다.

오늘의 학술대회는 한 해 동안 연구하신 귀한 연구 성과물을 발표하고 공유하는 대단히 뜻있는 자리라고 생각합니다. 오늘의 행사가 교수님이나 연구분야에 근무하시는 분들에게는 큰 학문적 성과가 있기를 바라며, 대학원생을 비롯한 후학들에게도 진로에 큰 도움이 되기를 바랍니다.

아무쪼록 조류관련 분야의 학술적·산업적 발전을 위해 개최된 학술대회에서 많은 성과가 있고, 특히 해조류 관련업이 잘 관리되길 바라겠습니다.

그리고 이곳 통영은 우리나라 수산업의 1번지이고, 문화관광도시로 인기가 많은 곳입니다. 행사가 끝난 후 동양의 나폴리 이곳 통영에서 바다 음식과 자연을 맘껏 느끼면서 힐링하는 자리가 되었으면 좋겠다는 생각도 가져 봅니다.

다시 한번 경상대학교 해양과학대학을 방문해 주신 조류기술분야의 전문가 여러분께 감사의 인사를 드리며, 맺음과 결실이 있는 계절에 한국조류학회의 큰 결실을 기원합니다. 감사합니다.

2017년 11월 2일
경상대학교 해양과학대학 학장 김 정 균

기조강연

[PL-01]

해조류 연구지식의 가치화(valorization)에 대한 고찰

한태준

겐트대학교 글로벌 캠퍼스

인천대학교 해양학과

최근 학술연구의 사회적 영향과 유용성에 대한 논의가 줄곧 진행되고 있는 가운데 과학 지식의 가치화, 즉 과학기술을 잠재력이 높은 상품, 서비스, 프로세스, 그리고 산업활동으로 전환하여 경제적 그리고 사회적으로 유용하게 만드는 작업에 대한 관심이 고조되고 있다. 이때, 가치화란 단지 '부'만을 의미하는 것이 아니라 '과학지식의 전수를 통해 창출될 수 있는 모든 영향력'을 포함한다. 한편, 빅데이터, AI, 클라우드 컴퓨팅, 사물인터넷 등으로 대표되는 4차 산업혁명시대가 시작되면서 사회는 정확하고 폭넓은 지식과 정보, 보다 빠른 소통 수단의 혜택을 누리고 정보통신기술과 전에는 관련이 없어 보이던 다양한 산업 사이에 융합적 접근이 이루어지기 시작하고 있다. 이러한 배경 하에서 영국의 경제 저널 [이코노미스트]가 양식 산업을 'Blue Revolution'이라 일컬으며 양식 산업이 첨단 기술 산업과 같은 고부가가치 주력산업 가운데 하나로 부상할 것으로 예측하고 있는 것에 주목할 필요가 있다.

본 강연에서는 해조류 기반 연구 지식의 가치화에 대한 예시와 향후 주요 해조류 바이오매스 생산기반으로서의 양식기술개발의 방향 제시를 통해 4차 산업혁명시대 해조류 관련 융합 연구가 가져올 다양한 혜택(생산적이고 성공적인 협동연구, 양질의 고용창출, 사회경제적 발전)에 대해 고찰하고 차세대 학자 및 후학들에게 시대를 선점하는 연구 동기 부여와 사회경제 발전에 대한 책임감을 고취하고자 한다.

[PL-02]

Ambivalence of Algae: *Microcystis aeruginosa* vs. *Ettlia* sp.

Hee-Mock Oh

Cell Factory Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 34141, Republic of Korea

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

On the other hand, microalgal biomass can be used as feedstock for several types of renewable fuels such as biodiesel, methane, hydrogen and ethanol. *Ettlia* sp. YC001, isolated from freshwater in Daejeon, is considered as a promising candidate for biofuel production. It can accumulate relatively high levels of neutral lipid and carotenoids under high CO_2 condition. To optimize the photoautotrophic culture conditions, combination of pH (regulated by CO_2 supply), dilution rate, and light intensity was systematically investigated for *Ettlia* sp. cultivation in a chemostat. The highest biomass and lipid productivities were 1.48 g L^{-1} d^{-1} and 291.4 mg L^{-1} d^{-1}, respectively, with a pH of 6.5, dilution rate of 0.78 d^{-1}, and light intensity of 1,500 μmol photons m^{-2} s^{-1}. With a sufficient supply of CO_2 and nutrients, the light intensity was the main determinant of the photosynthetic rate. Several ecophysiological and biochemical features of *Ettlia* sp. will be discussed

Consequently, CyanoHABs in lakes and reservoirs is mainly caused by inflow of wastewater containing high N and P, on the other hand, microalgal cultivation for biomass production needs N and P as major nutrients. Therefore, key nutrients in wastewater can be used for microalgae cultivation which can reduce the concentration of N and P in effluent resulting in reduction of CyanoHABs in lakes and reservoirs. Additionally, the cultured microalgal biomass can be used as a feedstock for microalgal biorefinery to produce fuels, foods, feed, cosmetics, pharmaceuticals, pigments, etc. The fundamental mechanism behind the dense and massive growth of CyanoHABs in nature can be applied reversely in order to stimulate the rapid growth of beneficial microalgal species in photobioreactor and raceway pond artificially. In other words, we can agree to a well-known proverb of “Extremes meet: Opposite extremes have much in common” in this case.

특별세션

[SS-01]

한국의 바다숲 복원 및 관리방향

김정하

성균관대학교 생명과학과

우리나라에서 바다숲의 중요성이 크게 부각되기 시작한 것은 이제 20년이 좀 넘는다. 1992년 제주해역의 갯녹음이 이슈화되면서 바다의 사막화가 심각한 해양환경문제로 대두되고, 국가사업으로서 바다숲 복원사업이 진행되면서 국립수산과학원에서 분리된 한국수산자원관리공단이 이 분야 사업을 주관하며 진행해오고 있다. 많은 노력과 성과 그리고 시행착오 또한 겪으면서 점점 심해져가는 바다사막화를 막고 훼손된 생태계를 본래의 숲으로 복원하려는 다양한 노력과 사업이 시도되고 있다. 이 발표에서는 현재까지 시도된 복원노력의 문제점을 진단하고, 보다 성공률을 높일 수 있는 생태학적 방안을 우리나라 해역별 특성에 맞게 제안해보고자 한다. 복원은 생태학 분야에서 가장 어려운 연구주제이다. 생물종간의 복잡한 상호작용과 여러 환경인자들의 복합적인 영향으로 불모지에 몇 십 개체의 옮겨놓은 모자반/감태로 자연은 쉽게 회복되지 않는다. 그러나 최근 동해안의 파일럿 연구에서 그 성공 가능성이 보였으며, 현재 재확인을 위한 반복연구가 진행 중이다. 바다숲의 복원은 끝이 아니며, 그 이후의 관리도 동등하게 중요하다. 자연 해조군락의 보존과 같은 맥락으로 해역별 특성을 고려한 과학적이고 세분화된 관리방안을 마련하여 해수부-수산자원관리공단-지자체-민간으로 구성되는 네트웍이 체계적으로 작동되어야 한다. 또한 바다숲 사업의 주관기관과 관련 학술분야의 전문가들과 지속적으로 생각, 지식, 경험을 공유하는 기회는 매우 중요하며, 본 특별세션이 향후 국제적인 전문가 네트웍 수준으로 발전되기를 희망한다.

[SS-02]

Manipulation of sea urchin density and application of metapopulation concept for recovery and maintenance of kelp forest in barren grounds

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Two different approaches have been conducting in two coastal areas, the east coast and Jeju coast in Korea, to recover kelp beds from existing urchin barrens. Korean east coast has been suffering marine deforestation last decades, comprising about 60% of all rocky shallow subtidal area, with the average density of urchins 7.8 individuals/m2 in the completely barren sites. Experimental manipulation of sea urchin density was conducted on the nine natural bed rocks of barren condition, each separated by sandy barriers in between. Three experimental conditions were applied: all urchin removal, "half"-removal, control for no-removal. At all removal sites, macroalgal community was recovered in good shape for three consecutive spring seasons (2015-2017), whereas barren state continued at the no-removal control sites. For the "half"-removal condition, we started with 4.0 individuals/m2, and then switched to 2.5 individuals/m2 to achieve an optimal density level, which may be necessary for the maintenance of kelp forest. In the case of Jeju coast, where sea urchin is not common, barren condition is presumably caused by multiple stress factors. We applied the metapopulation concept to artificial reefs (with different substrate types) to improve the chance of natural recruitment of seaweeds as the function of distance from nearby existing source kelp beds. On-going results will be shown in the presentation. The present studies provide a valuable guideline in controlling urchin density for community shift from barrens to forest and its maintenance

[SS-03]

Growth and Maturation of *Sargassum macrocarpum* in Cheongsan-Do Island in Southwestern coast of Korea

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Sargassum macrocarpum C. Agardh (Fucales, Phaeophyta) is a perennial brown alga and is highly differentiated into the hold fast, stem, main branches, vesicles, receptacles and so on. This species forms dense populations called *Sargassum* beds, which play a major role in the primary production in coastal ecosystems, and are important as nursery grounds for coastal fishes and other animals. The present study focused on the biological characteristics of *S. macrocarpum* with reference to its production ecology. Special attention was paid to the relationship between growth and maturation of the S. macrocarpum population on the flat rock area in Cheongsan-Do Island in southwestern coast of Korea, at the depth of 4 m, from October 2016 to September 2017. New main branches on perennial stem had been apparently observed in September, and grew increasingly through October to June in the next year, then reached the maximum length and biomass of the plants in June. Plants with two or more growth rings in holdfast matured and formed receptacles through May to June. The release of oospores and embryos was observed only in June. The minimum and maximum growth of plants was recorded in September (28.9±6.3 cm) and June (91.3±16.4), respectively. The maximum and minimum biomass were 21.70 kg wet wt.m^{-2} in June 2017 and 2.76 kg wet wt. m^{-2} in September 2017, respectively. This study provides fundamental methods and data on which to base marine afforestation, which is important for the enhancement of nursery grounds and for the preservation of environmental conditions in coastal ecosystems.

[SS-04]

A Study on the Selection of Suitable Sites for Sea-forest Enhancement

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This study was carried out to select the most suitable site for sea-forest enhancement with a habitat evaluation procedure at Yeondae-island, Korea. To calculate “quality” and “quantity” of suitable sites, the concept of HSI (Habitat Suitability Index) and GSDM (Gridded Spatial Distribution Map) were introduced to this study. HSI was calculated by geometric mean on 9 environmental factors (salinity, water temperature, light intensity, and so on), and GSDM was mapped by the method of Kriging interpolation. As the result analyzed by HSI and GSDM, area of 15.3ha was selected for the most suitable site for sea-forest enhancement(target species was *Sargassum*), and HSI showed a range of 0.90 to 1.0 (the maximum value is 1.0) in this site. The environmental factors that most affected selection of a suitable site were light intensity and current magnitude. Also, this method was verified by field data on native *Sargassum* patches distributed in study area, and an estimated location of suitable sites was an agreement with native *Sargassum* patches. Therefore, these results showed that this method was useful to determine “quality” and “quantity” of the most suitable sites for seaweed bed enhancement.

[SS-05]

동해안 특화자원인 도루묵 산란장(어소와 종묘부착판)의 조성효과

Effects of the artificial spawning area with seaweed plate and reef on local sailfin sandfish species *Arctoscopus japonicas* in the East Coast of Korea

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Sailfin sandfish *Arctoscopus japonicas*, is one of the local specialized species in East coast of Korea. They usually inhabit sandy and muddy sea floors in waters between 100 and 400 meters. To spawn, they migrate in shallow rocky beds of seaweeds during winter season. Recently, their spawning areas like seaweeds are largely decreasing due to marine pollutions and whitening events. Eggs drifting towards seashore during spawning season, in which affect the decline for rate of spawning and hatching. Therefore, this study is to increase the artificial spawning area of *A. japonicas* by seaweed plates and reefs fixed with brown algae *Sargassum* sp. Forty reefs and 1,500 seaweed plates were installed in Kuoam-ri, Goseong-gun, Junjin-ri, Namae 1-ri, Namae 2-ri and Yangyang-gun, Gangwon-do, Korea in October 2016. After 2 months, one hundred roe were approximately attached on a seaweed plate as well as 1,400 roe in a reef. A roe included in 1,200 eggs. Each site has 250 millions of eggs. The hatching and survival rate were estimated 10 % and 3 % respectively. These generations were expected to 750 thousands. The installation of seaweed plates and reefs may naturally enhance the productivity of *A. japonicas*. Based on this result, it is expected to provide a stable spawning and habitant of fishes as well as increase of other useful fisheries resources and restoration of marine ecosystem.

[SS-06]

2016년 바다숲의 생태적·경제적 가치평가

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본 연구는 FAO, UNEP 등 글로벌 기준 가치평가 매뉴얼에 기초하여 우리 사회에 제공하는 바다숲의 생태계 서비스 편익을 경제적으로 가치를 평가하고자 하였다.

본 연구의 주요 결과는 다음과 같이 종합할 수 있다. 첫째, 우리나라 바다숲이 우리 사회에 제공하는 유·무형 서비스 편익은 헥타르당 연간 771,121,551원의 가치를 지닌다고 할 수 있다. 둘째, 바다숲이 제공하는 서비스 편익별로 가치를 평가하면, 자원·공급서비스 편익 가치로서 수산물 잠재 생산량의 연간 가치는 헥타르당 58,512,271원에 달하며, 환경·조절 서비스 편익 가치로서 기후초절서비스 546,488원, 오염물질정화서비스 85,342원, 침식방지서비스 28,942,170원의 가치를 지니고 있어 환경·조절 서비스의 총 연간가치는 헥타르당 29,574,000원임을 보여주고 있다. 생태계유지 서비스로서 영양순환서비스는 헥타르당 연간 29,917,633원의 가치를 지니며, 문화·관광 서비스로서 스킨스쿠버와 바다낚시 서비스는 각각 5,011,765원과 10,305,882원으로 평가되어 문화·관광 서비스는 헥타르당 연간 15,317,647원의 가치를 지니고 있음을 보여주고 있다. 더욱이 바다숲의 비사용 가치 즉 보존가치는 헥타르당 연간 637,800,000원임을 보여주고 있다. 셋째, 바다숲의 가치가 단위면적에 비례하여 증가한다고 가정하면, 바다숲은 2016년까지 조성면적 12,208.2ha와 천연해조장 면적 4,272.6ha에 기초하여 연간 12조 7천억 원의 가치를 지니는 것으로 평가할 수 있다. 넷째, 향후 우리나라 바다숲의 가치가 미래에도 지속가능하다면, 한국개발연구원의 사회적 할인율 연 5.5%를 적용하여 바다숲의 총 경제가치는 2016년 기준 244조원으로 평가할 수 있다.

이와 같이 본 연구의 결과는 바다숲 생태계 서비스 편익의 가치를 화폐단위로 환산하여 제공함으로써 바다숲의 가치에 대한 인식을 증진시키고 바다숲 조성 정책의 타당성을 확보하는데 중요한 자료로 활용될 것으로 기대한다.

본 연구의 결과에 기초하여 정책적 제안은 다음과 같다. 첫째, 적극적인 홍보 전략 구축이 필요하다. 바다숲의 가치평가는 바다숲 조성 정책의 타당성을 확보하는 동시에 바다숲이 우리 사회에 제공하는 서비스 편익을 화폐단위로 환산함으로써 바다숲의 중요성과 가치 인식 증진을 위한 일환으로 이루어진다. 따라서 본 연구의 결과를 기초로 해서 적극적인 홍보 전략을 구축하는 것이 궁극적으로 한국수산자원관리공단의 설립 타당성과 당위성을 확보하는데 크게 기여할 것으로 보인다. 산림청은 국립산림과학원의 「2014년 산림의 공익적 가치」연구 결과인 산림의 연간가치 126조원에 기초하여 산림의 연간 평가액 126조원이 국내총생산액(GDP)의 8.5%, 농림어업총생산의 4배, 임업총생산의 65배, 산림청 예산(1.9조원)의 67배에 해당되며, 국민 1인당 249만원의 편익을 제공하고 있음을 적극적으로 홍보하고 있다. 둘째 권역별 바다숲 생태계

서비스 편익의 발굴 및 정기적인 가치평가가 필요하다. 우리나라 제주, 남해, 서해, 동해 연안바다는 쿠로시오 해류, 쓰시마 난류, 동한난류, 황해 난류, 쿠릴해류, 리만 해류, 북한 한류 등 난·한류 등의 영향을 받아 해조상이 다양하게 나타나고 있다. 이에 따른 바다숲의 생태적 특성으로 바다숲 생태계 서비스 편익 효과가 달리 나타난다. 따라서 제주, 남해, 서해, 동해 권역별 바다숲의 면적, 생태계의 특성 등을 고려하여 바다숲 생태계 서비스 편익을 발굴하고 이를 토대로 바다숲의 가치를 평가해야 한다. 한편 바다숲의 가치 인식을 증진하기 위해 권역별 바다숲 모니터링 및 효과조사와 함께 정기적인 가치평가를 실시할 필요가 있다. 예를 들면 산림청에서는 산림의 가치 인식을 증진하기 위하여 정기적으로 산림의 공익적 기능을 발굴하고 이에 기초하여 산림의 공익적 가치를 평가하고 있다. 셋째, 바다녹화사업의 지속적인 확대와 더불어 등급별 관리방안을 모색할 필요가 있다. 중앙정부는 미래의 건강한 연안생태 환경 조성과 어업생산성 향상을 위하여 바다녹화사업의 지속적으로 확대될 수 있도록 노력하여야 하며, 이러한 바다숲 조성 확대 전략과 더불어 바다녹화사업의 효과를 최대화할 수 있도록 사라지고 있는 천연해조장과 인공 바다숲을 등급화하여 등급별 관리방안을 모색할 필요가 있다. 예컨대, 바다녹화사업이 1978년부터 현재에 이르기까지 40여년 장기적이며 지속적으로 이루어지고 있는 미국의 체스피크만(Chesapeake Bay) 바다숲 복원 프로그램을 벤치마킹할 필요가 있다. 체스피크만 프로그램은 생태계 건강지표(ecosystem health indicator)를 A, B, C, D 등의 형태로 구분하고 현재 C등급에 맞추어 메릴랜드 주정부, 버지니아 주정부, 연방정부, 민간단체 등으로부터 예산을 지원받아 복원프로그램을 수행하고 있다. 넷째 향후 국가주도에서 벗어나 시민 참여형 바다숲 조성정책의 수립이 필요하다. 우리나라는 2002년부터 연안어업에 대해 국가 주도의 관리체계에서 벗어나 어업인 스스로 자율적인 어업관리체제를 지향하도록 개발된 자율관리어업을 도입하여 시행하고 있다. 그러나 자율관리주체인 자율관리공동체가 정부의 지원에 지나치게 의존하여 어장환경 개선과 어획량 및 어획노력량 등 자원관리활동에 소홀하다는 지적이 계속 제기되고 있다. 이와 같이 국가 주도와 생산자에 의한 자원관리로는 한계가 있으므로 최근에 자원관리의 대안으로 모색되고 있는 시민 또는 소비자 참여형 자원관리방안을 적극 도입하여 NGO, 환경단체, 소비자 단체 등이 참여하는 자원관리 및 조성정책이 필요하다. 일본의 경우 국가 주도의 바다숲 조성정책에서 벗어나 NGO, 환경단체 등이 참여하여 바다숲 조성정책을 결정하는 시스템으로 변화하려하고 있다. 끝으로, 바다숲의 사회경제적 효과조사 및 가치평가 매뉴얼의 개발이 필요하다. 바다숲 조성사업은 바다숲의 조성효과와 그 효과의 가치평가를 통하여 그 가치와 중요성을 확인하는 공익사업이다. 따라서 권역별 해역특성을 반영한 바다숲의 조성 효과 조사 지표를 생태지표와 사회경제적 지표를 구분하여 개발하고 이를 토대로 가치를 평가할 수 있는 평가 매뉴얼을 구축할 필요가 있다. 바다숲의 조성효과는 생물·생태적 효과와 사회경제적 효과로 구분할 수 있다. 현행 바다숲의 효과조사는 생물다양성, 생체량 등 생물·생태적 지표만을 고려하여 조사하고 있다. 향후에는 바다숲 조성사업에 따른 사회경제적 효과를 측정할 수 있는 사회경제적 지표도 효과조사에 포함하여야 한다. 일반적으로 사회경제적 지표는 바다숲에 대한 어업인, 지역주민, 일반시민의 인식도, 바다숲 조성해역의 가구 수, 상점 수, 낚시점 수, 스킨스쿠버 숍 수, 해양어촌관광객의 수 및 지출비용 등을 들 수 있다.

신진연구자발표

[AO-01]

What is the real species tree?

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The phylogenetic method based on several useful molecular markers has been used to discover inter-species relationships (i.e., species tree) for long times. Nowadays, the next-generation genome sequencing (NGS) technology led to construct massive genome databases (e.g., nuclear, plastid and mitochondrial genomes) from many eukaryotic organisms. For this reason, the species tree could be represented by the huge concatenated gene matrixes constructed from dozens to hundreds of genes. In many cases, however, each concatenated gene phylogeny from nuclear, plastid and mitochondrial genomes showed their own genetic histories with some conflicting inter-species relationships due to independent mutation, incomplete lineage sorting and species-level gene flow. Therefore, it is hard to define the standard marker loci for the species tree. To discover the real species relationship, we suggest the complex tree topology that each consensus tree topologies from nuclear, plastid and mitochondrial genomes were combined with their individual gene histories. To test this approach, we generated partial nuclear and complete organelle genome data from six coralline red algal species (*Lithothamnion* sp., *Neogoniolithon* sp., *Renouxia* sp., *Rhodogorgon* sp., *Sporolithon durum* and *Synarthrophyton chejuensis*). All available eukaryotic core genes (i.e., BUSCO), plastid and mitochondrial genes from our data with a published draft genome of *Calliarthron tuberculosum* were used for this analysis. We also discuss evolutionary history of coralline algae and the species concept.

[AO-02]

The study of endophytic green algae (Ulvophyceae) from Korea.

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Micro-filamentous green algae grow on a variety of solid substrata. Also they occur as epiphytes or endophytes of larger algae and seagrasses. Approximately more than 100 species of microfilametous ulvophycean taxa are reported in AlgaeBase, but the true number may be 200 species or more. Because they are difficult to find and identify due to similarities in their appearance and lack of information. The primary aims of this study were to identify these green endophytes and to characterize the abundance of the infections in Korea. In order to investigate the diversity of microfilamentous endophytic green algae in Korea, 16 species host strains (four green algae, one brown alga, ten red algae and one empty bivalve shell) were collected from 15 sites from Korea during August 2013 to February 2017. To provide information on the microfilamentous endophytic green algae from Korea, we analyzed the *tuf*A gene sequence and morphological characteristics of the endophytic algae isolated from the host. This study describes thirteen species, including six new candidate species of Korean marine algal flora. Among them, 12 species belong to Ulvophyceae: six *Ulvella* species (*Ulvella leptochaete, U. ramosa, U. viridis, Ulvella rotundata* sp. nov., *Ulvella jejuensis* sp. nov., *Ulvella complanata* sp. nov.), two Bolbocoleonaceae species (*Bolbocoleon piliferum, Bolbocoleon minus* sp. nov.) one Phaeophilaceae species (*Phaeophila dendroides*) and three species (*Dilabifilum arthropyreniae, Macula globosa* gen et sp. nov., *Phlegma teres* gen. et sp. nov) which are not yet located at the family level and belong to Ulvophyceae *Blastophysa rhizopus*, which has an unclear taxonomic position below the order level. Morphological and molecular phylogenetic analyzes of the endophytic algae were carried out to confirm the species diversity of Ulvophyceae.

[AO-03]

상주 공검지 퇴적층의 연대별 돌말류 분석을 통한 고대 환경 변화 연구

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담수습지는 해양과 비교하여 닫혀있는 환경으로, 물의 흐름, 강우, 바람 등 환경요인의 직접적인 영향을 받아 퇴적물이 쌓이게 되므로, 과거 환경 변화를 파악하는데 중요한 연구재료로 알려져 왔다. 특히, 돌말류는 단단한 규산질의 세포벽을 가지며, 다른 생물에 비해 퇴적층 속에 쉽게 화석으로 남을 수 있어, 전세계적으로 과거서식 환경을 대변할 수 있는 가장 대표적인 생물이다. 국립낙동강생물자원관에서는 2016년부터 국내 담수습지를 시추하여, 돌말류의 분석과 지질 분석을 통해 습지의 생성 역사를 밝히고, 고환경 복원을 위한 연구를 수행중에 있다. 2016년 연구 결과로, 조선시대 3대 저수지 중 하나로 알려진 상주 공검지 인근 4개 지점에서 시추(1지점: 7.6m, 2, 3지점: 7.0m, 4지점: 6.0m)를 수행하였고, 깊이별 돌말류 분석 및 연대, 입도 등의 지질 분석을 실시하였다. 돌말류는 대부분의 시추공에서 200cm～300cm 구간에서 집중적으로 출현하였으며, 1문 3강 14목 20과 36속 103종이 동정되었다. 이 중 6종은 국내에서 처음 보고되는 미기록종이었다. 또한, 지점별 우점종 변화 양상, 깊이별 지점별 출현 종수, 개체수, 종 다양성 등을 분석하였다. 이들 결과와 연대 결과를 비교 분석하여, 공검지 주변 고지형도의 변화를 유추하였으며, 실제 공검지는 현재 알려진 공검지 보다 상당히 큰 규모였음을 유추할 수 있었다. 2018년에는 공검지 내부 지점에 대한 시추를 수행하여, 연구를 수행 할 예정이며, 이를 통해, 정확한 공검지의 생성역사 파악이 있을 것이다

일반구두발표 Ⅰ, Ⅱ

[OO-01]

Pathogen-specific gene regulation in the red alga *Pyropia tenera* against the three most common diseases in sea farms

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Outbreaks of diseases devastate *Pyropia* aquaculture farms every year causing US$ multimillion dollar loss every year. The three most common diseases are *Olpidiopsis* blight and red-rot disease caused by oomycete pathogens and green-spot disease caused by PyroV1 virus. We hypothesized that a basic genetic profile of molecular defenses will be revealed by comparing and analyzing genetic response of *Pyropia tenera* against above three pathogens. RNAs isolated from infected thalli were hybridized onto an oligochip containing 15,115 primers designed from *P. tenera* ESTs. Microarray profiles of the three diseases were compared and interpreted together with histochemical observation. Massive amounts of reactive oxygen species (ROS) were accumulated in *P. tenera* cells exposed to oomycete pathogens. Heat shock genes and serine proteases were the most highly upregulated genes in all infection experiments. Genes involved in RNA metabolism, ribosomal proteins and antioxidant metabolism were also highly upregulated. Genetic profiles of *P. tenera* in response to pathogens were most similar between the two biotrophic pathogens, *Olpidiopsis pyropiae* and PyroV1 virus. A group of plant R-gene homologues were specifically regulated against each pathogen. Our results suggested that disease resistance of *P. tenera* consist of a constitutive defense using ROS signals and a genetic toolkit against specific pathogen.

[OO-02]

Revealing the distinct habitat ranges and hybrid zone of genetic sub-populations within *Pseudo-nitzschia pungens* (Bacillariophyceae) in the West Pacific area

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Genetic sub-populations (clades) of cosmopolitan marine diatom *Pseudo-nitzschia pungens* might have distinct habitats, and their hybrid zone is suspected in higher latitude area of the West Pacific area, however, it is still unrevealed because of technical difficulties and lack of evidences in natural environments. The aim of this study is to investigate the habitat characteristics of each clade of *P. pungens* on geographical distribution with the habitat temperature ranges of each clade and to reveal their hybrid zone in the West Pacific area. We employed the 137 number of genetic information of *P. pungens* and its sampling data (spatial and temporal scale) originated from the West Pacific area, and used field application of qPCR assay for intra-specific level of *P. pungens*. Only two genotypes, clade I and III, were considered in the West Pacific area. Clade I was distributed from 39 to 32.3 °N, and clade III were from 1.4 to 34.4 °N. The estimated habitat temperature for the clade I and clade III ranges were 8.1 - 26.9 ℃ and 24.2 - 31.2 ℃, respectively. The latitudal distributions and temperature ranges of each clade were significantly different. The qPCR assay employed, and results suggested that the hybrid zone for clade I and III has being created in the southern Korean coasts, and clade III population might be migrated from southern Pacific area. The cell abundances of clade III were strongly related with the higher seawater temperature and warm current force. Current study defined distinct habitat characteristics of genetically different sub-populations of marine phytoplankton, and revealed its hybrid zone in natural environment for the first time. Also, we provided strong evidences about dispersion of clade III population up to higher latitude in the West Pacific area.

[OO-03]

Improved Pigment Content of Microalgae by Use of CRISPR-CAS9 Technology

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There have been numerous commercial applications of microalgae in areas such as nutrition, pharmaceuticals, and biofuels. Overproduction of specific high-value biochemical in microalgae requires the modification of metabolic pathways. However, metabolic engineering in microalgae has been limited because specific transformation tools need to be developed for each microalgal species. Recently, we employed DNA-free RNA-guided engineered nucleases (RGENs) derived from the type II CRISPR-Cas9 system to the microalga *Chlamydomonas reinhardtii*. We first generated a specific knockout of the zeaxanthin (Zea) epoxidase gene to accumulate this xanthophyll in microalgae. Zea content was significantly increased (more than 10 times) in Δ*ZEP* mutants compared to the wild type, even under low-light growth conditions. To enhance productivity and to accumulate Zea in mass culture under bright sunlight conditions, we next generated double knockout mutants by transforming one of the Δ*ZEP* mutants with RGEN-RNPs targeting *CpFTSY*. We compared the photosynthetic productivity of the Δ*ZEP*/Δ*CpFTSY* mutant with that of the Δ*ZEP* single mutant. Quantum yields of photosynthesis of Δ*ZEP*/Δ*CpFTSY*, Δ*ZEP* and wild type were essentially the same, indicating that this parameter was not affected by the single or double mutation. Growth of the Δ*ZEP*/Δ*CpFTSY* mutant under high-light conditions was dramatically greater than that of the wild type and the Δ*ZEP* mutant. This simple RGEN RNPs method could be applied to other microalgae without the need for a laborious cloning step. Moreover, the resulting transformants would be exempt from GMO regulation, thus our results will facilitate applications of microalgae in the production of pharmaceuticals, nutraceuticals, food and animal feed, which will make the use of microalgae more attractive and lucrative.

[OO-04]

Learn from the Assembling Red Algal Tree of Life (RedToL)

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Red algae (Rhodophyta) include more than 7,000 species thrive in marine and freshwater habitats. Red algae play a critical role in the eukaryote tree of life as the donor through secondary endosymbiosis of the plastid that subsequently gave rise to chlorophyll-*c* containing groups such as diatoms, dinoflagellates, haptophytes, and cryptophytes. In order to increase our understanding of diversity and evolution of red algae, to make a linkage to the Assembling the Tree of Life we conducted taxon-rich multi-gene phylogeny of red algae. We assembled ten genes (plastid *rbc*L, *psa*A, *psa*B, *psb*A, and UPA, mitochondrial *cox*1 and cob, nuclear EF2, SSU and LSU rDNA) from 42 orders 570 taxa. Our best phylogeny based on individual and combined dataset provides highly resolved relationships in most taxonomic ranks. Based on the phylogeny we suggest new red algal taxonomic system.

[OO-05]

Integrated Multi-Trophic Aquaculture for Korea Waters

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Integrated multi-trophic aquaculture (IMTA) combines the fed aquaculture (e.g., fish or shrimp) with the extractive aquaculture (seaweed and shellfish) to create a more balanced ecosystem. In Korea, most open water fin- and shell-fish aquaculture practices occur in the southeast coastal areas of the country while the seaweed aquaculture mostly occurs in the southwest of the country. This disagreement of cultivation locations between organisms has caused environmental problems, such as harmful algal blooms near finfish farms and nutrient depletion at seaweed farms. A pilot scale IMTA system was introduced to Tongyoung, Gyeongnam, Korea. Sea cucumbers (*Apostichopus japonicus*), oysters (*Crassostrea gigas*) and seaweed (*Gracilariopsis lemaneiformis*) were cultivated with fifty thousand young *Pagrus major* (average weight of 2.2 g) in this IMTA system (1 hectare). Growth, biomass yields and tissue nitrogen contents of each organism were analyzed to evaluate nitrogen (N) discharge from the fish aquaculture and N extraction by the extractive aquaculture (sea cucumbers, oysters and seaweed) during the summer–fall growing season in 2016. Based on the findings in this study, a model IMTA system was developed for environmentally sustainable aquaculture in Korea.

[OO-06]

Development of methods for evaluation of natural seaweed beds in Korea

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The natural seaweed beds provides a nursery, spawning bed, shelter and feeding ground for useful fisheries organisms, human welfare and the marine environment. Consequently, evaluation of seaweed beds has become an important requirement globally. To estimate the environmental value of seaweed beds and to develop the evaluation of valuable natural seaweed beds, studies were carried out on the coast of Korea from June to November 2015. In this manuscript we not only develop such an evaluation method but also provide guidance to select appropriate indicators for relevant natural seaweed beds. We thus indicate how the evaluation method can be used in natural seaweed beds.

학생구두발표 Ⅰ, Ⅱ

[SO-01]

Genome sequencing and population genomic analyses provide insights into the adaptation to new environments of *Undaria pinnatifida*

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Undaria pinnatifida is one of the most popular multicellular kelp species that plays an important ecological role in its natural habitat in Eastern Asia. It is extensively cultivated in Korea (~500.000 tons/year) as food source and for its extracts. *Undaria pinnatifida* is also well known for being an invasive species. Indeed it was introduced to Europe in the 1970s associated with oysters introduced for fisheries purposes, initially to the Mediterranean coast and later to Brittany. In the late 1980s the species was also recorded in New Zealand. Introduced populations of *Undaria pinnatifida* are considered to cause considerable impacts to coastal ecosystems by forming dense canopies, displacing native species, and thus reducing biodiversity. It also causes economic impacts to fishing and aquaculture. To investigate the whole-genome adaptation of *Undaria pinnatifida* during invasions we produced the draft genome of *Undaria pinnatifida* from Korea and we re-sequenced the genomes of 22 individuals from various invasive populations around the world. We explored genome-wide variations between the different populations considered, and notably we identified putative selective sweeps at multiple loci. This study will provide new insights into the mechanisms by which genomes can rapidly adapt during an invasion. Furthermore, the genome sequence and its polymorphism represent a major resource for future crop improvement and biotechnology.

[SO-02]

Oxidative burst mediated by respiratory burst oxidase homologue in *Pyropia tenera* with pathogen attacks

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Disease management is the most serious concern for rapidly growing seaweed aquaculture industry. Oomycete and viral disease causes serious economic loss in *Pyropia* sea farms every year. Oxidative burst plays a pivotal role in defense to pathogenic infections in red algae *Pyropia* species. Histochemical staining and microarray profiles on disease infected *Pyropia tenera* showed that retrograde signaling from cell organelles is involved in the defense mechanism for infection. DAB staining on pathogen infected *P. tenera* blades showed an accumulation of hydrogen peroxide. Microarray gene profiles showed that respiratory burst oxidase homologue (RBOH) were specifically upregulated in the infected blades of *P. tenera.* As these enzymes are involved in disease resistance, we examined the role of RBOH on defense responses in *P. tenera* using Diphenyleneiodonium (DPI). DPI-pretreated *P. tenera* showed enhanced infection compared to the control, suggesting that RBOH protein was involved in defense responses to pathogens. These results suggest that *P. tenera* may have signal transduction pathway regulated by RBOH protein in response to pathogens and uses oxidative burst to inhibit the spread of oomycete diseases.

[SO-03]

The organelle inheritance and genome rearrangement in the brown algae with different types of fertilization.

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The brown algae (Phaeophyceae) are a photosynthetic Stramenopiles that all share a red algal-derived plastid via a secondary endosymbiotic event. In the different lineages of the brown algae, gametes exhibit several types of fertilization during sexual reproduction. It is distinguishable as isogamous, anisogamous or oogamous through the morphology of their gametes from female and male gametophytes. Anisogamous and oogamous species exhibit maternal inheritance of the plastid whereas isogamous species exhibit biparental inheritance of the plastid. A majority of the brown algae exhibit anisogamous or oogamous gametes and therefore their plastid is inherited from the maternal gamete. The order Ectocarpales represents an interesting exception, having isogamous gametes and therefore plastid transmitted birparentaly to the next generation. To investigate the effect of biparental inheritance on the plastid genome features, we newly characterized the complete plastid genomes of three species from the order Ectocarpales: *Scytosiphon lomentaria*, *Petalonia binghamiae*, and *Cladosiphon okamuranus*. Comparison between the plastid genomes of oogamous and anisogamous brown algae revealed that plastid genomes within the Ectocarpales had higher structural variation and rearrangements. We will discuss about the evolutionary history of plastid genomes within the Ectocarpales and how organelle inheritance impacts the structural variations of organelle genomes in the brown algae.

[SO-04]

Phylogeography of intertidal red algae, *Gloiopeltis*, (Gigartinales) reveals species complex in the North-Pacific

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The red algae, *Gloiopeltis* commonly distributed in rocky intertidal habitat along the North-Pacific, is good model to investigate the phylogeographic studies. To examine the genetic diversity within *Gloiopeltis* species in current distribution, we analyzed a total of 262 specimens collected from Korea, China, Japan, Russia, and Canada using two molecular markers of mitochondrial COI-5P and plastid *rbc*L. The phylogenetic trees and haplotype networks of both markers revealed at least nine highly divergent lineages in *G. furcata*, all of which were reciprocally monophyletic and clearly separated from congeners. Most lineages were diverged in Korea, except one lineage of which is extended from the northwest to northeast Pacific. In addition, we detected a novel species from Korea, *G. frutex* sp. nov, which was overlooked under phenotypic similarity to *G. complanata*. This result indicated that the genetic and species diversity of *Gloiopeltis* were substantially underestimated because high level of genetic divergence is not appeared at the morphological level. We assume that the environmental stress in the intertidal habitat may reduce gene flow generating speciation in the local region.

[SO-05]

Ultra-morphology and phylogeny of the genus *Phymatolithon* (Hapalidiales, Rhodophyta) with assessment of the features about a novel genus

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In the Hapalidiaceae, the genus Phymatolithon was established by Foslie (1898) for a single previously described species, P. polymorphum (L.) Foslie. The basionym of P. polymorphum, Millepora polymorpha L. is a superfluous substitute name for Millepora calcarea Pallas, and consequently the correct name of the type species of Phymatolithon is P. calcareum (Pallas) Adey & McKibbin. Since 1898, at least 47 specific and infraspecific taxa have been referred to the genus, and it has undergone several changes in circumscription. Currently, 15 species of Phymatolithon are recognized mostly based on morphological analyses. However, the genus Phymatolithon has been known as polyphyletic group during long time. A multigene phylogeny of the genus Phymatolithon, using COI-5P, psbA, and rbcL, was constructed to assess generic boundary. Based on our study about numerous collections and some type materials, we have concluded that some Phymatolithon species represent a distinct new genus. Here we also present detailed illustrated accounts of each of the species.

[SO-06]

Somatic cell fusion in a red alga *Griffithsia monilis* is mediated by two different signaling molecules

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When a cell in the red algal filament is wounded, a cascade of cellular event takes place in the adjacent cells. The dead cell is replaced through the somatic cell fusion between repair-shoot cell and repair-rhizoid cell produced from adjacent cells. During this repair process repair cells show attracted growth towards each other. Rhodomorphin released from repair-rhizoid cell has been reported to be responsible for this attracted growth between repair cells. However, our time-lapse videography showed that this attracted growth needs additional signaling molecule in addition to rhodomorphin, suggesting two different signaling molecules are involved in this process. The genes specifically expressed during the somatic cell fusion were isolated from the transcriptomes of *Griffithsia monilis* and their expression profile was studied using qPCR. Predicted gene model of wound-healing process of *Griffithsia monilis* will be discussed.

[SO-07]

Plastid genome evolution of genus *Porphyridium*

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The red algae (Rhodophyta) form a monophyletic lineage comprising around 7,100 species. The Rhodophyta consists of seven classes (Bangiophyceae, Compsopogonophyceae, Cyanidiophyceae, Florideophyceae, Porphyridiophyceae, Rhodellophyceae and Stylonematophyceae). Forty-eight available red algal plastid genomes have been reported mostly from two classes, Bangiophyceae (9 spp.) and Florideophyceae (27 spp.). The information on plastid genomes of early diverging red algal lineages, Porphyridiophyceae is clearly limited. Previous studies showed that plastid group II introns of four *Porphyridium purpureum* strains exhibit high genetic variation within a species. It suggests high genetic variation among plastid genomes of the Porphyridiophyceae.

Here, we completed seven plastid genomes from *Porphyridium aerugineum* (CCMP 1948) , *P. sordidum* (CCMP1380), *P. purpureum* (CCMP1328, SAG1380-1a, 1b, 1d) and *Porphyridium* sp. which is closely related to *P. purpureum*. Based on comparative genome analysis, here, we discuss a possible scenario of plastid genome evolution of the *Porphyridium* in this presentation.

[SO-08]

DNA barcoding for identification of hidden diversity in *Pyropia* (Bangiophyceae, Rhodophyta) from Korea

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A The red algal genus *Pyropia* commercially important algae is distributed from cold temperate to tropical waters. They are difficult to identify using solely morphological features because of lack of reliable diagnostic characteristics. DNA barcoding using mitochondrial COI-5P marker is now well established for red algae. We have been exploring the species diversity of the genus *Pyropia* from Korea based on the molecular analyses and morphological observations. We confirmed seven species including three unidentified ones: *Py. kuniedae*, *Py. seriata*, *Py. tenera*, *Py. yezoensis*, *Pyropia* sp.1, *Pyropia* sp.2, and *Pyropia* sp.3. In DNA barcode analysis, Korean *Pyropia* species were clearly distinguished with finding hidden diversity from unapproachable area to collect, such as Ulleung Island far from main land or deep underwater habitat over than 10m depth. This is the first time to apply DNA barcoding approach for the order Bangiales from Korea providing an efficient way to identify species level.

[SO-09]

Insights into the evolutionary history of the photosynthetic Stramenopiles using novel plastid genomes from four classes, Pinguiophyceae, Dictyochophyceae, Synchromophyceae, and Pelagophyceae (Stramenopiles)

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The photosynthetic Stramenopiles (heterokont algae) form a monophyletic group of algae that have been extensively studied since the 19th century. With more than 10,000 described species and an estimated one million species, it represents one of the largest and diverse eukaryote groups. Taxonomically, 17 classes are recognized within the Stramenopiles that were recently further grouped in three large clades: SI, SII, SIII clades. Those classes differ greatly in morphology and physiology. To this day, organelle genomic information is restricted to only six of the 17 classes of the Stramenopiles. This lack of information makes it difficult to understand the evolutionary history of the organelles in the Stramenopiles. Furthermore, phylogenetic relationships among these classes remain partially unresolved. In this study, we sequenced chloroplast genomes of seven micro-algal species belonging to four different classes of the Stramenopiles, *Pinguiococcus pyrenoidosus* and *Pinguiochrysis pyriformis* (Pinguiophyceae), *Rhizochromulina rina* and *ctyocha peculum* (Dictyochophyceae) *lamydomyxa montana* (Synchromophyceae), and *Sarcinochrysis marina and Chrysoreinhardia giraudii* (Pelagophyceae). Using this new data with publicly available organelle genome data, which cover most of the classes of the photosynthetic Stramenopiles, we discuss the evolution of organelle in the Stramenopiles as well as phylogenomic studies in an attempt to fully resolve the relationships among the classes in the photosynthetic Stramenopiles.

학생구두발표 Ⅲ, Ⅳ

[SO-10]

Effects of stocking density in productivity and nutrient removal of *Gracilaria vermiculophylla* in biofloc effluent

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application for nutrient bioextraction, this alga was cultured at different stocking density conditions (0.2, 2, 4, 8 g L^{-1} (FW)). *Gracilaria vermiculophylla* was cultivated in effluent from a juvenile *Paralichthys* biofloc tank culture system and von Stosch enriched (VSE) medium for 20 days. The total nitrogen and phosphorus concentrations in VSE was adjusted to those concentrations in biofloc (1000 µmol and 33 µmol, respectively). Other environmental conditions were maintained at 20 ℃, 12:12 L:D photoperiod and 140 µmol m^{-2} s^{-1} of light emitting diode (LED). The medium was changed every 5 days. The highest growth rate was observed at 0.2 g L^{-1} stocking density in both media (VSE: 17.39 %·d^{-1} and biofloc: 11.76 %·d^{-1}, respectively). As the stocking density increased, the growth rate decreased. However, the productivity was highest at the highest stocking density, 1.90 g·d^{-1} and 1.82 g·d^{-1} respectively. Tissue carbon contents were similar at all the conditions (33.7-34.9% in VSE and 33.1-34.0% in biofloc). Tissue nitrogen contents were also similar, ranged from 3.72% to 3.92% for VSE and 3.61% to 3.81 for biofloc. In VSE, nearly 70% of nitrate was removed at 8 g L^{-1} stocking density and over 90% of phosphorus at the stocking density of 2 g L^{-1} or higher in 5 days. In biofloc, nitrate was barely removed at all the stocking density conditions but approximately 32% of phosphorus was removed at the highest stocking density. Ammonium uptake of *Gracilaria* will also be presented. These results indicate that *Gracilaria vermiculophylla* may be a good species for nutrient bioextraction in biofloc effluent.

[SO-11]

The new reports on life cycle of *Heterosigma akashiwo* (Raphidophyceae)

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Heterosigma akashiwo (Hada) Hada (Raphidophyceae) is a noxious bloom-forming algal species that has damaged many fish farms in coastal waters during recent decades. Consequently, many studies focused on the population dynamics of *H. akashiwo*, while its life cycle was not well studied. In this study, we investigated veiled life cycle of *H. akashiwo* through culture based method. We cultured eight *H. akashiwo* strains originated from Korea, Japan, USA under various conditions (water temp., light intensity, salinity, pH). Morphological diversity of cells were observed via light microscopy and scanning electron microscopy. To observe nucleus of living cell, cells were stained with Hoechst and changes of cells in culture were observed through time-lapse. For observation of cysts and their germination process, cysts were isolated from sediment. As a results, it was revealed that *H. akashiwo* has extra small cell stage and large cell stage than known vegetative cell stage and cyst stage. Large cells are much bigger (20-45 μm) than vegetative cells. Large cell formation was resulted from fusion of vegetative cells. Small cells were very small (6.88 ± 0.85 μm), these cell divided from large cell or formed in germination process of cysts rarely. Small cells have lower motility than vegetative cells. These results improved the study of life stages of *H. akashiwo* and this fundamental investigation provide important new information and improve our understanding of the life cycle of *H. akashiwo*.

[SO-12]

Phenology of *Z. caespitosa* in Tongyeong, Southern Coast of Korea

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Seagrasses, marine flowering plant, are distributed on the whole world except Antarctica. There are about 60 seagrasses species in the world and among them 10 species are distributed in Korea. In this study, we investigated the variation of morphological features, density, biomass and characteristics of reproductive shoot on *Z. caespitosa*. This species was monthly monitored and collected during a year in Tongyeong (from Jan. 2016 to Dec. 2016). Morphological features, biomass and density significantly showed seasonal variation ($p<0.001$). Morphological features of above ground were recorded highest value in late spring to early summer and lowest value in winter. Average shoot density and biomass of *Z. caespitosa* were recorded each 1,223.4 shoots m^{-2} and 5,956.9 g w.w.m^{-2} and showed highest value in June. Reproductive shoot was occurred from April (13.3±1.1℃) to June (21±1.0℃). Pistils Erected outside sheath, anther dehiscing and small embryos were founded in April. Mature fruits and released seed were founded in June. The results suggest that this species showed high growth rate in late Spring and early Summer (15-20℃). Reproductive shoot of *Z. caespitosa* occurred at about 10-15℃ and mature fruits were observed at above 20℃. These results were similar to those of other studies on *Z. marina*. In conclusion, it is thought that the growth and maturity of *Z. caespitosa* are affected by temperature.

[SO-13]

Phosphatidylinositol-3-phosphate are involved in host cell entry of an oomycete pathogen *Olpidiopsis pyropiae*

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Host cell entry is the most crucial infection step in the obligate parasite, *Olpidiopsis pyropiae*, a causative agent of *Olpidiopsis* blight in *Pyropia* farms. Oomycete and fungal effectors can bind phospholipids, specifically phosphatidylinositol-3-phosphate (PI3P), and mediate cell entry via lipid raft-mediated endocytosis. The entry of *O. pyropiae* cell into the host, *Pyropia yezoensis*, was blocked with the treatment of Phosphatidylinositol-3-kinase (PI3K) inhibitors. PI3P binding proteins and inositol-phosphates that competitively inhibit effector binding to cell membrane also inhibited *O. pyropiae* infection. Fluorescent labeling showed that produces PI3P in zoosporangiums of *O. pyropiae*. We found two homologues of class Ⅲ PI3K from infected *P. yezoensis* transcriptome, and their expression profiles during the infection process were observed using real-time PCR. Our results show that the oomycete pathogen, *O. pyropiae* produce PI3P and may use a lipid raft-mediated endocytosis for its host cell

[SO-14]

Assessment of marine ecological health using diatoms

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Globally, diatoms are used to assess the ecological status of aquatic systems based on cosmopolitan nature, short life span and quick response to environmental and anthropogenic disturbances. Diatoms are meaningful, given that they are the one of main primary producers, contributing 40% of the primary productivity of the oceans and contributing approximately 20% of global carbon fixation.

In this study, the environmental and ecological health of tidal flat of Deokjeok island and Daeijak island were investigated and health of the coastal environment was evaluated by using diatoms.

As a result, both sites have high Shannon index values and species richness (2.9 ± 1) based on dominance by the genera *Navicula* and *Gyrosigma*. It showed both island sites were in relatively good ecological condition. Dominance by motile and live (healthy) frustules in the diatom communities (Dekojeck island is >75%, Daeijak island is >90%) also indicated that both islands were healthy.

In contrast, new diatom endpoints, lipid body characteristics, deformities and size reduction, indicated greater impacts at some sites of both islands. These sites might have been affected by some anthropogenic disturbance.

When compared with biochemistry results of same sites like as physico-chemical analysis (Chl-a), total organic carbon (TOC), chemical oxygen demand (COD), nutrients (N, P), microorganisms (*E. coli*, enteric bacillus, total *E. coli*), and evaluation of ecological water quality levels, it showed that there were clean area.

Conclusion of the present study is that Incheon islands are relatively ecologically healthy but needs future planning to maintain the near-pristine environment of the islands. Furthermore, it is also evident that investigation of diatom communities (especially periphytic and benthic communities) and new endpoint metrics (especially lipid body characteristics and frustule deformities) are meaningful tools for investigation of the ecological health of island environments.

[SO-15]

A silicon transporter PyLsi plays a critical role in stress tolerance in marine red alga *Pyropia yezoensis*

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Silicon is required for the protection of reproductive tissues in macroalgae. Although there are several evidences of the beneficial effects of silicon proven in macroalgae, the mechanisms regulating their transport activity are still poorly understood. Here, we show evidence that the expression patterns of PyLsi1 and PyLsi2 in both gametophytes and sporophytes phases. PyLsi were preferentially expressed in both sporophytes and gametophyte. Thus, *Pyropia yezoensis* may have only one silicon uptake mechanism of its generations. This is interesting because *P. yezoensis* was suggested using different sodium pump system in each of life stages. The expression of PyLsi1-1 was not effective under silicon stress, whereas PyLsi1-2 down-regulated activity in response to low silicon stress, suggesting that *P. yezoensis* adjusts the silicon transporter expression to adapt to silicon stress. Taken together, our results suggest that silicon transported by PyLsi in the mature zone is required for enhancing PyLsi activity.

[SO-16]

Development of a PCR-free marine biodiversity assessment methodology

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To understand the composition of ecological community from marine environments, DNA barcoding (or metabarcoding) that utilizes short genetic marker sequences amplified by universal PCR primer sets (e.g. COI, ITS, 16S rRNA, and so on) has been generally used as powerful tools to estimate the biodiversity of environmental samples. However, currently widely used DNA barcoding protocol has several technical hurdles (e.g., PCR bias, primers efficiency, and genetic marker dependency among different taxa) to be overcome. To remove these limitations, in this study, we establish a PCR-free marine biodiversity assessment method (hereafter, this method is called "***mitochondrial metagenomics***"). Shortly, in order to avoid the PCR bias and increase the efficiency of sequencing efforts, we extracted environmental DNA from not whole cells including nucleus but subcellular organelles (e.g. mitochondria and plastid) in environmental samples because in general total genomic DNA was mainly composed of nucleus DNA which is not sufficient genetic marker sequences compared with subcellular organelles.

To validate our method, we collected the environmental samples by filtration through two different pore-size filters from sea water at Yamido (Yellow sea) and Baealdo (South sea) in south korea. And, to test whether the taxonomic capturing capacity of our mitochondrial metagenomics method is better in terms of detecting the diversity of marine eukaryotes than existing one, it was compared to the consequences of DNA metabarcoding method employing four primary barcodes (COI, COI-5P, *tuf*A and *rbc*L). From environmental DNA, we prepared DNA libraries for DNA metabarcoding and mitochondrial metagenomics with paired-end 300 bp using Illumina Miseq. To obtain long-reads which were more efficient to taxonomy assign, the trimmed paired-end reads were merged to longer single-end reads. Finally, we carried out BLAST search to four NCBI nucleotide databases and assigned the taxonomy to reads based on NCBI taxonomy ID. As a result, in these analyses, we detect 1,034 species belonging to 776 genera and 1,017 species belonging to 718 genera using our method from sea water at Yamido and Baealdo respectively, but only 165 species assigned to 71 genera and 252 species assigned to 130 genera using DNA metabarcoding method. Moreover, these results were independent to aberration from the difference of raw-data size between two methods. We believe this method will present a useful alternative approach for evaluating marine environments by biodiversity and will be attractive to many marine biologists who are interested in marine ecosystems.

[SO-17]

방사무늬김(*Pyropia yezoensis*)의 살리실산 매개 질병 저항성

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식물은 병원체에 대응하여 세포벽이나 이차대사산물과 같은 방어 체계를 갖고 있을 뿐 아니라 감염에 대응하여 직접 유도되는 면역 반응도 가지고 있다. 고등 식물은 병원체의 감염 시에 살리실산 (salicylic acid)을 신호 호르몬으로 분비하여 세포 내 활성산소의 형성을 촉진하거나 세포자살을 통해 병원체의 증식을 억제한다. 홍조류 방사무늬김이 이와 같은 살리실산 매개에 의한 질병 저항성을 갖고 있는지 확인하기 위하여 살리실산 처리가 붉은갯병균 (*Pythium porphyrae*) 의 감염에 미치는 영향을 관찰하였다. 먼저 ELISA-test를 수행한 결과 방사무늬김은 다양한 자극에 의해 살리실산을 형성하는 것을 확인할 수 있었으며 붉은갯병균의 감염 시에 살리실산의 뚜렷한 증가는 관찰되지 않았다. 하지만, 방사무늬김에 살리실산을 전처리 한 후 감염 실험을 수행하였을 때 30초 정도만 살리실산에 노출되었을 때에도 감염률이 대조구에 비해 현저히 낮아지는 것을 볼 수 있었다. 살리실산 처리 후 DAB를 처리하여 과산화수소 (H_2O_2)의 축적을 관찰한 결과 감염된 방사무늬김의 세포 내에 더 많은 활성산소가 형성됨을 알 수 있었다. 또한 세포 자살 확인 시약인 트리판 블루를 처리하였을 때 살리실산을 전처리한 김에서는 대조구에 비하여 3배 이상 많은 세포자살이 관찰되어 엽체 위에서 붉은갯병의 균사가 성장하는 것을 막는 것이 확인되었다. 유기산인 살리실산은 방사무늬김의 면역력을 높일 뿐 아니라 잡조 제거 효과도 가지고 있어 활성처리제를 효과적으로 대체할 수 있을 것으로 사료된다.

[SO-18]

Optimization for protoplast isolation from the gametophytes of *Undaria pinnatifida* using response surface methodology

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Undaria pinnatifida is one of the most important commercial seaweeds around the world. Its gametophytes are good candidates for cellular biotechnology techniques, many of which rely on protoplasts (“naked” plant cells). Despite the importance of this species, there is no protocol for protoplast isolation using enzymes commercially available and the factors that affect its production have not been tested in detail. In this work, the effects of different enzymatic mixtures and chelating pre-treatment were tested in male and female cultures from *U. pinnatifida*. In addition, a full factorial split-plot design followed by a Box-Behnken design were used to optimize the protoplast yield. Temperature (X1), pH (X2), incubation time (X3) and concentration of enzymatic solution (X4) were considered as independent factors. True and viable protoplasts were obtained from male and female gametophytes using a mixture of 3 comemrcial enzymes (cellulase RS 1%, alginate lyase 2 U/ml and driselase 1%) with chelating pre-treatment. Additionaly, X3 and X2 had interactive effect only in female gametophytes. As temperature did not have a significant effect, it was set at 20℃ (normal culture temperature).

포스터발표

PA. 분류 및 형태

[PA-01]

Description and application of a marine microalga *Auxenochlorella protothecoides* isolated from Ulleung-do

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A unicellular green alga was axenically isolated from a tidal pool on Ulleung-do, Korea. Morphological, molecular, and biochemical analyses revealed that the isolate belonged to *Auxenochlorella protothecoides* and the current study is the first record of this species in Korea. The microalgal strain was named as *A. protothecoides* MM0011 and its growth, lipid and pigment compositions, and biomass properties were investigated. The strain was able to thrive at a wide range of temperatures (5~35℃) and to withstand up to 1.5 M NaCl. The results of GC/MS analysis showed that the isolate was rich in nutritionally important polyunsaturated fatty acids. Its major fatty acids were linoleic acid (27.6%) and α-linolenic acid (39.6%). Thus, this indigenous microalga may have potential as source of ω3 and ω6 PUFAs as an alternative to fish and/or plant oils. Also, the HPLC analysis revealed that the value-added antioxidant, lutein was biosynthesized as the accessary pigments by the microalga. A proximate analysis showed that the volatile matter content was 85.6% and an ultimate analysis indicated that the gross calorific value was 20.3 MJ kg^{-1}. Since 40.5% of total nitrogen and 27.9% of total phosphorus were removed from the medium, respectively, it also have potential as a future feedstock for biofuel applications which could be coupled to wastewater treatment. In addition, the biomass may also serve as an excellent animal feed because of its high protein content (51.4%). Therefore, *A. protothecoides* MM0011 shows promise for application in production of microalgae-based biochemicals and as a biomass feedstock.

[PA-02]

Species diversity of phytoplankton in Cheonjin lake, North-East South Korea

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The present study summarized the phytoplankton diversity in Cheonjin lake (small lagoon changed to freshwater) located in the North-East of South Korea from May 2016 to September 2017. A total of 305 taxa belong to seven main algal groups (Charophyta, Chlorophyta, Cyanophyta, Chrysophyta, Cryptophyta, Dinophyta and Euglenophyta) were identified. The highest number of species (161 taxa) was observed in September 2017, while the lowest(61 taxa) was observed in February. Desmids(44.2%) of Charophyta accounted for the most abundant group making up 135 taxa from 23 genera. Of these, 26 species of desmids including three new species, 7 species of Euglenophyceae, 4 species of Chlorophyceae and 1 species Chrysohyceae have not previously been recorded from Korea.

[PA-03]

Evolutionary Dynamics of Cryptophyte Plastid Genomes

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Cryptophytes are an ecologically important group of largely photosynthetic unicellular eukaryotes. This lineage is of great interest to evolutionary biologists because their plastids are of red algal secondary endosymbiotic origin and the host cell retains four different genomes (host nuclear, mitochondrial, plastid, and red algal nucleomorph). Here, we report a comparative analysis of plastid genomes from six representative cryptophyte genera. Four newly sequenced cryptophyte plastid genomes of *Chroomonas mesostigmatica*, *Ch. placoidea*, *Cryptomonas curvata*, and *Storeatula* sp. CCMP1868 share a number of features including synteny and gene content with the previously sequenced genomes of *Cryptomonas paramecium*, *Rhodomonas salina*, *Teleaulax amphioxeia*, and *Guillardia theta*. Our analysis of these plastid genomes reveals examples of gene loss and intron insertions. In particular, the *chl*B/*chl*L/*chl*N genes, which encode light-independent (dark active) protochlorophyllide oxidoreductase (LIPOR) proteins have undergone recent gene loss and pseudogenization in cryptophytes. Comparison of phylogenetic trees based on plastid and nuclear genome datasets show the introduction, via secondary endosymbiosis, of a red algal derived plastid in a lineage of chlorophyll-*c* containing algae. This event was followed by additional rounds of eukaryotic endosymbioses that spread the red lineage plastid to diverse groups such as haptophytes and stramenopiles.

[PA-04]

Complete mitochondrial genomes of two *Sargassum* species, *S. nigrifolium* and *S. yezoense*(Fucales, Phaeophyceae)

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Sargassum C. Agardh, one of the most important ecological genus on rocky shores, forms marine forests in tropical and temperate regions. Several species heve long been economically important as food and medicine. A total of 23 species are listed in the available literature for South Korea. Two *Sargassum* species, *S. nigrifolium* and *S. yezoense* are genetically very similar based on four gene anlaysis despite the morphological distinctiveness. We sequenced and characterized the complete mitochondrial genomes of two *Sargassum* species using next-generation genome sequencing methods. Genome size and GC content of *S. nigrifolium* and *S. yezoense* were slightly different as 34,788 nt vs. 34,767 nt, and 36.5% vs. 39.9%, respectively. Sixty-five genes of two *Sargassum* species were identified including 35 protein-coding genes, 2 open reading frames (ORFs), 3 rRNA genes, and 25 tRNA genes. The gene synteny was equal between *S. nigrifolium* and *S. yezoense*. There were gene length differences in *nad7, rns, cox2, rps3, trnW, tatC* and *rnl,* which were made genome variations between two species within the genus *Sargassum*. This will provide useful information on both population genetics and mitochondria genome evolution.

[PA-05]

Taxonomy and description of freshwater microalga

Mychonastes sp. Jangdong160806F

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Kyung June Yim, Eun Sun Joo.

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Genus *Mychonastes* is one of the small coccoid algal genus belonging to Chlorophyceae. In this study, we described a *Mychonastes* sp. Jangdong160806F strain. *Mychonastes* sp. was isolated from a freshwater sample in Jangdong reservoir and cultured in BBM medium at 20℃ with 16:8 LD-cycle. *Mychonastes* sp. cells are a spherical shape and measured 2.37~4.20 μm (2.99±0.49 μm) diameter. A motile stage has not been observed by light microscopy. Ultrastructural data showed each cell had a crescent-shaped chloroplast. The chloroplast consists of thylakoid lamellae arranged in six almost parallel rows without pyrenoid. Phylogenetic tree was inferred with combined gene sequences of partial small-subunit (SSU rDNA), internal transcribed spacer 1 (ITS1), 5.8s rDNA, internal transcribed spacer 2 (ITS2) and partial large-subunit (LSU rDNA) by maximum likelihood method. The tree showed *Mychonastes* sp. Jangdong160806F strain formed a separated clade from the *M. homosphaera* clade. And we are predicting ITS2 secondary structures of *Mychonastes* species.

[PA-06]

New records of diatoms (Bacillariophyceae) and floristic survey in Korea

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A study on the indigenous diatoms was carried out at 12 sites during February to October 2016 from the brackish-waters and the freshwaters in around the Gyeongsang-do, Gangwon-do and Jeju Island from Korea. An ultra-structure of small-sized diatoms was examined using a light and scanning electron microscopy. Seventy six species of diatoms were identified and composed of 3 class, 18 order, 28 family and 43 genus. We newly recorded five diatom species in Korea; *Entomoneis paludosa*, *Gomphonema cholnokyi*, *Punctastriata mimetica*, *Urosolenia eriensis* and *Pinnularia lignitica*. The historical synonyms of the diatom species are presented for the floristic informations and this study will contribute the knowledge of the species diversity level of diatom in Korea

[PA-07]

Surirella nnibria sp. nov. in freshwater, South Korea

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The genus *Surirella* were recorded about 1300 species, of which 249 species have been identified as currently accepted taxonomically. Many of *Surirella* species distributed from tropical and sub-trophic areas in different countries. In this study, a new freshwater diatom, *Surirella nnibria* Yun, Lee & Kim sp. nov., was found from Hoeryongpo, Yeong river, Yujeon river and resorvoir Gyeongcheon, Korea. Samples were analyzed using the light and scanning electron microscopy. The species compared with related species (*S. angusta*, *S. ovalis* and *S. linearis*). *Surirella nnibria* is characterized by solitary cells, dumbbell-form, valves with constrict outline on the central area. The species have the straight apical axis, isopolar valve, and symmetrical transapical axis. Ultrastreucture in the intra-valve was not developed.

[PA-08]

Morphological Characteristics of Sand-Dwelling Benthic Dinoflagellates as Newly Recorded Species to Korean Waters

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Some recent ecological reports have revealed that tropical/subtropical species in many kinds of taxa occur around Korean Peninsula due to climate changes such as global warming. We have tried to find out such species occurrence of planktonic and benthic dinoflagellates in Korea waters since early 2000. In this study we focused on sand-dwelling benthic dinoflagellates in order to get some evidences of such alien species occurrence in Korean waters. Samples were periodically collected from sand sediments at several stations of intertidal beach and subtidal coast from December 2016 to April 2017. Each individual cells were isolated by picking method, then incubated. Species identification was done by light and scanning electron microscope. We add five sand-dwelling benthic dinoflagellates such as *Gymnodinium dorsalisulcum*, *Prorocentrum bimaculatum*, *Prorocentrum tsawwassense*, *Thecadinium kofoidii*, and *Togula britannica*, as newly recorded species to Korean waters and describe morphological characteristics in the present study.

[PA-09]

Complete organelle genome and “flip-flop” structure of chloroplast genome of *Capsosiphon fulvescens* (Ulotrichales, Ulvophyceae)

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A filamentous green alga, *Capsosiphon fulvescens* has been consumed as food with unique flavor and soft texture to treat stomach disorders and hangovers, and its economic value justifies studying its nutritional and potential therapeutic effects. In contrast to these applications, the genome on this genus has never been reported. To better understanding of organelle genome of *C. fulvescens*, we sequenced and annotated its complete chloroplast and mitochondrion genome in this study. The cpDNA length is 111,998 bp with 31.3% GC content. The circular cpDNA contains 108 genes including 77 protein-coding genes, two copies of rRNA operons and 25 tRNAs. The mtDNA length is 43,578 bp with 30.7% of GC content. The circular mtDNA contains 53 genes including 23 protein-coding genes, one copy of rRNA operon and 28 tRNAs. To determine its phylogenetic position in the class, we used chloroplast and mitochondrial genome to construct phylogenetic trees. Additionally, we found that the special structure of cpDNA consists of two types of form called flip-flop. In this presentation, we will discuss about organelle genome of *C. fulvescens* and unique feature of *C. fulvescens* chloroplast genome and evolutionary trends in green algae.

[PA-10]

Morphological observations and phylogenetic position of the parasitoid nanoflagellate *Pseudopirsonia* sp. (Cercozoa) infecting the marine diatom *Coscinodiscus wailesii* (Bacillariophyta)

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The marine diatom *Coscinodiscus wailesii* cells infected by a novel parasitoid nanoflagellate were observed during a sampling at Nokdong harbor, southern coast of Korea in January 2017. While the development process of the trophosomes of the parasitoid was more similar to that of *Pseudopirsonia mucosa*, division pattern of the auxosomes was similar to that of *Pirsonia* species. Phylogenetic analyses inferred from 18S rRNA gene sequences revealed that the parasitoid infecting *C. wailesii* fell within the cercozoan groups and branched as a sister lineage of the clade consisting of *Pseudopirsonia mucosa* and the undescribed *Cercomonas* sp. SIC7235, with the sequence dissimilarity of 7.3% with *Pseudopirsonia mucosa*. All of these developmental and molecular characteristics suggest that the parasitoid nanoflagellate infecting the diatom *C. wailesii* is a new *Pseudopirsonia* species.

[PA-11]

Three new Antarctic *Asterochloris* species (Trebouxiophyceae) from King George island, Antarctica

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The genus *Asterochloris* is one of the most common lichen photobionts. We collected few species of the lichen genera Cladonia and Stereocaulon from the King George Island, Antarctica, and isolated many single photobiont cells by using Pasteut capillary pipette and established them as unialgal culture strains. To understand phylogenetic relationships and species diversity of the genus *Asterochloris* known as one of most common photobionts in the thallus of lichen, we analyzed molecular and morphological data by using light microscopy, confocal laser microscopy and three molecular markers; nuclear encoded internal transcribed spacer (ITS) rDNA, actin and *rbc*L protein coding gene. Phylogenetic analyses based on the nuclear ITS rDNA, actin and *rbc*L gene sequence data indicated that Antarctic strains divide into three separate lineages and form a monophyletic clade respectively with high support values. The new species were characterized by unique compensatory base changes (CBCs) and hemi-CBCs in the nuclear ITS transcripts and chloroplast morphologies.

[PA-12]

New candidate species of endophytic green algae *Bolbocoleon minus* sp. nov. (Ulvophyceae) from Korea.

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Bolbocoleon Pringsheim (Chaetophoraceae, Chlorophyta) are small genus that contain only two species. We would like to propose to *Bolbocoleon minus* sp. nov. as a new species within the genus *Bolbocoleon* Pringsheim based on Korean specimens collected from jeju. This plants formed dark olive green irregular clumps up to 5 mm in diameter. Cells were narrower than those observed in *B. piliferum* isolates with circular cells measuring 6-10 µm in diameter and elongated cells measuring 2.5-5 µm in diameter and 3-5 times longer than broad. Vegetative cells contained a parietal chloroplast with 1(-3) pyrenoids. Sporangia were formed from intercalary cells with a exit tube. In the phylogenetic tree, based on *tuf*A sequences, this species are nested in the same clade as *Bolbocoleon.* However, there was no same species. In this study, this species are newly recorded in the Korean marine algal flora, based on the morphological and molecular data.

[PA-13]

경상남도 산지습지에서의 규조류 군집분포

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사자평 고산습지, 신불산 고산습지, 화엄늪은 경상남도의 대표적인 산지습지로 해발 1000m내외의 영남알프스 지역에 위치한다. 최근 하천 최상류 수분공급원인 산지습지의 보전가치가 높은 것으로 인식 되면서 다양한 연구가 진행되고 있으나, 생태계 최하위 계층인 규조류의 군집특성에 대한 연구는 부족한 실정이다. 따라서 본 연구에서는 산지습지에서의 규조류의 군집특성과 이화학적요인의 비교 분석을 통하여 산지습지에서의 독특한 군집구조를 파악하고자 하였다. 조사는 2016년 3월부터 11월까지 수행하였다. 온도 및 pH는 현장에서 즉시 측정하였으며, 종 동정을 위해 Permaganate method (Hendey 1974)로 세정한 후 Pleurax로 봉입한 영구표본을 이용하여 광학현미경과 주사전자현미경 사진을 촬영하여 동정하였다. 현장에서 측정한 pH는 5.66-6.84 범위로 약산성을 나타냈으며 3월 사자평 화엄늪에서 가장 낮았고 6월 사자평고산습지에서 가장 높았다. 온도는 5.4-31.8 범위로 6월 신불산 고산습지에서 가장 높게 나타났다. 이번 조사에서 동정된 규조류는 총 27속 117종이었으며, 이 중 호산성종은 49종, 호알칼리성종은 10종으로 산성종의 비율이 알칼리성종에 비해 많이 나타났으며, 호산성종은 *Pinnularia*속과 *Eunotia*속에서 각각 13종과 12종으로 가장 많이 관찰되었다. 계절별 출현종은 3월 신불산에서 가장 많았으며, 9월 신불산에서 가장 적었다.

[PA-14]

Comparative genomics of plastid and mitochondria in Minerva aenigmata and Pyropia pulchra (Rhodophyta)

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Minerva aenigmata is a species in the Bangiales that has unbranched, erect thalli, initially forming uniseriate filaments that become multiseriate at maturity. This simple filamentous structure is morphologically indistinguishable from other filamentous Bangiales taxa. *M. aenigmata* is known as the earliest diverged species of Bangiales that is distributed in the upper intertidal zone along the New Zealand. Currently, several Bangiales plastid genomes are available, however, these taxa all belong to the stem group of the Bangiales. To better understand organelle genome evolution, we sequenced and annotated the complete plastid and mitochondrial genomes of the early diverged *M. aenigmata*. The plastid genome length is 189.5kbp with 32.3% GC content. The circular plastid genome contains 243 genes including 199 protein-coding genes, 6 rRNAs and 37 tRNAs. The mitochondrial genome of *M.aenigmata* is 26.8kbp in size with 30.8% of GC and encodes 25 protein-coding genes. In mitochondrial genome of *Pyropia pulchra* that size was 33,203bp with 30.7% GC content, and contained 27 protein-coding genes, 2 rRNA, 24 tRNA genes and 2 intron ORF in *cox1* gene and rnl regions. Comparative analysis of organelle genomes show highly conserved genome structures including genome sizes, gene contents, gene orders and intron regions both in plastid and mitochondrial genomes. We calculated and classified value of dN analysis result on a functional basis about 199 plastid protein-coding genes and 25 mitochondrial genes. Through gene classification by function in each organelle gene set, we estimated relationship between function and gene evolutionary rates.

[PA-15]

곰피(*Ecklonia stolonifera*)의 양식과 품종 구분을 위한 형질분석

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국제식물신품종보호동맹(UPOV) 가입과 의무 규정에 따라 국내 해조류 분야는 2012년부터 품종보호 관련 업무가 시행 되었다. 다양한 해조류 종들이 식용, 의약용, 공업용, 사료용 및 화학용 등 산업적으로 널리 이용되고 있지만, 수산 분야의 품종 출원은 육상 식물에 비하여 매우 적은 수에 그치고 있다. 경제성 있는 해조류를 대상으로 한 연구 로드맵 중 ‘유전자원 탐색 및 종자 소재 개발’과 ‘종자 특성 표준화’와 관련한 접근이 기반 연구로서 시급하다. 최근 보급되기 시작한 갈조 곰피(*Ecklonia stolonifera*)와 감태(*E. cava*) 양식의 경우도 향후 다양한 품종 개발이 이어질 것으로 예상된다. 따라서, 이를 효율적으로 지원하기 위한 곰피의 신품종 개발 및 재배심사에 필요한 표준화 기술 개발이 시급한 실정이다. 본 연구는 곰피의 형질특성조사와 이를 바탕으로 한 특성조사요령 작성을 위하여 양식장 재배 개체 조사와 자연개체군 조사를 병행하고, 확보한 표본들을 바탕으로 곰피의 형태적 특성을 분석하였다. 곰피의 주요 식별형질과 양식 과정에서 이들 형태적 특성의 변화를 연속적으로 조사하였다. 2016년 5월부터 2017년 10월까지 초기 채묘 과정부터 가이식 및 본 양성 단계까지 월별 조사를 수행하였다. 이를 통하여 품종 구분에 적합한 것으로 판단된 1차엽과 부착기 등의 양적 형질을 포함하여 27개 특성을 선별하였다. 품종 확인을 위하여 선별한 이들 형질 특성에 대하여 양식 개체군과 자연개체군을 대상으로 식별형질들의 유의성을 검토하고, ‘특성조사요령(안)’을 위한 항목으로 어린 개체에서 7개 기본적인 양적 형질을 선택하였고, 성체에서는 질적 형질 6개, 양적 형질 14개의 20개를 선택하였다. 또한, 각 항목별로 조사 시기 및 조사방법을 규정하였다. 본 연구의 ‘특성조사요령’은 곰피 양식을 위한 표준화기술 개발에 기여할 것으로 판단된다.

[PA-16]

홍조식물 *Griffithsia monilis*의 형태 발생에 대한 DNA-methylation 저해제 5-azacytidine의 영향

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식물의 형태 발생은 동물과 마찬가지로 후성유전학적 조절에 의해 결정되나 전형성능 (totipotency)를 갖는 식물에서는 종종 이미 분화된 조직의 세포로부터도 전체 개체를 다시 유도할 수 있다. 이와 같은 후성유전적 역전은 DNA-demethylation 기작에 의해 일어난다. 다핵의 거대세포를 갖는 홍조식물인 *Griffithsia monilis*를 재료로 하여 형태 발생에 있어 후성유전학적 결정 과정을 조사하였다. 2차원 전기영동 조사 결과 정단부와 가근부의 단백질체는 상당히 다른 패턴을 갖는 것이 관찰되었다. *Griffithsia monilis*의 사상체를 정단 부위와 중간 부위 및 가근으로 구분 하여 얻어진 단일 세포의 분화 과정을 추적하였을 때 정단 부위에서 분리된 세포는 거의 모두 정단부와 가근을 갖는 기본 형태의 개체로 분화되었으나 가근 부위의 세포를 분리하여 배양하였을 때에는 기본 형태로의 분화에 훨씬 많은 시간이 소요되었으며 가근세포 보다는 정단 세포의 분화가 더 두드러졌으며 전체의 50% 정도만 정단부와 가근을 모두 갖는 개체로 분화하였다. DNA methyltransferase inhibitor인 5-azacytidine을 다양한 농도로 처리한 후 오랜 시간 배양하였을 때 대조구에 비해서 50 μM의 농도에서 더 빠른 성장과 생물량의 증가를 관찰할 수 있었다. 이와 같은 속성이 후성유전적으로 고정되었는지를 보기 위해 저해제를 제거하고 다시 단일 세포부터 배양하였을 때에도 위와 같은 특성이 계속 유지되는 것을 볼 수 있었다. 이상의 결과는 단순한 체제를 갖는 다핵성 홍조식물에서도 세포 분화가 후성유전적으로 결정되며 일단 일어난 변화는 상당 기간 유지됨을 보여준다.

[PA-17]

A new report of two marine *Mallomonas* species (Synurophyceae) from Korea

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The genus *Mallomonas* is a single-celled flagellate that generally has siliceous scales and bristles on cell surface. *Mallomonas* is one of well-known freshwater algae. However, we report two new marine *Mallomonas* species collected from the Dongho Beach, Jeollabukdo, Korea. To understand taxonomy of the species, we performed molecular phylogenetic analysis based on a concatenated dataset and observed morphological characters under light and electron microscope. For the phylogenetic analysis, we used a combined dataset from five gene sequences; nuclear SSU and LSU rDNA and plastid LSU rDNA, *rbc*L and *psa*A genes. The new species *M. cuspis* sp. nov. Dongho022517B3 was grouped together with *M. heterospina* and *M. oviformis* in the section *Planae*, and was characterized by scale morphology such as broad shield marked with v-shaped across internal ridge and lack of submarginal rib structure and dome. The other new species *M. marina* sp. nov. Dongho031817J was grouped together with *M. cratis*, *M. pseudocratis*, *M. asmundiae* and *M. striata* var. *serrata* in the section *Striatae* and have well developed posterior submarginal rib, transversal ribs, dome with striped silica scale.

[PA-18]

Diatoms (Bacillariophyta) from a tidal sandflat of the western coast, with emphasis on the richness and diversity of epibenthic species

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Coasts and estuaries, boundaries between seas and continents, are ecosystem transition areas, with large geomorphic changes and diverse breeding grounds for living organisms. Overall, species diversity of biological organisms is higher in coastal areas than in ocean or inland waters, and diatoms are no exception, as recent studies have revealed that diatom community structure and diversity are influenced by geographical factors independent of environmental conditions. Furthermore, this region features vast (up to 10 km wide) open intertidal mudflats from the southeast to the northwest of Korea. Approximately 3,000 small islands are scattered over the flats. One sample from a tidal flat of the western coast of Korea, in Byeonsan of Buan, was selected to show an abundance and richness of benthic diatoms in intertidal areas. It is noted that F. Hustedt identified 388 taxa, including 93 new to science, from just two samples of mud from Beaufort coast, North Carolina, in 1955. Many diatom taxa occurring in intertidal areas are remained unidentified or unrecorded. This data highlights the need of more floristic studies to properly clarify the diatom diversity over intertidal sediment off the western coast of Korea. The present report enhances the species diversity or richness of diatom in the country

[PA-19]

Isolation and computational characterization of glutathione peroxidase gene from *Pyropia yezoensis*

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Oxidative stress caused by accumulation of reactive oxygen species seriously jeopardized the production of seaweed cultivation worldwide. Glutathione peroxidases (GPXs, EC 1.11.1.9) are key enzymes of the antioxidant network in seaweed. In the present study, we aimed at understanding the roles of the antioxidant enzymes in *Pyropia yezoensis* by focusing on the GPX family. We identified the genes which indicated their putative chloroplastic, mitochondrial and cytoplasmic location in *P. yezoensis*. The exon-intron organization of these genes exhibited a conserved pattern closely related among plant *GPX* genes. Multiple environmental stresses and hormone response related *cis*-acting elements were predicted in the promoters of *PyGPX* genes. The gene and protein expression profiles of PyGPXs in response to high levels of salinity and osmotic stresses were investigated using real-time RT-PCR and western blotting analysis. Our result showed that different members of the *GPX* gene family were coordinately regulated under specific environmental stress conditions, and supported the important roles of PyGPXs in salt and drought stress response in *P. yezoensis*.

[PA-20]

The crustose coralline alga, two new *Phymatolithon* species (Hapalidiales, Rhodophyta) from Korea

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The genus *Phymatolithon* Foslie (1898) was established based on *P. polymorphum* (= *P. calcareum*). *Phymatolithon* is characterized by monomerous thallus construction, rounded or flattened outermost walls of epithallial cells, subepithallial initials that are usually as short as or shorter than their immediate inward derivatives, cells of adjacent filaments linked by fusions, absence of protective cells in spermatangial initials, branched and unbranched spermatangial filaments, absence of a conspicuous central fusion cell in mature carposoporophyte, and having multiporate tetrasporangial conceptacles. 15 *Phymatolithon* species are currently listed from the worldwide. Of them, only one species, *P. repandum*, has been reported in Korea. In this study, we described two new candidate species of *Phymatolithon* from Korea. They are distinguished from other species by their substrate, initially growing forms, thallus thickness, and marginal construction in vegetative structures and presence or absence of flush pore plugs than other roof cells, size of pore plate, diameter of pore plug, number of pore plugs in pore plate, and roof thickness in tetra/bisporangial structures. Phylogenetic analyses of COI-5P and *psb*A also reveal that these two new species are placed in *Phymatolithon* and distinguished from congeners. The sequence divergence between them is 8% in *psb*A gene and 10% in COI-5P gene.

[PA-21]

A new record of epilithic coralline algae *Lithothamnion japonicum* (Hapalidiales, Rhodophyta) from Korea

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The genus Lithothamnion is one of the biggest genera in Hapalidiaceae with 75 species. Lithothamnion japonicum reported as endemic species to Japan and is described by having protuberances, raised mound-like male conceptacles, branched spermatangial filaments, buried senescent male conceptacle chambers, confluent tetra/bisporangial conceptacles, flattened pore plant, and deeply embedded senescent tetra/bisporangial conceptacles. In this study, we collected numerous unidentified samples along the coastlines of Korea. It is compared to the holotype of L. japonicum and the holotype of L. fretense (=L. japonicum). Furthermore, we analyzed DNA sequence data of COI-5P and psbA to determine their phylogenetic relationship. Here, we newly report L. japonicum for the first time from Korea and present more detailed morphological characters and taxonomic re-evaluation of this coralline algae.

[PA-22]

The ITS2 genetic polymorphisms within *Pseudo-nitzschia pungens* (Bacillariophyceae) resulted from the sexual reproduction

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The bio- and genetic diversity of species could prevent the extinction from natural selection and provide the primary abilities to adapt to the various habitats. The pennate diatom, *Pseudo-nitzschia pungens* is cosmopolitan, and regarded as a common component of marine phytoplankton. The genetic diversity and distinct three genotypes (clades) of *P. pungens* have been studied quite enough, however the experimental proof of genetic polymorphism phenomenon has not been provided until now. We analyzed morphological features using LM and TEM images, and examined the ITS2 rRNA gene using genetically different (clade I and III) two parental and its two offspring *P. pungens* strains through cloning PCR. There were no morphological differences between parental and offspring strains, however the offspring strains showed recombinant sequences types in ITS2 region completely. The ITS2 sequences of offspring were composed by the sequences of clade I or III. Additionally, the high ratios (38.6 and 65.1%) of single nucleotide polymorphism (SNP) were observed in ITS2 region of offspring strains. Our results implicated that the genetic polymorphism phenomenon such as genetic recombination and SNP generation resulted from sexual-reproduction should contribute to maintain the genetic diversity and to produce the new genotypes within this species. Furthermore, the diverse hybrid types might provide adaptive strategies to various natural environments and may even be the source of new recombinant species in the future.

[PA-23]

한국산 돌말류 속 이상의 분류군의 국명화 연구

이진환

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1993년 12월 생물다양성협약 발효 이후 2010년 10월 당사국 총회에서 나고야 의정서가 채택되고, 2014년 10월 12일 발표됨에 따라 각국의 생물자원의 파악은 최대 급선무로 부상하였다. 국립생물자원관에서는 자생 생물자원에 대한 총괄 관리 및 나고야 의정서에 따른 생물다양성 보존 및 관리 등의 기반이 되는 국가 생물종 목록을 구축하고 있다.

우리나라 자생 생물종 47,003종(2016년 12월 기준) 중 학명은 있으나 국명이 없는 종이 13,292종(전체 종의 28.3%)이며, 이 중 해산 및 담수 미세조류(微細藻類) 15.2%(2,015종)는 국명이 전혀 없다. 다만, 1995년 연구에서 강, 목, 과, 속 수준에서 국명 부여가 수행되었으나, 그 후 20년 이상 지나 많은 분류학적 연구가 수행되어 일부 보완되기도 하였다.

국명화의 과거의 연구를 보면 정영호(1968)의 한국동식물도감(담수조류 편)에서 일부 속의 국명을 붙였고, 최중기・이진환・이경(1995)에 한국산 돌말류(硅藻類)의 분류학적 연구의 일환으로 분류체계와 분류계급의 한국명화(韓國名化)에서 1강, 2목, 5아목, 21과, 5아과, 146속의 우리말 이름을 붙였다. 그리고 대한민국 생물지 담수산 돌말류에서 이정호 (2012)가 20여 속의 명칭을 붙였다.

이번 연구에서는 국립생물자원관 사업으로 이진환・조경제(2015)에 의해 작성된 국가생물종목록집(돌말류)에 실린 속명이상의 분류군에서 국명으로 명명되지 않은 28과(Family), 83속(Genus)에 대하여 새로이 명명하였기에 보고하는 바이다.

돌말류의 속 이상의 분류군에 국명을 부여하므로서 중·고교, 대학, 전공학자, 일반국민, 산업계 등에 어려운 학명을 보다 친숙하고 알기 쉬운 이름을 제공할 수 있으며, 국가 생물종에 대한 이해를 높이고 생물주권 확보에 기여할 수 있을 것으로 판단된다.

[PA-24]

Cloning of a novel Cyclophilin B gene in the red tide dinoflagellate *Cochlodinium polykrikoides*: molecular characterizations and transcription to environmental stresses

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The marine dinoflagellate *Cochlodinium polykrikoides* is one of the most common ichthyotoxic species that causes harmful algal blooms (HABs), which leads to ecological damages and huge economic loss in aquaculture industries. Cyclophilins (CYPs) belong to the immunophilin superfamily, and they may have a role in the survival mechanisms of the dinoflagellate in stress environments. In the present study, we identified a novel cyclophilin gene from *C. polykrikoides*, and examined physiological and gene transcriptional responses to biocides copper sulphate ($CuSO_4$) and sodium hypochlorite (NaOCl). The full length of *CpCYP* was 903 bp, ranging from the dinoflagellate splice leader (DinoSL) sequence to the polyA tail, comprising a 639 bp ORF, 117 bp 5' UTR, and a 147 bp 3' UTR. Motif and phylogenetic comparisons showed that CpCYP was affiliated to group B of CYP. In biocide stressors, cell counts, chlorophyll *a* and photosynthetic efficiency (*Fv*/*Fm*) of *C. polykrikoides* were considerably decreased with both exposed time- and dose-dependent manners. In addition, *CpCYP* gene expression was significantly induced after 24h exposure to the biocide-treated stress conditions. These results indicate an effect of the biocides on the cell physiology and expression profile of *CpCYP*, suggesting that the gene may play a role in environmental stress responses.

[PA-25]

Description of *S. coreanum* sp. nov. in the Korean coasts

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Despite the recent description of *Stenogramma guleopoense* in Korea, the issue on *S. interruptum* in northwestern Pacific is still a matter of debate. We analyzed 24 *rbc*L sequences from specimens collected in Korea, including a longer fragment of *rbc*L from the type of *S. guleopoense*, in combination with morphological observations. Phylogenetic analysis of *rbc*L sequence revealed a new distinct clade that differed from *S. guleopoense* from Korea and other species of *Stenogramma*. The morphology and anatomy of the Korean clade supported its distinct position in the genus *Stenogramma*. Based on these results, we herein describe a new species, *S. coreanum*, from Korea. *Stenogramma coreanum* is distinguished by a combination of its large size (up to 24 cm) of fan-shaped or irregularly leveled thalli with up to nine times divided branches, wider blades with laciniate segments, one to two layers of cortical cells, two to three layers of medullary cells, and a gradient of one to two layers of smaller cells between the cortex and medulla, and not continuous cystocarps on the center of frond. *Stenogramma coreanum* occurs mostly along the south coast of Korea and *S. guleopoense* along the west coast. The implication for biogeography in *Stenogramma* is discussed.

[PA-26]

Revision of the genus *Streblocladia* (Rhodomelaceae) in New Zealand, with genetic evidence for a new species

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Early European collectors described a red alga from southern New Zealand under several different names, eventually resolved as *Streblocladia glomerulata*. The close relationship between this and another heavily corticated species of *Polysiphonia sensu lato, P. muelleriana* has been known for several decades, with the transfer of *P. muelleriana* to *Streblocladia* foreshadowed by research of Hommersand & Adams (Adams 1991) and L. Phillips (2001). To confirm the relationships of these species, we conducted a molecular-assisted investigation using the plastid *rbc*L gene, as well as the morphological observations. Our molecular analyses indicated that *P. muelleriana* should be transferred to the genus *Streblocladia,* with these species characterized by sympodially branched, corticated main axes, the absence of trichoblasts, and spermatangia replacing the whole trichoblast in a unilateral. Additionally, new taxonomic entity of this genus is confirmed on the basis of the genetic evidence and we will present the distinguishing features of possible candidate for a new species in New Zealand. In our analyses New Zealand materials of *Streblocladia* forms the monophyly with strongly supported bootstrap value and is clearly separated from other species of *Polysiphonia sensu lato*.

[PA-27]

New auxiliary cell ampullae based on foliose red algae, *Nesoia* gen. nov. (Haleminiaceae, Rhodophyta) from Korea

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The family Halymeniaceae is characterized by unique reproductive organs composed of carpogonial branch ampullae and auxiliary cell ampullae. The type of auxiliary cell ampullar has been considered as the key characteristics in the family Halymeniaceae. The continuous surveys into subtidal region from Korea including morphology and *rbc*L molecular analyses give a chance to reveal a new evolutionary lineage in the generic level. As a result, we propose a new genus, *Nesoia* gen. nov., with description of *N. delicatula* sp. nov., *N. pulchella* sp. nov., and *N. latifolia* comb. nov. which is a new combination from *Halymenia latifolia*. The genus *Nesoia* gen. nov. shows foliose vegetative thallus composed of single layered cortex and anticlinal medulla. This new genus is characterized by monoecious gametophytes and auxiliary cell ampullae consisted of three-ordered ampullar filaments. The auxiliary cell as the basal cell of the second-order is borne from the secondary or tertiary cell of the first-order ampullar filament having two second-order ampullar filaments bilaterally. This new auxiliary cell ampullae as a mediate type between *Halymenia*-type and *Aeodes*-type will provide more effective resolution to delimit taxonomic boundaries among genera of Halymeniaceae.

[PA-28]

Molecular and morphological investigations of the genus *Scinaia* (Nemaliales, Rhodophyta) from the northern Pacific

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The red algal genus *Scinaia* is characterized by a thallus having a non-calcified, dichotomously branched, and filamentous medulla with utricles at the outer cortex. Except *Scinaia latifrons* showing flat thallus with inflated margin, it is difficult to distinguish species based on external morphology only. To identify *Scinaia* species distributed in the northern Pacific, we analyzed *rbc*L sequences of sixty seven *Scinaia* specimens and revealed eight species: *Scinaia articulata*, *S. confusa*, *S. japonica*, *S. johnstoniae, S. latiforns*, *S. okamurae, S. tokidae* and a new species. *S. articulata*, *S. johnstoniae* and *S. tokidae* are monophyletic, showing 5.0% interspecific divergence between *S. articulata* and *S. johnstoniae*, and 7.7% between *S. tokidae* and *S. johnstoniae*. In morphology, the utricles' size is distinct among them. *S. japonica* has the epidemis composed of inflated utricles and one-layered pigmented cells. *S. articulata*, *S. johnstoniae*, *S. tokidae S. confusa* and *S, japonica*, including *S. latifrons*, have compactly arranged cortical surface view composed of polygonal utricles' apex, and they formed a large clade. Unlike, *S. okamurae* and *Scinaia* sp. showed rosette arrangements in surface view. *S. okamurae* and *Scinaia* sp. formed an independent clade, which was separated to the former clade with 9.1-13.6% pairwise distance. *Scinaia* sp. was distinguished from *S. okamurae* by utricles' size and apex's shape, showing 5.9% interspecific divergence to *S. okamurae* in *rbc*L analysis. In conclusion, the molecular investigation of *rbc*L sequences with morphological observation provides more accurate resolution to identify *Scinaia* species from the northern Pacific, and further it will be useful to describe species diversity and to reveal the phylogenetic relationships of *Scinaia* species globally distributed.

[PA-29]

Transfer four species of *Haraldiophyllum* (Delesseriaceae, Rhodophyta) to *Neoharaldiophyllum* gen. nov. based on cystocarp development and molecular data

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The new genus *Neoharaldiophyllum* J.C. Kang *et* M.S. Kim belonging to the tribe Myriogrammeae, subfamily Phycodryoideae of the Delesseriaceae, is described. This new genus consists of four species, namely *Neoharaldiophyllum udoense* (M.S. Kim *et* J.C. Kang) *gen. et* comb. nov. from Jeju Island Korea as the type species, *Neoharaldiophyllum nottii* (R.E. Norris *et* M.J. Wynne) J.C. Kang *et* M.S. Kim comb. nov. from the Hood Canal, Mason County, Washington, U.S.A., *Neoharaldiophyllum mirabile* (Kylin) comb. nov. from Canoe Island, San Juan County, Washington, U.S.A., and *Neoharaldiophyllum erosum* (Harvey) J.C. Kang *et* M.S. Kim comb. nov. from Garden Island, Western Australia. The morphological traits of the new genus are very similar to the genera *Haraldiophyllum* and *Myriogramme* in terms of the vegetative and reproductive structures. There are differences among the three genera in the developmental patterns of the carposporophyte: the primary gonimoblast cells of *Neoharaldiophyllum* are prostrate on the floor cells of the cavity of the cystocarp and fuse together secondarily, whereas in the two other genera they remain free without a secondary incorporation with the floor cells; the carposporangia of *Myriogramme* are borne in short chains terminating the gonimoblast filaments, while those in the other two genera are borne as solitary structures. The molecular phylogenies based on *rbc*L and LSU sequences strongly support the significance of the developmental patterns of the carposporophyte and support the separation of *Neoharaldiophyllum* from *Haraldiophyllum* in the tribe Myriogrammeae.

[PA-30]

Species boundary of *Scinaia johnstoniae* (Nemaliales, Rhodophyta) from the northern Pacific using molecular analysis

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The genus *Scinaia* has been identified in species level based on the morphological characters, such as pattern of thallus segments, size and shape of utricles, shape and layer of pigmented hypodermal cells, cortical arrangement in surface view, and location of spermatangial sori. *Scinaia articulata* from California and *S. tokidae* from Korea and Japan were synonymized as *S. johnstoniae* on the basis of morphology only. To reveal the species boundary and distribution of *S. johnstoniae*, we conducted the *rbc*L analysis for the specimens of cylindrical type *Scinaia* from Korea and California, USA. We confirmed three genetic groups of *S. johnstoniae* specimens from the type locality, California including specimens from Korea. One Korean group revealed as *S. tokidae*, distinguished from *S. johnstoniae* by utricle size, the other groups composed of *S. articulata* and *S. johnstoniae*. *S. johnstoniae* exhibited 5.0% and 7.7% interspecific divergence with *S. articulata* and *S. tokidae*, respectively. The *rbc*L analysis of *Scinaia* resolved the limitation of species identification based on the morphology only. In conclusion, two synonyms of *S. johnstoniae* should be resurrected as taxonomic entities, *S. articulata* and *S. tokidae*.

[PA-31]

Cryptic species diversity of the genus *Herposiphonia* (Rhodomelaceae, Rhodophyta) from the south-eastern coast of Spain

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In Spain, the genus *Herposiphonia* has been recorded only two species, *H. secunda* (C. Agardh) Ambronn and *H. tenella* (C. Agardh) Ambronn. These species are having considerable taxonomic confusion and controversy because of their morphological variations. *Rbc*L and COI-5P genes are well established to delimit species boundaries in red algae. We collected *Herposiphonia* specimens from the south-western Spain and confirmed three species based on the morphological difference and *rbc*L molecular analyses. Two species are identified as *H. secunda* by having d/i branching pattern and *H. tenella* by d/d/d/i branching pattern with presence of vegetative trichoblast. The third species is similar to *H. nuda* Hollenberg, by slender (50-60 μm) and long (2-3 mm) determinate branches with absence of vegetative trichoblast. In COI-5P DNA barcoding analysis, we compared our samples with 13 Hawaiian, 4 Spanish and 2 Portuguese sequences from GenBank. The results showed that these sequences were separated to several independent clades. Interestingly, only one sequence of our samples, as similar with *H. nuda*, was matched to Spanish one (KF648513). In conclusion, four species are distinguished from Spanish specimens rather than two. We need to investigate the phylogenetic relationships of Spanish *Herposiphonia* species from the Atlantic coast.

[PA-32]

Taxonomy and Phylogeny of the genus *Phymatolithon* (Hapalidiaceae, Rhodophyta)

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In the Hapalidiaceae, the genus *Phymatolithon* was established by Foslie (1898) for a single previously described species, *P. polymorphum* (L.) Foslie. The basionym of *P. polymorphum*, *Millepora polymorpha* L. is a superfluous substitute name for *Millepora calcarea* Pallas, and consequently the correct name of the type species of *Phymatolithon* is *P. calcarea* (Pallas) Adey & McKibbin. Since 1898, at least 47 specific and infraspecific taxa have been referred to the genus, and it has undergone several changes in circumscription. Currently, 15 species of *Phymatolithon* are recognized mostly based on morphological analyses. Since the original description of *Phymatolithon*, further features were provided as diagnostic characters such as the absence of arborescent thallus, monomerous thallus construction, contiguous filaments connected by cell fusions, subepithallial initials that are usually as short as or shorter than their immediate inward derivatives, rounded to flattened outermost walls of epithallial cells, absence of protective cells in spermatangial initials, branched and unbranched spermatangial filaments, and absence of a conspicuous central fusion cell in mature carposporophyte. Although only one species, *Phymatolithon repandum* has been recorded from Korea, no detailed studies have been undertaken, and past record do not indicate which species are present. The aim of this study is to provide an account of species of *Phymatolithon* occurring in Korea by detailed morphological observations and molecular works.

[PA-33]

Protoplast regeneration from male and female gametophytes of *Undaria pinnatifida*

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Protoplast regeneration is an important requisite for cellular biotechnology techniques. This work describes the regeneration of cell wall from protoplasts derived from male and female gametophytes of *Undaria pinnatifida.* A mixture of commercial enzymes (cellulase RS 1%, alginate lyase 2 U/ml and driselase 1%) was used for protoplast isolation under optimized conditions. Regeneration medium consisted on Provasoli enriched seawater (PES) supplemented with NaCl as osmoticum and 5 mM $CaCl_2$. Cell wall regeneration started after 3 hours in culture and was completed by day 5. First cell division was observed 2 days after. Regeneration of female gametophyte protoplasts started with a first asymmetric division division and, after one month in culture, typical new thallus had formed. 57% of them presented reproductive structures and in some cases (18%) callus-like structures developed from the oogonia. We also observed the development of whole plant from protoplast. In the case of male gametophyte protoplasts, regeneration was characterized by the outgrowth of multiple rhizoid-like protrusions, however no reproductive structures were observed after one month in culture

[PA-34]

New insights of the taxonomy of *Pyropia pseudolinearis* complex: Proposal a new cryptic species, *Pyropia donghaeensis* S.M. Kim et H.-S. Kim, from the east coast of Korea (Bangiaceae, Rhodophyta).

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Species delineation by using molecular markers has been widely accepted in taxonomy and brought a lot of knowledge to evaluate the evolutionary history of various algal groups, including red algal family Bangiaceae. Due to the economic importance, much molecular data of the bladed Bangiaceae (*Porphyra sensu lato*) at global scale have been accumulated. For this reason, it is easier to estimate the regional entities of the bladed Bangiaceae using DNA sequences, but there remains still some problem to fit action to the binomial Linnaean naming system for the numerous *Porphyra* sequences, which registered in GenBank as unidentified names. Our preliminary survey of the species of *Pyropia* in Korea, based on sequence analysis of molecular markers (*rbc*L, SSU, ITSI) and complemented with the information on morphology and micro-environmental habitat, revealed the occurrence of several cryptic or unreported species especially in the east coast of Korea. The dioecious oblong-lanceolate thallus of *Pyropia* in the east coast of Korea has been identified as *Py. pseudolinearis* without doubt before using molecular marker for identification. Based on *rbc*L sequences data, Kim and Kim (2011) divided *Py. pseudolinearis* complex into three species as *Py. pseudolinearis*, *Porphyra akasakae* Miura, and *Porphyra irregularis* Fukuhara. However, the three species in the east coast of Korea must be revised in detail through the expansive collection data. In this study, 75 samples of Korea and Japan *Py. pseudolinearis* complex were newly deterimined DNA sequences and reconstructed the phylogeny based on concatenated rbcL+rSSU sequence data. Our result suggested that *Py. pseudolinearis* complex is an endemic lineage in East Sea (=Sea of Japan) and northern Japan and should be identified into three taxonomic species as *Py. Pseudolinearis, Py, akasakae* (Miura) comb. nov., and *Py. donghaeensis* sp. nov., based on molecular phylogeny and biogeography. The three species, however, showed considerable genetic differences between Korean and Japenese populations. The biogeographical isolation of genetic lineages in these three species are considered a reflection of vicarient event during Quaternary climatic oscillations, which have played a major role in shaping the present geographical distribution of temperate species.

[PA-35]

New candidate species of endophytic green algae *Phlegma teres* gen. et sp. nov. (Ulvophyceae) from Korea.

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New candidate species endophytic alga was isolated from *Bryopsis rhizophora* and *Lychaete dotyana* (Ulvophyceae, Chlorophyta), which collected from Jeju and cultured in the laboratory in order to examine morphological characteristics. And a phylogenetic analysis based on chloroplast-encoded elongation factor *tuf*A gene was performed to identify this endophytic alga. In the culture, this plant was distinguished easily by morphologically. While most endophytic species were filamentous but this species did not formed a filament or thallus. This species surrounded by mucilage. Initially, only a single cell and then grows get together after formed mucilage. When it grows and forms a lump and cells divided. Vegetative cells had a chloroplast with many pyrenoids. Mature plant, nearly all cells have become sporangia. Vegetative cells had a chloroplast with many pyrenoids. Hairs were not observed. In a phylogenetic reconstruction based on the chloroplast-encoded *tuf*A gene, the sequence for the new Genus and species were clearly distinct from any the other genus sequence available for this gene. Their phylogenies support the taxonomic status of *Phlegma teres* gen. et sp. nov. as a new candidate species.

[PA-36]

Rediscovery of the *Ochromonas* type species, *Ochromonas triangulata* Wysotski, from sample of the type locality.

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Molecular markers have become a major component of any modern systematic study because they can identify and distinguish species with confidence. However, for microalgae that were described before gene sequencing was invented and have not been studied during the molecular era, the holotype is often an ink drawing. Despite being a perfectly acceptable holotype, the ink drawing cannot be used in molecular phylogenetic analyses. Furthermore, cryptic speciation, biogeographic isolation and convergent evolution are potential problems when anchoring an old species name with modern gene sequences. Therefore, to avoid possible confusion caused by misidentified microalgal culture from a different locality, the best approach is to sequence genes from alga re-collected from the type locality.

The genus *Ochromonas* is a large, polyphyletic genus containing approximately 125 species and varieties. To resolve the taxonomic and nomenclatural problems created by the polyphyly, it is necessary to include the type species. The type species, *Ochromonas triangulata* Wysotzki 1887, is described from the salt lake, Lake Veysove, in the Ukraine; however, this species was not reported again until now. It is rare that the type species goes unobserved for 130 years. In some cases, the type description is vague and this leads to doubt; however, Wysotzki's description is very thorough and includes not only the triangulate and non-triagulate cell shapes, but also descriptions and illustrations of the cyst, palmelloid cells, cell division and illustrations of what is now known as flagellar transformation. Here we report the rediscovery of *Ochromonas triangulata* from its salt lake type locality, Lake Veysove. The alga was brought into culture and re-examined. Along with light microscopical observations, we produced sequences for the nuclear encoded SSU rRNA and the plastid encoded *rbc*L and *psb*A genes. We discuss the phylogenetical position of the type species for *Ochromonas* and more broadly the uniflagellate/biflagellate and the pigmented/colorless polyphyletic assemblages within the class Chrysophyceae.

[PA-37]

Multigene phylogeny reveals pattern of evolution of the multicellularity in the Heterokontophyta SI clade.

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The heterokont algae are an exceptionally diverse group. The most recent phylogenetic analyses showed that there are three major clades, called the SI, SII and SIII clades. Only the clade SI has true multicellular organisms, which are limited to the Phaeophyceae. Interestingly phylogenetic analyses placed many filamentous algae near the Phaeophyceae and the Xanthophyceae.

To investigate the *de novo* appearance of multicellularity in the clade SI we sequenced five genes for a majority of those filamentous algae. Here we report the results of our phylogenetic analyses and light microscopic observations. The coccoid forming class Raphidophyceae was the first to diverged. Within the remaining lineages four strongly supported subclades were identified: 1) the Aurearenophyceae and Phaeothamniophyceae, 2) the Phaeophyceae and Schizocladiophyceae, 3) the Chrysomerophyceae + *Tetrasporopsis*, 4) the Xanthophyceae + *Phaeobotrys / Pleurochloridella* + *Chrysowaernella.* We will discuss the phylogenetic relationships in the clade SI and their implication on the evolution of multicellularity.

[PA-38]

Chromatophore genome of *Paulinella longichromatophora*: Changes during endosymbiotic organogenesis

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The thecate filose amoeba *Paulinella chromatophora* is a good model organism for understanding plastid organellogenesis because it has two sausage-shaped plastids termed chromatophores that were derived from an alpha-cyanobacterium. The primary endosymbiosis of *P. chromatophora* occurred relatively recently (90-140 Mya), whereas the primary endosymbiosis that gave rise to the Archaeplastida occurred before 1,500 Mya. This event was completely distinct from the major plastid organellogenesis. Up to date, three different photosynthetic *Paulinella* has been reported; *P. chromatophora*, *P. micropora*, and *P. longichromatophora*. In this study, we sequenced chromatophore genome of *P. longichromatophora*; the genome was 979,356 bp in total length, the GC content was 38.8%, and 915 genes were annotated. Multi-gene phylogeny showed that photosynthetic *Paulinella* species were monophyletic and *P. longichromatophora* clustered together with *P. micropora*. Comparative genomic analysis with *Synechococcus* species and chromatophore of *Paulinella* showed several genomic changes during endosymbiosis. Orthologous gene set of *Synechococcus* species were compared with chromatophore genome of *Paulinella* in functional group category. Oxidative phosphorylation, photosynthesis, and ribosome gene are under greater purifying selection compared to other functional categories.

[PA-39]

The genomic analysis of *Apophlaea lyallii* (Florideophyceae, Rhodophyta); the algal-fungal symbiosis

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Red algae are diverged from the other primary endosymbiosis groups more than 1,400 million years ago. During this long evolutionary history, the red algae lineages have survived and diversified as a distinct algal group which led red algae to adapt to a wide variety of environments. The genus *Apophlaea* (Florideophyceae, Rhodophyta) are well known for their resistance to various stresses including ultraviolet radiation and desiccation which are only found in intertidal zones of a New Zealand. Furthermore, the genus *Apophlaea* form mycophycobioses; obligate symbiosis with a marine fungus. However, this symbiotic relationship is a little is known about its establishment of the symbiotic relationship and their physiological mutual association. To investigate these questions, we have sequenced *Apophlaea lyallii* using Next Generation Sequencing (NGS) with various method and constructed the draft genome. In this presentation, we will briefly describe about newly sequenced genome and address the new insights on the evolutionary history of red algae brought by new genome sequences; most notably, we will comment on the algal-fungal symbiotic relationship and environmental tolerance.

[PA-40]

Pleurostomum flabellatum genomics; New paradigm to unveil the adaptation of extreme salinity

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Pleurostomum flabellatum, a member of the Heterolobosea, thrives in extremely high salt (optimal 300‰ of salinity) environment (e.g., salt pond), which is the highest among the eukaryotes. This halophilic extremophile likely developed genetic tools to overcome significant restricting components in the harsh habitats. Many heteroloboseans have adapted to various extreme environments; halophilic, acidophilic, thermophilic, and anaerobic conditions however, these lineages are considerably understudied despite their enormous ecological and morphological diversity. To investigate the molecular adaptation in halophilic extremophilic habitat of *P. flabellatum*, we have conducted whole-genome sequencing and RNA-seq. We compare genome data with the available heterolobosean genome of *Naegleria gruberi*. We predicted protein-coding sequences as well as functional annotation based on transcriptome assembly. We also performed comparative orthologous gene analysis between *P. flabellatum* and *N. gruberi*. Based on the comparative genomic analysis, 4,876 orthologous gene families (OGFs) with 4,787 OGFs groups contained sequences from the two analyzed species.

Also, a total of 14,269 annotations were determined from assembled contigs. Future more, 4,629 genes/transcripts were selected for future annotation with targeted manual curating. In this presentation, we will discuss our results in more detail.

[PA-41]

A new endophytic green algal species: *Ulvella jejuensis* sp. nov. (Ulvellaceae, Chlorophyta) from Korea.

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Benthic marine macroalgae are host to a wide range of green, red, and brown endophytic algae. Traditionally, these have been assigned to genera such as *Ulvella* (=*Acrochaete*) in green algae. Recently, we isolated an endophytic alga from *Lesleigha yamadae*; it had been collected from Moon Island, Jeju and cultured in a laboratory, so that we could examine its morphological characteristics. Phylogenetic analysis based on the chloroplast-encoded elongation factor *tuf*A gene was performed to identify this endophytic alga. In the culture, this endophytic alga was filamentous and formed clumps. Branching was irregularly alternate. The cylindrical part of the cells measured 4–8 µm in diameter and were up to 4–5 times longer. Each cell had 2-4 pyrenoids without hairs. Sporangia developed from the cylindrical cells. In a phylogenetic reconstruction based on the chloroplast-encoded *tuf*A gene, the sequences for the *Ulvella jejuensis* sp. nov. were clearly distinct from any other *Ulvella* sequence available for this gene. Their phylogenies support the taxonomic status of *Ulvella jejuensis* sp. nov as a new species.

[PA-42]

Nitrogen uptake and growth of thalli of *Pyropia yezoensis* under several culture conditions

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Pyropia is one of the most important maricultured seaweeds in the world. Due to its commercial economic value as food, this species has been cultivated for several hundred years in Asia. However, occasionally, nitrogen has been considered the limiting nutrient at *Pyropia* cultivation farms. Chlorosis event damage was increased by the lack of nitrogen concentrations. We investigated the dissolved inorganic nitrogen (DIN) uptake rates in thalli of *Pyropia yezoensis* under several culture conditions. The experiment was conducted with nine DIN concentrations (0.23 ~ 312.90 μmol L^{-1} DIN). Conditions common to all treatments were one temperature (8℃), one photon flux density (PFD, 100 μmol photons m^{-2} s^{-1}), and one photoperiod (12:12-h, light–dark cycle) with light provided by cool-white fluorescent tubes. The rate of nitrogen uptake per hour was the highest at 8.06 μmol L^{-1} DIN concentrations and the lowest at 0.23 μmol L^{-1} DIN concentrations. Also, the nitrogen uptake rate was significantly lowered at higher DIN concentrations than 8.06 μmol L^{-1} ($p < 0.05$). The relative growth rate (%) was the highest in the 23.61 μmol L^{-1} DIN concentrations and the lowest in the 0.79 μmol L^{-1} DIN concentrations ($p<0.05$). Here, we describe the effects of nutrient concentrations on nitrogen uptake in thalli of *P. yezoensis.*

PB. 생태

[PB-01]

Short-term variations of the phytoplankton species composition and environmental parameters in Youngsan River estuary

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This study aims to investigate the tidal effects during neap-spring tide on the phytoplankton species composition and environmental parameters in Youngsan River estuary at sampling station, Station A, which is situated near the Youngsan dike. The study was conducted by the Marine Microbial Ecology Laboratory of Mokpo National Maritime University during12th-13th August (wet season neap tide) and 17th-18th August (wet season spring tide on year 2012. The physical data were obtained onsite through the use of YSI* Model 6600 multiparameter. Phytoplankton were identified through compound light microscopy. The selected parameters include freshwater discharge from the dike and tide level, water temperature (℃), salinity (psu), and phytoplankton species composition.

There were no significant changes observed between the physical parameters as the tide level changes. The average phytoplankton cell count during neap tide was 1121.06 cell/mL compared to the 633.41 cell/mL during spring tide. Species group differentiation showed that diatoms were abundant during the neap tide while dinoflagellates dominated during spring tide. The diatom *Nitzschia sp.* dominated during neap tide while the cyanobacteria *Microcystis aeruginosa* dominated during the spring tide. The number of species range from 6 to 14 species with an average of 9 species during neap tide while during spring tide, the range was 4 to 9 species with an average of 5.41 species. Based on the results of the Sørensen’s index (similarity coefficient), there is only 36.92% similarity between the phytoplankton community during neap and spring tide. The results of this study could provide more understanding on estuarine dynamics in Youngsan River estuary.

[PB-02]

Ecological Study in Macroalgal Assemblage of Ulleungdo on East Coast of Korea

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A subtidal marine benthic algal flora vegetation at two sites in Ulleungdo was investigated to clarify the community structure by a quadrat method in May and August 2016, respectively. A total of 83 species including 6(7.2%) of green algae, 24(28.9%) of brown algae, 53(63.9%) of red algae were collected and identified. The dry weight biomass in May is 68.7 g dry wt. m^{-2} and August in 282.6 g dry wt. m^{-2} during the study period. The maximum biomass depth was 95.7 g dry wt. m^{-2} middle zone in May and August was 340.0 g dry wt. m^{-2} middle zone. In May, the dominant species were *Sargassum horneri*, *Undaria pinnatifida* in upper zone, *Myagropsis Myagroides*, *Peyssonnelia caulifera* in middle zone, *Halopteris filicina*, *Agarum clathratum* in lower zone. In August, the dominant species were *Eisenia bicyclis*, *Amphiroa beauvoisii* in upper zone, *Ecklonia cava*, *Eisenia bicyclis* in middle zone, *Ecklonia cava*, *Carpomitra costata* in lower zone. In May the R/P and (R+C)/P value reflecting flora characteristics were 2.5 and 2.8 and August were 2.4 and 2.9 respectively. Community structure of subtidal benthic marine algae at Ulleungdo was similar with previous studies.

[PB-03]

영산강 하구의 담수유입에 따른 생태적 영향

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본 연구에서는 목포 영산강 방조제에 의한 인공적인 담수방류 전후로 미치는 수질환경 및 생태적 변화에 대한 현장조사 자료를 분석하여 하구역 관리를 위한 연구기초자료를 제공하고자 하였다. 현장조사 정점은 하구언 내 수역 1개의 정점(St.R)과 하구언 아래 해역 3개의 정점(St.1-3)을 선정하였고, 수문개방에 따른 방류 전후 조사가 실시되었다. 수질은 YSI(6600V2, YSI, USA)를 이용해 각 정점의 수온, 염도, DO, pH등을 측정되었고, 식물플랑크톤의 Chlorophyll *a* 자료 분석을 통해 생태학적 영향을 조사하였다. 수온과 DO는 방류 전 담수역(St.R)에서 해수역(St.1-3)에 비해 높게 측정되었고, 염분과 pH는 해수역(St.1-3)에서 담수역(St.R)에 비해 높게 확인되었다. 방류 후에는 수온과 DO가 담수의 영향으로 해수역(St.1-3)에서 높아진 값을 보였고, 염도는 방류 전 후 15.32 psu로 절반가량 떨어졌으나 시간경과 후 회복 되었다. pH는 방류 전후 차이값이 적었다. 식물플랑크톤 크기구조 변동 비율을 비교한 결과, 담수역에서 방류 전 보다 방류 후에 Micro size Chl.*a* 비율이 증가하고 Nano size Chl.*a* 비율이 감소하는 경향을 보였고 해수역(St.3)에서는 반대경향을 나타냈다. Chl.*a* 전체양은 방류 전 담수역(St.R) 10.28 ㎍ L^{-1}, 해수역(St.1-3) 0.37-0.45 ㎍ L^{-1} 값으로 측정되었고 방류 후 담수역(St.R) 5.16 ㎍ L^{-1}, 해수역(St.1-3) 1.43-2.20 ㎍ L^{-1} 으로 담수역의 식물플랑크톤이 해수역으로 방류되어 영향을 미치는 것을 확인하였다. 이와 같이 방조제의 담수 방류에 의한 환경적 조건은 담수와 해수에 각각 영향을 미치게 되어 생태적 변화가 불가피하여 기존 환경을 우점하던 종과 달리 기회종이 서식할 조건이 형성될 것으로 사료된다.

[PB-04]

Seasonal growth and reproduction of *Gelidium coreanum* and *G. elegans* (Rhodophyta) from the east coast of Korea

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Despite its production of agar and agarose, growth and reproduction of *Gelidium* species in Korea remain less studied. To compare growth rate, we have seasonally surveyed length and reproduction of plants in *G. coreanum* and *G. elegans,* from the east coast of Korea, where is mostly under influence of cold temperate water. *Gelidium coreanum* plants grew attached to rocks slightly buried in the sand on wave-exposed beaches, usually exposed to strong waves. The maximum length was 3.51 cm in August. Plants were sterile in March and May, while they formed tetrasporangia in August. *Gelidium elegans* plants grew attached to artificial cement bed in a small fishery harbour, very sheltered location. The maximum length was 9.20 cm in August. Plants were vegetative in March, while they formed tetrasporangia in May and August. *Gelidium elegans* had more branches, forming more biomass and revealed early reproduction than *G. coreanum*. Our on-going work is to develop suitable species of mass culture for increasing biomass of agar-producing red algae.

[PB-05]

목포해역 식물플랑크톤 Chlorophyll *a*의 계절별 크기구조

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본 연구에서는 계절적인 환경변화가 목포해역 내 식물플랑크톤 Chlorophyll *a*에 어떤 영향을 미치는지 확인하고자 조사를 수행하였다. 조사지역인 목포해역은 주요 채널을 따라 6개(A~F)의 정점을 지정하여 2014년12월~2015년10월까지 총 4차례에 걸쳐 계절별 조사를 실시하였다. 또한 환경인자로 작용할 수 있는 수온, 염분, pH, 용존산소와 식물플랑크톤의 생체량 및 크기구조 변동을 파악하여 서로의 상관성을 분석 하였다. 수온은 겨울, 여름 차이로 최대 14.6℃ 차이를 보였고, 염분 (29.68±3.3 psu)와 pH (7.8±0.3) 2가지 환경인자는 연 중 일정하게 유지되었다. 용존산소는 가을철 (7.7±0.3 mg/L)을 제외한 겨울, 봄, 여름 모두 10.4±0.1 mg/L 수준으로 유지되고 있었다. 식물플랑크톤 크기구조 변동 비율을 계절별로 확인한 결과 전반적으로 봄철에 크기가 작은 식물플랑크톤(Nano, Pico size)이 77.95%로 높은 비율로 우점하는 경향을 나타냈다. 그 외 겨울 (62.28%), 여름 (54.96%), 가을 (45.81%) 순으로 작은 식물플랑크톤 비율을 확인하였다. Chl.*a* 생체량은 모든 정점에서 여름, 가을, 봄, 여름 순으로 많게 확인되었고 그 중 담수방류 시 가장 영향이 큰 St. A 정점에서 4계절 평균량이 51.05 ㎍ L^{-1}으로 가장 높게 측정 되었다.

[PB-06]

Holocene environmental changes from a diatom record in Korea (Reservoir Gonggeomji, Sangju City)

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The paleo-environmental history was reconstructed using fossil diatom analysis of sediment core GG01, 02, 03 and 04 from the Reservoir Gonggeomji-si Korea. The diatom record in core sediment samples revealed well-defined hydrological change and paleo-environmental conditions during the Holocene period. The fossil diatom assemblages was composed of benthic diatom in freshwater. The highest diatom concentrations in GG01, GG02, GG03 and GG04 were at 325–225 cm, at 300–225 cm, at 300–225 cm and 250–175 cm, respectively. And, the species richness and diversity were also very high. The Cymbella, Eunotia, Gomphonema, Gyrosigma, Navicula and Pinnularia were the dominant genera in four core sediments. The distribution of fossil diatom in sediment core and the sedimentological analysis indicated the paleo-ecological environments changes in Reservoir Gonggeomji, which were resulted by freshwater input and human activity (e.g. build an embankment and farmland) during the last about 2,300 years.

[PB-07]

Akashiwo sanguinea 적조 발생 및 미 발생시의 환경변화 차이

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Akashiwo sanguinea 적조 발생시의 환경요인 변화 및 식물플랑크톤 군집의 1년의 변화를 파악하기 위하여 2016년 6월 27일부터 2017년 6월 16일까지 주 1회를 기본으로 하여 조사를 실시 하였으며, *A. sanguinea* 적조 발생했던 33일간(2016년 11월 11일~12월 13일) 매일 조사를 거제 장목만에서 수행하였다. *A. sanguinea*는 2016년 10월 31일부터 2017년 1월 30일까지 관찰되었으며, 적조 발생시 *A. sanguinea*의 최대 개체 수는 2,935 cells/mL 이었다. *A. sanguinea*는 저수온기에 적조를 유발시키는 종으로, 적조 발생 당시 평균수온은 15.4℃로 나타났다. 평균염분은 31.9psu로 큰 변화를 보이지 않은 반면, 용존산소는 *A. sanguinea*의 개체 수에 따라 급격히 증가(최대: 13.84 mg/L)하였다가 감소하는 경향을 보였고, 용존무기인(발생 전: 0.379μM, 발생시기: 0.571 μM, 발생 후: 0.131 μM)과 용존규소(발생 전: 11.29μM, 발생시기: 22.9 μM, 발생 후: 6.68 μM)는 적조 발생기간 동안 높은 농도를 보인 반면, 용존무기질소(발생 전: 4.7μM, 발생시기: 2.3 μM, 발생 후: 3.8 μM)는 적조 발생기간 동안 감소하였다. 박테리아 군집은 *A.sanguinea* 적조 발생 이후 용존무기인이 감소를 보일 때, 점점 증가하였으며 당시 최대 개체 수는 29 x10^6 cells/mL로 나타났다. 본 연구결과 *A. sanguinea*의 적조발생은 저온 시에 발생되며, 적조 발생시 용존무기질소를 급격히 소모하는 반면, 용존무기인은 크게 소모하지 않는 것으로 판단된다.

[PB-08]

Effects of salinity on growth and photosynthetic performance of *Ulva ohnoi* (*Chlorophyta*)

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제주 연안의 유해녹조대발생은 매년 여름철에 발생하여 경제적으로 큰 피해를 야기하고 있다. 유해녹조대발생의 원인종은 *Ulva pertusa*와 *U. ohnoi*로 알려져 있지만 *U. pertusa*에 비해 *U. ohnoi*의 생리생태학적 정보는 부족한 실정이다. 본 연구에서는 염분 구배에 따른 *U. ohnoi*의 광합성 생리생태 연구를 수행하였다. 연안환경에서 강우 및 지하수 유입에 의해 변동가능한 염분조건(15, 20, 25, 30, 35 psu)을 조성하여 8일간 노출실험을 진행하였고, 성장 및 광합성률(산소발생률 및 엽록소 형광분석)을 측정하였다. 성장율은 염분 구배에 의한 유의한 차이를 보이지 않았다. 또한 엽록소 형광분석 및 산소발생률의 결과에서도 염분에 의한 차이는 관찰되지 않았지만 저염분 조건인 15 psu와 20 psu에서는 오히려 산소발생률이 약간 증가하는 경향을 보였다. 이러한 결과는 제주지역의 유해녹조대발생 원인종인 *U. ohnoi*가 넓은 염분범위에 생리적으로 잘 적응하는 것을 알 수 있었고, 강우의 영향을 많이 받는 여름철에도 저염 스트레스를 받지 않는다는 것을 예측할 수 있다.

[PB-09]

Surveys on high-temperature resistant natural populations of *Pyropia* species in Korea

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Species of *Pyropia* are commercially important edible red algae in Korea, regarded as a low energy density food, rich in dietary fiber and containing high contents of vitamins, minerals, and antioxidants. In Korea, the yearly production of *Pyropia* is ca. 250,000-400,000 ton/yr and worth up to $ 2 billion dollars, and the farming proceeds from October to March. The *Pyropia* gametophytes (i.e. the blade stage) are not grown in the summer months in the sea farms, as they prefer colder seawater and air temperatures and deteriorate fast at temperatures exceeding 20℃. Due to increasing domestic consumption and export, more demands for *Pyropia* production have arisen during the last decade. In order to find high-temperature resistant strain or *Pyropia*, which can tolerate seawater temperature over 20℃ we surveyed the western and southern coasts of Korea and found several natural populations of the gametophytes growing in the warmer months. Carpospores released from the blades in the laboratory were settled on the suspended dead oyster shells, and the conchocelis phase of two *Pyropia* species was obtained. The conchospores released from the mature sporophytes developed into blades, completing the life cycle in 1 year. The *rcb*L and SSU rRNA gene sequencing results showed that our temperature-resistant strains belonged to the clade including *P. haitanensis* and *P. dentata* from Japan, China and Taiwan, but are different from the strains recorded in those countries. Our molecular-phylogenetic analyses showed that sequences in each group (i.e. '*haitanensis*' and '*dentata*') were very heterogeneous; for example, in *rbc*L gene, different isolates of *P. haitanensis* and *P. dentata* had 95.8-100% and 93.3-100% identity, respectively. In SSU rRNA gene, different isolates of *P. haitanensis* and *P. dentata* had 74.7-99.7% and 82.7-78.2% identity, respectively. Even isolates of the same species from the same country varied significantly suggesting the locality of each strain overlapping in Far Eastern countries.

[PB-10]

한국 연안에 서식하는 군소(*Aplysia kurodai*)의 섭식생태

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군소 (*Aplysia*)속은 연체동물문, 복족강 (Gastropoda), 군소목 (Aplysiomorpha), 군소과 (Aplysiidae)에 속하는 1년생 연체동물로 전 세계에 약 40여종이 있으며, 그 중 23종이 인도양과 태평양에, 12종이 대서양에 서식하고 있고 몇몇 종은 지중해에서 보고되고 있다. 국내의 군소에 관한 연구로는 Kim and Choe (1981)가 군소 *(A. kurodai*)는 울릉도와 독도 연안에서 서식하는 것으로 보고한 후, Choe and Lee (1994)가 독도 연안에서 군소와 검은테군소 (*A. parvula*) 두 종을 보고하였다. 이후 Seo (2009)는 부산 연안에서 군소의 성장과 생식주기를 밝혔으며 최근에는 Ryu et al. (2012)이 독도에서 군소, 검은테군소, 안경무늬군소 (*A. oculifera*) 및 갈색군소 (*A. sagamiana*) 4종을 추가로 보고하였다. 그러나 군소의 주먹이인 해조류에 대한 연구는 없는 실정이다.따라서 본 연구는 해조류를 주 먹이원으로 하는 군소의 섭식생태를 밝힐 목적으로 동해안의 추암, 북평, 대보와 남해안의 청산도 지리 연안에서 잠수조사를 통해 채집한 군소의 위내용물 분석을 수행하였다. 남해와 동해에서 나타난 군소의 주 먹이 중 서식지에 관계없이 출현하는 종은 구멍갈파래 (*Ulva pertusa*), 고리매 (*Scytosiphon lomentaria*), 참도박 (*Grateloupia elliptica*), 잔금분홍잎 (*Acrosorium polyneurum*), 마디잘록이 (*Lomentaria catenata*)이로 나타났고, 이상의 연구결과 군소는 서식지 주변에 서식하는 해조류를 주로 먹으며 특정한 종의 해조류를 주 먹이로 하는 경향은 나타나지 않았으나 주로 녹조류와 홍조류를 주 먹이로써 선호하는 경향을 나타내었다. 그러나 군소의 먹이 선호도와 선택성에 대해서는 다양한 먹이 해조류 공급을 통한 사육실험을 통해 명확히 구명할 필요가 있을 것으로 판단된다.

[PB-11]

갯벌에서 광량에 따른 저서미세조류의 영양염 흡수율

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저서미세조류(microphytobenthos)는 갯벌의 주요한 일차생산자로서 연안생태계의 영양염순환에 중요한 역할을 하지만 정량화 연구는 많이 이루어지지 않았다. 본 연구에서는 저서미세조류가 서식하는 서천 갯벌에서 저서미세조류에 의한 영양염 흡수율에 대한 연구를 수행하였다. 현장에서 채집한 퇴적물을 순환식 배양수조에 넣은 후 4 개의 광조건(45, 90, 145, 220 μmol photons m^{-2} s^{-1})에 일주일간 배양하였고, 해수를 채집하여 분광광도법으로 질산염(NO_3^-), 아질산염(NO_2^-), 인산염(PO_4^{3-}) 농도를 지속적으로 모니터링 하였다. 그 결과 모든 영양염은 시간이 지남에 따라 농도가 낮아지는 경향을 보였다. 아질산염의 흡수율은 광량에 따라 큰 차이가 나타나지 않았지만, 질산염과 인산염 흡수율은 유의하게 증가하였다. 본 연구에서 질산염+아질산염과 인산염의 흡수율 비는 1.46 으로 계산되었다. 이 결과를 바탕으로 저서미세조류는 광량에 따라 영양염 제거 효율이 높아지는 것을 알 수 있었다. 특히 저서미세조류의 광저해 현상이 나타나지 않는 특성을 고려했을 때 갯벌의 잠재적 영양염 흡수율이 매우 높을 것으로 예측할 수 있다.

[PB-12]

통영해역에서 출현하는 식물플랑크톤 변동 특성 1: 차세대 염기서열 및 현미경 분석을 통한 규조류의 변동 차이

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차세대 염기서열 (NGS) 및 현미경 분석을 통한 통영해역에서 규조류에 대한 변동 특성을 파악하기 위해 2013년 10월부터 2016년 2월까지 매월 통영 해역 두 정점을 선정하여 채집을 실시하였다. 현미경 분석결과, 규조류의 개체수는 11-2,116 cells mL^{-1} (평균 140±370 cells mL^{-1})이며, 전체 식물플랑크톤의 8.5-100.0% (평균 84.3.0±17.1%)를 차지하였다. 규조류의 계절적 주요 출현 양상을 살펴보면, *Chaetoceros* 속(*C. curvisetus, C. debilis, C. decipiens*)과 *Pseudo-nitzschia pungens*는 여름과 가을, *Asterionellopsis glacialis*는 가을, *Skeletonema dohrnii-marinoi* complex는 겨울, *Thalassiosira* sp.와 *Nitzschia* sp.는 가을과 겨울에 높게 출현하였다. 21,759~222,006 (평균 109,010±46,087)의 read counts의 NGS 분석결과, 주요 규조류는 *Chaetoceros* groups, *Thalassiosira-Shionodiscus-Minidiscus* group, *Pseudo-nitzschia* group, *Skeletonema* groups, *Cerataulina pelagica*, *Hemiaulus-Campylosira* group으로 나타나, 현미경 분석의 우점종과 일부 차이를 보였다. NGS 분석을 통한 계절적 변화는 현미경 분석과 유사하였다. 형태학적 분류는 연구자의 분류학적 지식 및 장기간의 숙련이 필요한 반면, NGS 분석은 다량의 시료를 빠르게 분석할 수 있다. 그러나, 유전자의 분석 부위 및 분석 길이에 따라 종 수준의 분석의 어려움 및 결과의 차이를 보인다. 따라서, 두 방법을 상호 보완할 수 있는 분석 방법의 개발이 필요하며, 이를 통하면, 더 정확한 규조류의 생태계 변화를 이해할 수 있을 것이다.

[PB-13]

Abundance of three *Alexandrium* species in the South Sea, Korea during the summer 2017

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Alexandrium, a major genus of paralytic shellfish poisoning (PSP) toxin producing red-tide forming dinoflagellates, has been found around the coastal area of Korea and worldwide, and causes significant damages in aquaculture industry, human health and the marine ecosystem. Although routine monitoring the harmful algae is important to prevent or reduce these damages, identifying and precisely quantifying *Alexandrium* species in the field are challenging tasks. Here, we introduced a new effective technique using droplet-digital polymerase chain reaction (ddPCR) to quantify the abundance of three *Alexandrium* species targeting the internal transcribe spacer (ITS) in the marine environment. The species-specific ITS primers were validated against purified DNAs from related genres by conventional PCR and the ITS copy numbers per each cell were acquired using the known cell amounts. The species-specific ITS copy number by ddPCR was applied to estimate the abundance of *Alexandrium* species in the environmental samples collected in the nearshore and offshore of southern Korea in August 2017. *A. affine* was a dominant species found in the wide area, and also three *Alexandrium* species were differently distributed in spatially. The method offer not only identifying species, but quantifying each species accurately. Our highly sensitive approach to determine the abundance of three *Alexandrium* species, *A. affine, A. catenella*, and *A. pacificum*, can be applied in quantifying other *Alexandrium* species and harmful algae, which is efficiency in time- and labor-saving manners.

[PB-14]

Quantification of inorganic carbon removal efficiency by *Pyropia* aquaculture bed

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연안에 서식하는 해조류 식생의 높은 생산력은 해수 중 많은 양의 이산화탄소를 필요로 하기 때문에 해양의 탄소 격리(carbon sequestration)에 중요한 역할을 한다. 특히 고밀도의 해조류 양식은 높은 이산화탄소 및 영양염 제거 효율을 보이기 때문에 인간활동으로 인해 야기된 산성화 및 부영양화와 같은 환경변화에 긍정적인 역할을 할 것으로 기대하고 있다. 본 연구에서는 남서해안에 분포하는 김 양식장 3곳에서 김 엽체를 채집하여 2016년 12월에서 2017년 3월까지 광합성률을 측정하였다. 그 결과 김 양식이 이루어지는 시기 동안 광합성률은 양식장 위치와 무관하게 유사한 광합성 능력을 보이고 있었다. 광합성 결과를 바탕으로 무기탄소 흡수율과 광량의 비선형 회귀 방정식을 얻을 수 있다. 또한 현장 광량과 김 양식 생산량을 바탕으로 김 양식장의 순 생산량을 추정이 가능하며, 이를 바탕으로 김 양식장의 잠재적 무기탄소 제거 효율을 평가할 수 있다.

[PB-15]

Effect of red algal blooms on trophic structure of macrobenthic food web in the southern coast of Korea revealed by C and N stable isotope analyses

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Red algal blooms occur over the world and are known for playing an important role in modifying ecosystem structure and function. This study aimed to evaluate the effect of red algal blooms, *Cochlodinium polykrikoides*, on trophic structure of the macrobenthic food web in the southern coast of Korea. We compared the community structure of phytoplankton and trophic structure of macrobenthic consumers between July (bloom season) and October (non-bloom season) in the coastal waters around Namhae Island, using HPLC and stable isotope analyses. Significant differences in phytoplankton biomass and community composition (dinoflagellates to diatoms) were observed between two seasons. Temporal variations in the δ^{13}C and δ^{15}N of phytoplankton-derived and sedimentary organic matters were determined, displaying that their isotope values in the bloom season were higher than those in the non-bloom season. Similarly, with the exception of several non-selective deposit feeders, more ^{13}C- and ^{15}N-enriched values for most macrobenthic consumers were found in the bloom season than in the non-bloom season. Considering that macrobenthic consumers and their potential food sources had relatively higher values with a significant elevation in the bloom season, our results suggest the increased availability of organic matter derived from *C. polykrikoides* in the bloom season. Finally, our findings suggest that coastal food webs might be characterized by isotopic changes due to the red algal blooms that seem to influence the trophic contribution of organic matter sources to the macrobenthic consumers.

[PB-16]

춘계 제주도 연안의 유독 착생 와편모류 *Ostreopsis*의 분포와 분자계통학적 위치

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최근 지구 온난화의 가속화에 따라 국내 연안에서 열대 및 아열대성 유독 와편모류의 출현이 보고된 바 있다. 본 연구에서는 2017년 4월 춘계 제주 연안에서 총 7개의 정점(협재, 이호테우, 함덕, 성산, 표선, 남원, 사계)을 선정하여 해조류에 부착하여 서식하는 유독성 착생 와편모류 *Ostreopsis*의 분포를 조사하고 분자계통학적 분석을 실시하였다. 본 연구 결과에서 수온은 15.7℃ - 34.9℃의 범위로 정점 2(이호테우)에서 가장 높게 나타났고, 정점 5(표선)에서 가장 낮았으며, 염분은 33.4 ~ 34.9psu의 범위로, 정점 5(표선)에서 가장 높았으며 정점 2(이호테우)에서 가장 낮았다. 본 연구해역에서 정점 5를 제외한 6개의 정점에서 모두 *Ostreopsis* sp.가 출현하였으며, 그 중 정점 6(남원)에서 출현한 홍조류인 참지누아리(*Grateloupia filicina*)에서 단위 무게(g)당 *Ostreopsis*의 출현밀도가 243 cells/g으로 가장 높은 출현밀도를 나타내었고, 정점 3(함덕)에서 출현한 갈조류 지충이(*Sargassum thunbergii*)에서 2 cells/g를 나타내어 가장 낮은 출현밀도를 나타내었다. 분자계통학적 분석을 위해 각 정점에서 *Ostreopsis*를 단일세포로 분리 배양하여, LSU rDNA (D8/D10 영역)를 이용하여 분자계통수를 분석한 결과, 현재까지 알려진 *Ostreopsis*의 9개 분기군 가운데, 본 연구해역에서 출현한 *Ostreopsis*는 모두 *Ostreopsis* sp. 1 분기군에 속하는 것을 확인하였다. 이 그룹은 다른 아열대 및 열대 해역에서는 지금까지 출현이 보고되지 않았으며, 본 연구해역을 비롯하여 온대역인 일본 연안에서만 분포하는 것으로 보고되었다. 따라서, 향후 제주에서 출현한 *Ostreopsis*의 기원과 유입경로 및 온대기후에서 적응한 수온 범위에 대한 추가적인 연구가 필요하다. 뿐만 아니라, 다른 분기군에 비해 *Ostreopsis* sp. 1은 가장 강한 독성을 가지는 것으로 알려져 있어 향후 우리나라에서 분리한 *Ostreopsis*의 독성과 독의 추이에 대한 연구가 필요하다.

[PB-17]

한국산 방사무늬김(*Pyropia yezoensis*)의 건조 스트레스에 의한 붉은갯병(red rot disease) 감염률 비교

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방사무늬김(*Pyropia yezoensis*, Rodophyta)은 일반적으로 조간대에 서식하기 때문에 간조 때의 높은 염분과 강한 광, 건조 스트레스 등의 극심한 환경에 노출된다. 2016년부터 2017년까지 우리나라 주요 김 양식장을 대상으로 붉은갯병균(*Pythium chondricola*)에 의한 붉은갯병 발병률을 비교해 본 결과 전남지역(해남)이 전북지역(군산)보다 김양식 기간 동안 높은 발병률을 보였다. 두 지역은 각각 노출식, 무노출식 부류식으로 양식방법에 차이가 있으므로, 지역간 양식방법에 따른 붉은갯병의 발병률을 확인하기 위하여 건조 스트레스에 따른 붉은갯병 감염률을 실내실험으로 비교해 보았다. 감염 후 48시간 후에 관찰하였을 때 30분에서 1시간 건조 조건에서는 전체 엽체들 중 30%가 감염되었지만, 2시간에서 3시간 사이의 건조 조건에서는 감염률이 70~80% 로 증가하였다. 반면 무노출 실험군은 실험 초기 대비 40%만 감염되었다. 붉은갯병에 감염된 김의 감염 진행율을 보기 위하여 건조 스트레스를 2시간 준 다음 48시간 후 감염면적을 관찰하였다. 그 결과 무노출 실험군은 감염 초기 대비 239배로 감염면적이 증가한 반면에, 건조스트레스를 주었던 김은 감염면적이 65배만 증가하였다. 따라서 본 실내실험 결과 김의 건조 스트레스는 질병의 진행을 저해시키지만 일정시간 이상의 노출은 오히려 발병률을 증가시켰다. 앞으로 다양한 온도 및 광 조건하에서의 상관관계와 야외에서의 실험을 통하여 현장적용 가능한 기초자료가 필요할 것이다.

[PB-18]

Practicality of mitochondrial marker for diatoms community monitoring of the west coast of Korea

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The diatoms are ubiquitous and an important primary producer in coastal ecosystems. They are involved in carbon, nitrogen, and silicate exchanges between the water column and sediments as part of the biological pump. Despite of ecological importance of diatoms in mudflat, systematics and ecological studies have largely relied on morphological and ultrastructural characteristic and handful genes of nuclear and plastid i.e., LSU and SSU rRNAs, and *rbc*L. In present study, we used all available mitochondrial genomes (mtDNA) of diatoms from public DB (10 spp) and including newly determined mtDNAs, such as two benthic species, *Berkeleya fennica* TA424 GenBank accession NC_026126 (35,509 bp, 29.7% GC) and *Navicula ramosissima* TA439 NC_031848 (48,652 bp, 31.7% GC) isolated from the Taean, and one pelagic species, *Skeletonema marinoi* JK029 NC_028615 (38,515 bp, 29.7% GC) isolated from an intertidal site of the Sihwaho, the west coast of Korea. All CDS of mtDNAs were aligned and compared for new primer sets. Based on the statistical tests and preliminary sequencing by using culture strains, we selected three markers (cob, cox2, and nad5) for diatoms community monitoring on the west coast of Korea. We described and discussed new markers' theoretical and practical utilities for diatoms monitoring based on preliminary results of field samples from the Geunsoman mudflat.

[PB-19]

Impact of ocean acidification and warming on chlorophyll *a* fluorescence and growth of the canopy forming alga *Sargassum horneri*

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Recently, canopy forming brown alga *Sargassum horneri* received peculiar attention as an invasive seaweed at the West Coast of United State. Also, drifting patches of *S. horneri* are frequently observed around South Sea of Korea. Thus, forecasts of future population trajectories of *S. horneri* is quite a necessary to reduce the damage caused by drifting *S. horneri*. In this study, indoor mesocosm study was conducted to evaluate ecophysiology under simulated future climate conditions at two life stage of *S. horneri* (embryo and adult thallus). Three experimental conditions (acidification: high CO_2 + ambient temp., warming: ambient CO_2 + high temp., and greenhouse: high CO_2 + high temp.) were established with well-controlled carbonate chemistry system. Photosynthetic performance was measured using PAM fluorometry (Diving PAM, Walz, Germany) after 7 days exposure to experimental treatments. Results indicate that photosynthesis of embryo was not significantly influenced by acidification, but was increased under warming and greenhouse conditions. Also, similar tendency of photosynthetic properties of adult thallus was represented under simulated future ocean conditions. Based on this study, seawater warming create more positive ocean conditions for photosynthesis of embryo and adult thallus of *S. horneri* than seawater acidification.

[PB-20]

Mapping distribution of cysts of recent dinoflagellate and *Cochlodinium polykrikoides* using next-generation sequencing and morphological approaches in South Sea, Korea

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The total dinoflagellate cyst community and the cysts of *Cochlodinium polykrikoides* in the surface sediments of South Sea (Tongyeong coast), South Korea, were analysed using next-generation sequencing (NGS) and morphological approaches. Dinoflagellate cysts can be highly abundant (111–4,087 cysts g-1 dry weight) and have diverse species composition. A total of 35 taxa of dinoflagellate cysts representing 16 genera, 21 species (including four unconfirmed species), and 14 complex species were identified using the NGS analysis. Cysts of S*crippsiella* spp (mostly *Scrippsiella trochoidea*) were the most dominant and *Polykrikos schwartzii*, *Pentapharsodinium dalei*, *Ensiculifera carinata*, and *Alexandrium catenella/tamarense* were common. Thus, a combination of NGS and morphological analysis is effective for studying the cyst communities present in a given environment. Although *C. polykrikoides* developed massive blooms during 2013-2014, microscopy revealed low density of their cysts, whereas no cysts were detected by NGS. However, the vegetative *C. polykrikoides* not appeared during 2015-2017 in spite of the observation of *C. polykrikoides* cysts. This suggests that the *C. polykrikoides* blooms were not due to development of their cysts but to other factors such as currents transporting them to a marine environment suitable for their growth.

[PB-21]

남, 동해 하천 하구역의 부착규조를 이용한 수생태계 건강성 평가

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남, 동해 하천의 하구역을 대상으로 총 53개 지점에서 2016년 5월과 9월에 환경요인 및 부착규조군집과 부착규조를 이용한 수생태 건강성 평가를 실시하였다. 이번 조사에서 출현한 부착규조류는 2목 3아목 9과 40속 247종 27변종 2품종으로 구성된 총 276종이 출현하였고 *Achnanthes minutissima, Navicula atomus* var. *permitis, Nitzschia inconspicua, Nitzschia fonticola* 와 *Nitzschia frusturum* 등이 주요종으로 출현하였다. 1차 조사 시 *N. atomus* var. *permitis*는 53개지점 중에 12지점에서, *N. inconspicua*는 8지점에서 우점종으로 출현하였고, 2차 조사 시 *N. inconspicua*는 19지점 지점에서, *A. minutissima*는 7지점에서 우점종으로 출현하였다. 상관분석 결과, 염도와 전기전도도가 0.87 정도의 높은 상관을 보였으며, COD와 탁도, DO와 총인이 비교적 높은 상관을 보였다. 또한 DAIpo와 TDI는 0.73의 상관을 보였다. 부착규조를 이용하여 수생태계의 건강성을 평가한 결과, 동해권 하구역과 남해권 하구역의 평균 TDI는 각각 35.4와 22.9로 나타나 동해권 하구역이 남해권 하구역보다 TDI가 다소 높았으나 두 권역 모두 D등급(나쁨)으로 평가되었다.

[PB-22]

통영 연안 해역에서 여름철 Chlorophyll *a* 연속 관측 및 식물 플랑크톤 군집 변화

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통영 해역에서 여름철 chlorophyll-*a* 연속적인 변화 및 식물플랑크톤 군집의 변화를 파악하기 위하여 2017년 7월 29일부터 9월 28일까지 60일간 연속 관측 및 주 1-2회 식물플랑크톤 군집을 분석하였다. 연속 관측 정점은 통영 바다목장 기지에서 수행하였으며, multi-parameter(YSI EXO2 sonde)를 표층 1.5 m에 설치하여 매 5분 간격으로 수온과 chlorophyll-*a* 및 기본 환경요인(염부, pH, 용존산소)을 측정하였다. 조사기간 동안 수온은 35일동안 일 평균 25℃ 이상의 고수온기(8월 1일~9월 5일)를 나타내었다. 또한 조사기간 중 chlorophyll-*a*가 급격히 증가하는 변화가 3회 발생하였다. 첫 번째 chlorophyll-*a*변화(8월 7일~8월 14일: 고수온기)에서는 오후 2-4시 높은 증가가 반복적으로 나타났다. 이때 식물플랑크톤 군집 중 최우점종은 *Alexandrium affine*로 오전 9시에는 저층에서, 오후 12시와 4시에는 표층에서 높게 나타나는 일주 수직 운동을 보였다. 두 번째(8월 24일~8월 30일)와 세 번째(9월 12일~9월 16일) chlorophyll-*a*변화는 수온 및 시간에 관계없이 증가하였다. 이때 식물플랑크톤 군집은 규조류가 우점하였으며, 특히 *Chaetoceros curvisetus*가 높게 차지하였다. 이처럼, 연속 관측을 통해서만 관찰이 가능한 *A. affine*의 일주 수직 운동 및 규조류의 급격한 증가 등 다양한 변화가 관찰되었다.

[PB-23]

와편모조류 *Oxyrrhis marina*의 섭식 과정 중 편모의 역할에 대한 초고속 촬영 분석

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종속영양 와편모조류 *Oxyrrhis marina*는 원생생물의 세포 생리학적 연구와 해양 생태계의 탄소와 영양염 순환에 대한 모델 생물로 섭식 과정에 대한 많은 연구가 수행되어 왔으나 먹이의 인지와 가공 과정에 대해서는 여전히 알려진 바가 적다. *Oxyrrhis marina*의 섭식 과정은 먹이 탐색(searching), 접촉(contact), 포획(capture), 가공(processing), 그리고 섭취(ingestion)의 단계로 구성된다. 먹이 가공 과정에 대한 초고속 촬영을 통한 분석의 결과 *Oxyrrhis marina*는 살아있는 먹이 외에 유기질의 덩어리를 섭취할 때에도 종편모를 사용해 가공하는 것을 관찰할 수 있었으며, 이 과정에서 먹이의 성공적인 섭취가 결정됨을 알 수 있었다. 먹이 생물로 *Oxyrrhis marina*가 선호하는 와편모조류 *Amphidinium carterae*와 선호도가 낮은 은편모조류 *Rhodomonas salina*를 제공하고 섭식 과정을 추적한 결과 섭식 단계 중 먹이 탐색과 접촉 및 포획 단계에서는 두 먹이 간 차이가 관찰되지 않았으나 가공 단계의 성공률에서 큰 차이가 나타났다. 먹이를 가공하는 단계에서 종편모는 계속 먹이를 두드리거나 다듬는 운동을 반복하였고 편모 운동의 속도도 이동 시보다 컸다. *Rhodomonas salina*는 가공 과정 중 탈출하는 비율이 *Amphidinium carterae*보다 현저히 높았고 탈출 후 사망하는 비율도 낮았다. 이상의 결과는 *Oxyrrhis marina*의 먹이인지와 가공 과정에서 종편모의 역할이 매우 크다는 것을 보여준다.

[PB-24]

채취법에 따른 우뭇가사리 종조성 및 생물량 변화 양상

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우뭇가사리(*Gelidium elegans*)는 전통적으로 어업인들의 주 소득원이었으나 자원량이 점차 감소하고 있는 실정이다(2010년 대비 2014년 생산량 약 17% 감소). 따라서 본 연구는 감소하고 있는 우뭇가사리의 자원량 증대 및 지속이용을 위해 고랑식 채취법에 따른 생물량(회복량) 변화를 모니터링하고, 어업인 자율관리 모델을 제시하는데 그 목적이 있다.

2016년 6월 제주연안 우뭇가사리 군락지역에 25m × 50m의 직사각형 시험구 3개를 설치하였다. 전량채취구는 일반해조류를 제외한 우뭇가사리류를 전량 채취하였고, 2/3채취구는 보존구역과 채취구역을 각각 1/3, 2/3로 3개씩의 소구역을 교대로 설정 후 2/3에 해당하는 소구역 내의 우뭇가사리류를 전량 채취하였다. 1/2채취구는 균등하게 6개의 소구역으로 분할 후 교대로 소구역 3개의 우뭇가사리류를 전량 채취하였다. 그 후 2016년 8월과 10월, 그리고 2017년 4월 각각의 소구역에 0.5m × 0.5m 방형구를 2개씩 설치하고 방형구 내 해조류를 전량 채취하여 종조성 및 습중량(wet.g.m^{-2})을 비교하였다.

해조류 출현종수는 2016년 8월 전량채취구에서 31종(녹4, 갈5, 홍22), 2/3채취구에서 18종(녹1, 갈3, 홍14), 1/2채취구에서 19종(녹4, 갈3, 홍12)이 출현하였고, 10월에는 전량채취구에서 18종(녹2, 홍16), 2/3채취구에서 19종(녹2, 갈3, 홍14), 1/2채취구에서 17종(녹1, 갈2, 홍14)이 출현하였으며, 2017년 4월에는 전량채취구에서 25종(녹1, 갈1, 홍23), 2/3채취구에서 22종(녹1, 갈3, 홍18), 1/2채취구에서 22종(녹1, 갈2, 홍19)이 출현하였다.

우뭇가사리 생물량은 2016년 8월에 1/2채취구(334.8g) > 2/3채취구(212.3g) > 전량채취구(109.4g) 순으로 나타났고, 10월에는 2/3채취구(132.6g) > 1/2채취구(103.3g) > 전량채취구(74.3g) 순으로 나타났다. 2017년 4월에는 1/2채취구(742.9g) > 2/3채취구(218.7g) > 전량채취구(139.3g) 순으로 나타났다.

1차 모니터링 결과 전량채취구에서 비교적 많은 해조류 출현종수를 나타내었으나, 우뭇가사리 생물량(회복량)은 1/2채취구에서 많게 나타났다.

[PB-25]

Benthic invertebrate community structure in natural and restored *Zostera marina* beds in Seosan, Korea

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Restoration project of *Zostera marina* beds has been carried out for recovery of seagrass beds, which were destroyed due to anthropogenic and natural disturbances in coastal waters of Korea.

In the present study, to examine recovery of benthic invertebrate community in the restored seagrass beds, species abundance, density, and biomass of macro-benthic invertebrates inhabited in transplanted and natural reference *Zostera marina* beds, and bare mud flats in Seosan, Korea were monitored from October 2015 to May 2017.

Species abundance, biomass, and density of benthic invertebrates gradually increased throughout the experiment periods in the restored *Z.marina* bed. The 65 species and 323.7g/m^2 of benthic invertebrates were observed in the natural reference *Z.marina* bed, whereas 66 species and biomass of 519.2g/m^2 were observed in the restored bed in May 2017.

Community structure of benthic invertebrates in the restored *Z.marina* bed was more similar to that in natural *Z.marina* bed, compared to that in bare mud flats, at the end of this experiment. According to the result of this experiment, restored seagrass beds may also provide ecosystem services similar to natural seagrass beds.

[PB-26]

Treatment of secondary wastewater effluent using High Rate Algal Ponds in New Zealand

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To demonstrate the feasibility of a High Rate Algal Pond (HRAP) to treat secondary wastewater effluent, two pilot-scale HRAPs were installed and operated over six months in New Zealand climatic conditions. Initially (NZ autumn; February to April) the HRAPs were operated in series with a daily inflow rate of 428 L/d (combined HRT of the two HRAPs: 7 d), while in winter (June to August) the HRAPs were operated in parallel with a daily inflow rate of 300 L/d for each HRT (winter HRT: 5 d). The wastewater treatment performance was monitored twice a month in terms of TSS/VSS, total/soluble BOD_5, nutrients (N and P) and *E. coli* removal. The HRAP algal culture (predominantly *Pediastrum* sp.) grew well until mid-April, with an average VSS concentration of ~120 mg/L in HRAPs. However, when the HRT of the HRAPs was reduced from 7 days to 6 days in mid-April, *Pediastrum* sp. was quickly replaced by the unicellular alga, *Chlorella* sp. Our previous studies showed that a high dominance of unicellular algae reduces algal removal efficiency by gravity settling. However, the unicellular algae (*Chlorella* sp.) formed large algal aggregates (>1 mm) possibly due to algal bioflocculation under nitrogen limiting conditions, resulting in >80% TSS removal in the algal settlers (HRT: 6.5 h). The HRAPs produced a high quality final effluent throughout the experimental period with the following average concentrations: TSS <30 mg/L; $cBOD_5$ <8 mg/L; NH_4-N <0.6 mg/L; NO_3-N: <1.0 mg/L; DRP: <1.0 mg/L, and *E. coli* <100 cfu/100 ml, (>2 log reduction).

[PB-27]

Influence of salinity on growth, nutrient uptake and nutrient bioextraction capacity of seaweeds

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The objective of this study was to evaluate the influence of salinity on growth, nutrient uptake and nutrient bioextraction capacity of *Gracilariopsis chorda*, *Gracilaria vermiculophylla, Ulva prolifera* and *U. compressa.* These seaweed species were cultivated in von Stosch enriched medium for 15 days at different salinity conditions (5, 10, 15, 20, 30, 40 and 50 psu). Results showed that under salinity regimes from 20 to 40 psu, daily growth rates of all species were higher than other salinity conditions. The maximum nitrate and phosphorus uptake rates of *Gracilariopsis lemaneiformis* were 11.7 and 0.9 $\mu\mathrm{mol}\cdot\mathrm{g}^{-1}\cdot\mathrm{d}^{-1}$ at 30 psu, respectively. The maximum nitrate and phosphorus uptake rates of *Gracilaria vermiculophylla* were 17.2 (15 psu) and 1.4 (40 psu) $\mu\mathrm{mol}\cdot\mathrm{g}^{-1}\cdot\mathrm{d}^{-1}$, respectively. The maximum nitrate and phosphorus uptake rates of *U. prolifera* were 27.5 (10 psu) and 4.3 (15 psu), respectively. The maximum nitrate and phosphorus uptake rates of *U. compressa* were 32.4 and 2.5 $\mu\mathrm{mol}\cdot\mathrm{g}^{-1}\cdot\mathrm{d}^{-1}$ at 20 psu, respectively. The nutrient removal rates of *Gracilariopsis lemaneiformis* were markedly higher at 30 psu (0.4 $\mathrm{mgN}\cdot\mathrm{g\ DW}^{-1}\cdot\mathrm{d}^{-1}$). Under salinity regimes from 15 to 40 psu, nutrient removal rates of *Gracilaria vermiculophylla* were higher than other salinity conditions. The nutrient removal rates of *U. prolifera* were not significantly at different salinity conditions. The nutrient removal rates of *U. compressa* was markedly higher at 10 psu (1.7 $\mathrm{mgN}\cdot\mathrm{g\ DW}^{-1}\cdot\mathrm{d}^{-1}$). These results suggest that *Ulva prolifera* may be a good species for nutrient bioextraction, but considering the economic value, *Gracilaria vermiculophylla* can be more suitable to be used in a nutrient bioextraction system.

[PB-28]

Seaweed Cultivation in Northeast America for Food, Feeds, Fertilizer, Ecosystem Services & Biofuels

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Seaweeds have significant value in US agriculture as organic fertilizers, feeds, as well as functional foods, nutraceuticals, and alternative medicinal products. After more than three decades of efforts by scientists, industry, state and federal agencies, seaweed aquaculture is now developing as an environmentally responsible practice and offers new opportunities for expansion of US coastal waters including the EEZ with the announcement of the ARPA-E (US DOE) MARINER Program. The World Bank estimates that farming kelp in less than 5% of US territorial waters could create as many as 50 million direct jobs. With the nursery and open water technologies developed at the University of Connecticut (UCONN) and GreenWave, the cold water brown seaweeds, *Saccharina latissima* and *S. angustissima*, have been successfully cultivated in the Northeast during the past 7 years. The biomass yields vary from 1.7 - 20 kg FW m^{-1} in *S. latissima* after 6 months (Dec.-May) of open-water cultivation in the northeastern US coastal waters. Yields of up to 25 kg FW m^{-1} for *S. angustissima* have been attained over a two-year period of study. The harvests from the northeast US kelp farms have been processed using a mobile kelp-processing machine developed by UCONN. In 2016, over 4.0 MT of sugar kelp was processed in southern New England using this processing system at GreenWave. Seaweed aquaculture provides ecosystem services by removing excess nutrients (carbon and nitrogen) from ecosystems, and thereby helps to improve water quality through ‘nutrient bioextraction.’ We are now planning to apply advanced breading technologies with the beginning of the MARINER program.

[PB-29]

Study of Community Structure and Algal Flora of Gageodo Island, West-southern Coast, Korea

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This study was conducted to elucidate the marine algal flora of Gageodo Island located in the west-southern coast of Korea. The materials were collected by SCUBA diving from August 2013 to March 2015 at the coastal zone of Gageodo Island. In analysis of the marine algal flora, R/P value of Feldmann’s(1937) and (R+C)/P value of Cheney’s(1977) method which represents the characteristics of the marine algal flora according to the seawater temperature were used. According to the study, 11 species of Chlorophyta, 30 species of Phaeophyta, and 95 species of Rhodophyta, a total of 136 species of marine algae were identified. Among 136 species in this study, by using R/P and (R+C)/P value, comparative analysis between Gageodo Island along with Chujado, Heuksando, Hongdo, Hataedo, Manjaedo, and Jindo was conducted. As a result, Gageodo Island shows 2.6 and 3.0 value which represents the characteristics of temperate marine algal flora including Chujado, Hueksando, and Hongdo. To find out variation of the species composition in comparison with the previous study, 45 species including 4 species of Chlorophyta, 8 species of Phaeophyta, and 33 species of Rhodophyta were added. To analyze the characteristics of the marine algal flora in the West-southern coast, more accurate study on Gageodo Island is needed.

[PB-30]

Study of Ecological Structure and Flora in Marine Macro algae on East Coast and Jeju Island, Korea

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A subtidal marine benthic algal flora vegetation at five sites in Korea was investigated to clarify the community structure and the pattern of geographical distribution by a quadrat method between January 2016 and December 2016. A total of 147 species including 14(9.5%) of green algae, 41(27.9%) of brown algae, 92(62.6%) of red algae were collected and identified. The dry weight biomass ranged from 53.8 to 175.7 dry wt m^{-2} during the study period. The maximum biomass region was Ulleungdo, and the minimum was Wangdol-cho. The dominant species were *Ecklonia cava*, *Ecklonia stolonifera*, *Myagropsis myagroides*, *Sargassum horneri*, *Eisenia bicyclis* at study site. The R/P and (R+C)/P value reflecting flora characteristics were 2.9 and 3.3 respectively. A cluster analysis produced three groups that differed meaningfully: one included the sites Munseom, Ulleungdo, Dokdo and another included the site Nam-hyeung-je-sum, the other included the site Wangdol-cho.

[PB-31]

Trophic structures of benthic microalgae to benthos in marine ecosystems of Korea using stable isotopes and food web analyses

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The trophic importance of benthic microalgae as the food source of primary organic matter for benthic invertebrates was studied in the *Halophila*-invaded ecosystems of the south coast of Korea using stable carbon and nitrogen isotope ratios. The stable carbon and nitrogen isotope ratios of benthic microalgae, phytoplankton, epiphytes, suspended particulate organic matter (POM), soil organic matter (SOM), two seagrasses and macrozoobenthos were identified at three different habitats (invasive seagrass bed, native seagrass bed and a shallow subtidal flat). Although the carbon stable isotope values of benthic invertebrates considerably varied among consumers in three habitats, the isotope signatures of consumers showed similarities among different sites. Cluster analysis based on their isotopic similarity showed that the isotopic variability of the benthic consumers was related more to functional feeding groups rather than to habitats or taxonomic groups. Moreover, the results of the SIAR model based on the carbon and nitrogen isotope ratios suggested that benthic microalgae and phytoplankton play an important role in supporting the benthic food web in summer and fall. Our findings suggest that benthic and pelagic microalgae made a large contribution to benthic consumer diets, while invasive seagrass, *H. nipponica* may not have a large role in supporting benthic food webs in this subtidal ecosystem.

[PB-32]

홍조류 진두발 야외개체군의 계절 및 조위에 따른 생장과생식변화

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진두발의 계절별 생물량, 밀도, 습중량과 G:T 비율(배우체:포자체)이 진두발 개체군이 서식하는 곳의 상부와 하부에서 조사되었다. 본 연구를 통하여 아래의 3가지 가설을 확인하였다. (1) 진두발의 생장은 상부에 비하여 환경스트레스가 적은 하부에서 좋을 것이며, (2) 배우체는 돌가시리과에 포함되는 많은 종들에서처럼 상부에서 우점할 것이며, (3) G:T 비율은 환경이 변화가 있는 계절과 조위에 따라서 변화할 것이다. 진두발의 생물량과 개체별 습중량은 하부에서 높았고 최대 생물량은 7월에 1,695 g wet wt./m^{2}였고 최대 개체별 습중량은 10월에 797.27 mg였다. 하지만, 엽체의 밀도는 계절과 조위에 따른 차이는 발견되지 않았다. 배우체는 상부에서, 사분포자체는 하부에서 우점하였다. 사분포자체와 과포자체의 조위별 패턴은 유사하였고, 생식기를 가진 엽체는 10월에 가장 많았고 4월에 최소였다. 진두발의 G:T 비율은 0.05- 2.45였으며, 계절과 조위에 따른 차이를 보였다. 본 연구 결과, 조간대의 환경스트레스는 진두발의 생장과 성숙을 결정하는 중요한 요인이며, 주 생장시기는 여름이고 생식시기는 가을과 겨울로 확인되었다.

PC. 생리 및 유전

[PC-01]

Overexpression of a *S-Adenosylmethionine Synthetase* gene from *Pyropia tenera* confers enhanced tolerance to salinity stress

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Pyropia tenera is an intertidal red alga of commercial significance owing to its popularity as a health-promoting seafood product. This alga grows in marine environments and is frequently exposed to high salinity and osmotic stress, which impact its growth. Therefore, the enhancement of stress tolerance in *P. tenera* is critical. In the present work, we aimed to elucidate the mechanisms underlying abiotic stress tolerance in this species; specifically, we identified the *P. tenera* S-adenosylmethionine synthetase-encoding gene (*PtSAMS*) gene and characterized its biological function. This gene, which is known to play a role in stress tolerance in other plants, was cloned and overexpressed in *Escherichia coli* under high-salinity conditions. The *PtSAMS* gene was found to encode a 385-amino-acid protein with a molecular weight of 41.8 kDa. In silico sequence alignment and phylogenetic analysis of the PtSAMS amino acid sequence showed that the encoded protein comprises three conserved domains and two motifs that are highly conserved in other plants. Growth assay results indicated that *PtSAMS*-overexpressing *E. coli* cells exhibit enhanced tolerance to salt stress. The present study is the first to describe the role of the *SAMS* gene in enhancing abiotic stress tolerance in marine plants. Furthermore, the results suggest that *PtSAMS* expression is induced by a combination of ion toxicity and osmotic stress resulting from exposure to high salinity in marine environments, and that this gene is expressed at housekeeping levels owing to growth in such conditions. The findings suggest that *PtSAMS* could be used as a potentially valuable bioresource with utility in the genetic engineering of salt stress-tolerant crop plants.

[PC-02]

Biomass analysis of four domestic microalgae strains using wastewater treatment for different types of applications

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Microalgae has been suggested as a promising candidate for biofuels due to its several advantages such as high lipid content and biomass productivity. However commercial-scale cultivation encounters high cost for operating process. To overcome the economic feasibility problem growing microalgae with wastewater was studied for cost-cut as well as nutrient removal. In this study, municipal wastewater treatment and biomass analysis was investigated using four indigenous strains *Scenedesmus* sp., *Asterarcys* sp., *Desmodesmus* sp. and *Pseudopediastrum* sp.. *Desmodesmus* sp., attained the highest growth rate, chlorophyll contents, biomass productivity and over 90% of removal efficiency in total nitrogen, total phosphorus and ammonia in 7 days of culture. In biomass analysis, *Desmodesmus* sp., also had almost 40% of protein and the highest omega 3 contents among them. This indicates that microalgae cultivation using municipal wastewater has potential for microalgal production, wastewater treatment and biomass application.

[PC-03]

RNA-seq analysis for the study of circadian gene expression in multicellular red algal *Gracilariopsis chorda*.

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Circadian rhythms expressed with a period of approximately 24 hrs are ubiquitous among living organisms at almost all levels of biological organization. Although there is a rich history of clock studies essential for their metabolism and development in many model organisms, but not yet in algae. Red algae, in particular, have few such studies and it is concentrated mostly on *Cyanidioschyzon merolae* which is one of representative single-cell red algae. This study is the first to investigate circadian clock system on major multicellular red algal *Gracilariopsis chorda*. Here, we performed genome-wide transcriptome profiling to detect circadian oscillation of *G. chorda* under constant light (LL) following light-dark (LD) conditions, and identified 1802 cyclically expressed genes, representing 16.7% of *G. chorda* gene set. We additionally analyzed to explore the 24 hr rhythmic gene expression regulated by the light rather than circadian under LD cycle because most biological rhythms have proved to be a mixture of endogenous (circadian) and exogenous (diel) components. As a result, the total number of rhythmic genes increased to 2483, indicating that at least 23% of the gene set present in *G. chorda* is under diel and/or circadian control across a wide range of biological functions and processes. Our strong periodic gene expression data will identify functional relationships established by prior studies and be a valuable new resource for investigating a variety of biological processes including photosynthesis and other key metabolic pathway in *G. chorda*.

[PC-04]

Alteration of inorganic carbon acquisition on geniculate coralline alga *Corallina officinalis* under hypoxia and warming

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Calcareous coralline algae are commonly distributed in the coastal rocky shore, and provide many ecological functions (i.e. accrete cement components and capture inorganic carbon), might be very sensitive to climate change. With the anthropogenic activities, overloading of allochthonous nutrient at coastal area was significantly increased, and it causes many environmental problems (i.e., eutrophication, harmful algal bloom, acidification and hypoxia). Among these problems, hypoxia is likely to influence on macroalgal physiology because decreased oxygen concentration affecting on CO2 affinity and competition between O2 and CO2 at the active site of RuBISCO. In this study, mesocosm experiment was conducted to evaluate alteration of carbon acquisition strategies of geniculate coralline alga *Coralline officinalis* under hypoxia and warming conditions. *C. officinalis* was grown under 4 experimental treatments with individual and combination environments of hypoxia(4 mg O_2L^{-1})and warming(18℃) conditions compared with ambient conditions (8 mg O_2L^{-1}and15℃). Carbon anhydrase (CA) activity and affinity of CO_2 and HCO_3^- were investigated by measurements of photosynthetic oxygen evolution. In the hypoxia condition, *C. officinalis* was more preferable CO_2 than HCO_3^- with decreased in intracellular CA(iCA). These results indicate that characteristics of carbon acquisition seem to be affected by lowered levels of dissolved oxygen, but this effect was mitigated by increasing temperature.

[PC-05]

DNA methylation is involved in regeneration and differentiation of protoplasts in the *Bryopsis plumosa*

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When cell membrane of the marine coenocytic green alga *Bryopsis plumosa* is destroyed, the protoplasm expelled in seawater generates numerous protoplasts *in vitro*. Protoplasts were surrounded by a polysaccharide envelope from the beginning of formation, which acted in a similar way to the cell membrane until this developed within several hours. We constructed 2-DE protein maps and transcriptome database of protoplasts at different stages of formation and attempted to elucidate characteristic genes expressed at each stage. The profiles of proteome as well as transcriptome changed dramatically at each stage of cell rebuilding process. Most proteins, which were up-regulated during the early stage of cell rebuilding disappeared or reduced significantly by 24-48 h. About 70-80% of proteins spot detected at 48 hours after the wounding were newly appeared ones, which was rarely seen in any other proteomes studied to date. DNA methylation seems to be involved in cell-rebuilding process of *B. plumosa.* DNA methylation is often utilized to silence and regulate genes without changing the original DNA sequence. To prove this hypothesis, DNA methylation assay was carried out using regenerating protoplasts at different stages. A dramatic de-methylation occurred in the regenerating cells for 24 hours after the release of cytoplasm in seawater. These results show that an epigenetic modification drives differential expression of the large gene sets specifically regulated at each developmental stage of cell-rebuilding process in *B. plumosa*.

[PC-06]

Interactive effects of temperature and light properties (intensity and wavelength) on the photosynthesis and growth of red alga *Pyropia dentata* (Bangiales, Rhodophyta) in a conchocelis phase

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In this study, photosynthetic performance and growth of *Pyropia dentata* in a conchocelis phase was investigated under various culture conditions, specifically combination of temperature (10, 15 and 20^{o}C), light intensity (20 and 70 μmol photons m^{-2} s^{-1}), and light properties (LED_{Blue}, LED_{Red}, $LED_{Blue+Red}$, and fluorescent lamp). Photosynthesis was measured using chlorophyll fluorometry (Mini-PAM, Walz) after 3 weeks acclimated under various experimental conditions. Also, growth was calculated by image analysis for estimating 2-dimensional area of complicated structure of conchocelis. Our results show that growth rate was significantly higher under higher temperature (15 and 20^{o}C) than 10^{o}C condition, but light intensity was not significantly influence on photosynthesis and growth. $LED_{Blue+Red}$ and LED_{Blue} show greater growth rate and photosynthetic efficiency than LED_{Red} and fluorescent lamp after 3-weeks acclimation. Also, the photochemical properties (maximum quantum yield) in this condition showed similar tendency with growth rate. Based on these results, we established optimized laboratory cultivation conditions of conchocelis phase of *P. dentata*. Specifically, this species requires higher temperature for optimal growth and photosynthesis. Also, mixed red and blue or solitary blue light could be an efficient light source for stabilized laboratory cultivation.

[PC-07]

해양 낭균에 감염된 홍조식물 엇가지풀의 전신획득저항성

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식물은 개체 일부분이 병원체에 노출 되었을 때 그 신호를 전신에 전달하여 비감염조직에 방어태세를 유도하는 전신획득저항성이 존재한다. 이러한 전신획득저항성이 홍조식물 엇가지풀에도 존재하는지 알아보기 위해 연구를 진행하였다. 엇가지풀에 낭균(*O. heterosiphoniae*)을 감염시킨 후 감염시간에 따른 감염률과 성장 속도, 저 염도에서의 생존율을 현미경으로 관찰하고 낭균에 노출된4일, 1달 후 숙주세포의 유전자 발현을 분석하였다. 그 결과 낭균(*O. heterosiphoniae*)에 감염된 엇가지풀은 수 개월 동안 감염률이 유지되며 병원체와 공생할 수 있고 대조군에 비해 감염이 오래된 엽체 일수록 성장 속도는 느려지지만 저 염도 환경에 대한 내성은 강해진다. 또한 낭균에 노출된 4일 후에 세포벽 합성에 관여하는 유전자의 발현이 증가하였다. 낭균 (*O. heterosiphoniae*)에 감염된 엇가지풀의 감염이 진행되지 않은 부분에서 이러한 생리적, 형태적 변화가 일어나는 것은 홍조식물 엇가지풀도 식물과 같은 전신획득저항성이 존재한다는 것을 시사 한다. 그리고 세포벽에 관여한 유전자의 발현이 증가하는 것은 엇가지풀의 이러한 변화에 기여하는 것으로 사료된다.

[PC-08]

Viral infection enhances resistance to oomycete pathogens in *Pyropia yezoensis*

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Green spot disease (GSD) causes serious economic loss in *Pyropia* sea farms in Korea every year. The causative agent of this disease is a chloroplast RNA virus (PyroV1). Proteomic studies and fluorescent microscopy on PyroV1 infected *Pyropia yezoensis* showed that retrograde signaling from cell organelles is involved in the defense mechanism for the viral infection. When the blades of *P. yezoensis* were pre-exposed to GSD infected blades the resistance the oomycete pathogens enhanced. DCF-DA staining on PyroV1 infected *P. yezoensis* blades showed an accumulation of ROS in the cells undergoing viral lysis. Mitochondrial inner membrane ATPase and fructose-bisphosphate aldolase were specifically up-regulated in the infected blades of *P. yezoensis.* As these enzymes are involved in mitochondrial energy metabolism we examined the enzymes involved in the mitochondrial alternative respiratory cycle. KCN-pretreated *P. yezoensis* showed enhanced infection suggesting that alternative oxidase is involved in defense response to PyroV1. These results suggest that a *P. yezoensis* may have a basic defense mechanism enhanced by different pathogens.

[PC-09]

홍조식물 *Bostrychia moritziana*의 성 특이적 importin alpha 유전자의 규명

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성의 분화는 생명의 진화 과정에서 가장 다양한 유전자의 출현을 촉진한 시발점으로 종의 생존에 결정적인 영향을 미치는 유성생식의 양상을 결정한다. 홍조식물 *Bostrychia moritziana*의 성 분화 과정을 밝히기 위하여 유성생식 생활사 중 나타나는 수배우체, 암배우체 및 사분포자체에 대하여 HiSeq sequencing을 수행하여 총 30Gb의 대용량 발현유전체를 확보하고 RNAseq분석을 수행하였다. 한 쪽 성에서만 특이적으로 출현한 유전자는 거의 없었으나 importin alpha 유전자는 암수 배우체 모두에서 나타나는 isoform과 각각의 배우체 특이적으로 나타나는 isoform들이 있다는 점에서 주목되었다. Genomic PCR을 통한 분석 결과 각각의 성 특이적 importin alpha isoform은 한 쪽의 배우체에만 있다는 것을 알 수 있었으며 서로 간에 DNA 염기서열이 77.5%, 아미노산 서열이 80.6%로 낮은 유사도를 나타내었다. 수정과정을 전후하여 성 특이적 importin alpha 단백질의 발현을 qPCR로 확인한 결과 수배우체 특이적인 importin α (BmMS1)는 수정 후 과포자체 발달 과정에서 6배이상 발현이 증가하는 것을 볼 수 있었으며 암배우체 특이적인 importin α (BmFS1)는 수정과정 중 수정모에 정자가 부착한 30분 후에 암배우체에서 발현이 크게 증가하는 것이 관찰되었다. 수배우체 특이적인 importin α (BmMS1)의 RNA 발현 정도를 확인하기 위해 *RNA in situ* hybridization으로 정자핵 양끝에 발현됨을 관찰되었다. 이상의 결과들은 *B. moritziana*의 성이 성염색체에 의해 결정되며 importin alpha의 isoform들이 성분화의 각 단계에 깊숙이 관여한다는 것을 보여준다.

[PC-10]

Labyrinthula zosterae 감염에 의한 거머리말(*Zostera marina*)의 Mn-SOD 유전자 발현

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생물체는 생태계에서 고온, 병해와 같은 다양한 환경스트레스를 받을 수 있으며, 이러한 스트레스로 인하여 생체 내의 산소(O_2)가 반응성이 높은 독성 활성산소종(reactive oxygen species)으로 변하여 광합성 억제 등의 심각한 생리적 장애를 일으킬 수 있다. 활성산소에 대한 방어기작으로는 항산화물질 및 항산화효소의 체내 활성산소 형성 억제 및 생성된 활성산소 제거 등이 있으며, 그 중 Superoxide Dismutase (SOD)가 가장 대표적이다. Mn-SOD (manganese superoxide dismutase)는 SOD의 family gene으로 Mn이온에 의존적인 효소이며, 수생식물인 거머리말(*Zostera marina*)에서도 항산화와 관련된 유전자로 보고된 바 있다. 본 연구에서는 1930년대에 북대서양, 북아메리카 및 유럽에서 자생 거머리말의 90%를 대량폐사 시킨 바 있는 wasting disease와 거머리말의 Mn-SOD의 상관관계를 조사하였다. Wasting disease의 원인균인 *Labyrinthula zosterae* (Labyrinthulomycetes)를 실험실에서 인위감염 시킨 후 정상 잎과 감염된 잎에서 각각 RNA를 추출하였다. 이후 Mn-SOD 유전자의 발현을 quantitative PCR을 통하여 확인하였다. 그 결과 거머리말의 wasting disease 감염부위에서 정상부위보다 Mn-SOD의 발현이 28배 높은 것으로 나타났다. 따라서 Mn-SOD는 거머리말의 wasting disease 발생시 방어 기작의 하나일 것으로 사료되며, 추후 다른 SOD 유전자의 발현 및 항산화활성 측정실험을 통하여 상관관계의 규명이 필요하다.

[PC-11]

양식 김 엽체의 기계적 절단에 의한 무성포자 방출 유도

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최근 김 산업 수출액이 2007년 대비 6배의 상승세를 보이면서 3억 6천만불에 달해 김이 우리나라의 최대 수출 농수산물이 되었으며 김 가공 산업의 빠른 성장에 따라 원재료인 물김에 대한 수요도 어느 때보다 증가하고 있다. 김 양식 과정 중 무성포자 방출은 7-8회에 달하는 수확 사이에 새로 성장하는 어린 엽체를 추가하여 김의 품질 및 생산량 증가에 큰 영향을 미치므로 종묘의 개량에 매우 중요한 요인으로 간주되나 무성포자의 방출을 촉발하는 직접적 환경 요인에 대해서는 아직까지 알려진 바가 없다. 양식장에서 엽체를 절단하여 수확한 이후 무성포자의 방출이 활발해지는 현상에 착안하여 기계적 절단이 무성포자 방출을 유도하는지 보기 위해 방사무늬김(*Pyropia yezoensis*) 엽체를 다양한 크기로 절단한 후 배양하였다. 대부분의 실험구에서 기계적 절단 후 5일 후부터 무성포자의 방출이 시작되는 것을 관찰하였다. 절단된 엽체를 다양한 빛 조건에 노출한 결과 빛을 쪼여준 조건에서만 방출이 유도되었고 좀 더 강한 빛에 노출 될수록 더 많은 무성포자가 방출되었다. 기계적 절단과 강한 빛이 야기하는 산화적 스트레스가 무성포자 방출의 직접적인 촉발 요인인지를 확인하기 위해 엽체에 H_2O_2를 처리한 결과 양식 김의 품종에 따라 민감도가 다름을 알 수 있었다. 참김(*Pyropia tenera*)과 방사무늬김(*Pyropia yezoensis*)은 비교적 낮은 농도에서 무성포자의 방출이 이루어진 반면 내병성 계통주인 골드1호는 강한 산화적 압력 하에서만 무성포자의 방출이 이루어졌다. 양식 김 엽체의 성장률, 크기, 수확 시기를 결정하는 요인 중 하나인 무성포자 방출의 촉발 요인 분석은 새로운 품종 개량에 있어 중요한 기초자료로 활용될 수 있을 것이다.

[PC-12]

녹조식물 해캄(*Spirogyra varians*)의 phototropin 분석

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녹조식물 해캄(*Spirogyra varians*)의 사상체는 적색광 하에서 불규칙적으로 구부러지는 운동을 보이는 반면에 청색광 하에서는 뚜렷한 양성 굴광성을 보인다. 청색광 수용체 phototropin의 신호전달자인 phosphoinositide 3-kinase를 wortmannin과 LY294002를 통해 저해하였을 때 해캄의 청색광 운동이 관찰되지 않았다. 발현유전체를 분석하여 해캄의 phototropin 2종(*SvPHOTA*, *SvPHOTB*)을 선별하고 유전자를 분리하였다. *SvPHOTA*와 *SvPHOTB*는 48.7 %의 아미노산 서열 유사도를 보였다. 계통분석에서 SvphotA는 접합조강(Zygnematophyceae)의 photA 계통군에 속했지만 SvphotB는 다른 photB 계통군과 분리되었다. 해캄의 광반응 운동에서 두 유전자의 발현은 *SvPHOTA*가 감소하고 *SvPHOTB*가 급격하게 증가하는 차이를 보였다. Phototropin이 결여된 애기장대(*Arabidopsis thaliana*)에 *SvphotA-GFP*와 *SvphotB-GFP*를 각각 이형발현 시켰을 때 모두 원형질막에 정상적으로 위치하였다. 각 형질전환체는 엽록체의 세포 내 위치와 청색광 반응이 일부 회복되었으며, 특히 *SvphotA-GFP*는 잎이 평평한 표현형으로 phototropin 기능 회복이 뚜렷하게 관찰되었다. 이상의 결과를 종합하여 해캄의 청색광 운동을 조절하는 *SvPHOTA*와 *SvPHOTB*의 분화와 특성을 규명하였다.

[PC-13]

세 가지 갯병에 대한 참김 (*Pyropia tenera*)의 특이적 면역 반응 분석

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해양 질병은 수산양식에 경제적으로 큰 위협이 되고 있다. 수산양식의 발전과 점점 밀집되는 양식 환경은 기존 질병의 전파와 새로운 질병의 발병을 가속화 시켰다. 김 양식장에서 가장 흔히 나타나는 갯병들은 대표적으로 난균강에 속하는 붉은 갯병과 낭균병, 바이러스 질병에 속하는 녹반병이 있다. 본 연구에서는 서로 다른 질병원에 대한 참김 (*Pyropia tenera*)의 분자적 반응을 분석하고 면역 반응에 대해 연구하고자 하였다. 식물에 가장 기본적인 면역 반응인 활성산소 생성을 확인하기 위해 질병 감염된 김에 DAB와 NBT 염색을 수행하였고 유전자 변화를 확인하기 위해 Microarray 분석을 사용하였다. DAB와 NBT 염색을 수행한 결과 붉은 갯병과 낭균병에 감염된 김에서는 활성산소의 축적이 뚜렷하게 나타났지만 녹반병에 감염된 김에서는 뚜렷한 패턴을 찾을 수 없었다. Microarray 분석 결과 모든 갯병 감염구에서 공통으로 Heat shock protein과 Serine protease와 같은 스트레스 저항 및 면역 반응에 관여하는 유전자의 발현이 증가하는 것을 확인하였다. 반면 각 갯병 감염에 특이적으로 발현이 증가하는 유전자들의 패턴은 갯병에 따라 매우 달랐으며, 같은 난균강에 속하는 붉은 갯병과 낭균병 보다 감염 기작이 비슷한 낭균병과 녹반병의 유전자 발현이 더 비슷한 것을 확인할 수 있었다. 본 연구 결과를 통해 김이 각 갯병에 대한 특이적인 질병-대응 기작을 가지는 것을 확인할 수 있었으며 이를 이용해 갯병 방지에 대한 새로운 기술 개발에 기초 자료로 사용할 수 있을 것으로 기대된다.

[PC-14]

방사무늬김(*Pyropia yezoensis*) 6개 품종의 신안지역 적합성 확인을 위한 생장 비교

김지건, 모기호, 김영희, 이지은, 허진석, 박은정

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우리나라 김의 생산량은 40만톤, 생산금액은 4,472억 원으로 해조류 양식산업의 약 68%를 차지하고 있다. 특히 김 수출은 2010년 1억 달러 달성 이후 지속적인 증가로 2016년에는 3.5억 달러를 달성하여 우리나라를 대표하는 수출품목으로 성장하였다. 김 산업의 지속적인 발전을 위해서 물김의 안정적 생산이 필요하며, 이를 위해 각 해역에 맞는 다양한 형질의 신품종 개발 및 산업화가 필요하다.

이에 본 연구는 해당 지역에 맞는 형질의 신품종을 개발하고 산업화 가능성을 확인 하고자, 우리원에서 개발 중 인 6개 품종(A, B, C, D, E, F)을 대상으로 주요 김 생산 지역인 신안에 2016년 10월에 시설하여 2주 간격으로 양식장 환경 및 김의 엽장, 엽폭, 엽장/엽폭비 그리고 형질 특성을 조사하였다.

김 양식장 환경은 수온 7.30~20.00℃ 범위, 염분은 30.72~32.80psu, 용존산소는 6.05~10.46㎎/L의 범위를 보였다. 품종별 최대 엽장은 B(최대 370.00㎜, 평균 256.17㎜), F(최대 370.00㎜, 평균 273.00㎜)가 8주차, A(최대 295.00㎜, 평균 211.69㎜), C(최대 355.00㎜, 평균 263.53㎜), D(최대 455.00㎜ 평균 304.67㎜), E(최대 340.00㎜, 평균 255.67㎜)가 12주차에 평균 최대 엽장을 보였다. 엽폭의 경우 C(최대 77.62㎜, 평균 48.05㎜), D(최대 47.30㎜, 평균 28.85㎜) 이 8주차, E(최대 95.36㎜, 평균 54.59㎜)는 10주차, A(최대 60.66㎜, 평균 30.71㎜), B(최대 96.09㎜, 평균 45.57㎜), F(최대 76.00㎜, 평균 41.70㎜)가 12주차에 평균 최대 엽폭을 보였다. 엽장/엽폭 비의 평균 결과 D(12.65), F(9.99), A(8.60) 3품종은 선형으로 B(4.83), E(4.65), C(4.28) 3품종은 도란형으로 나타났다.

김은 엽체의 형질에 따라 생산, 가공법이 달라지기 때문에 각각 양식지역에서 선호하는 김의 형질 또한 상이하다. 본 연구 해역인 신안지역의 양식 어민들은 재래김(김밥 김)등을 주로 양식하기 때문에 선형보다 도란형을 선호하는 것으로 사료되며, 이에 도란형 3품종(B, C, E)이 신안에서 양식하기 적합할 것으로 판단된다.

[PC-15]

방사무늬김 우량계통주 선발을 위한 저준위 감마선조사

김지건, 모기호, 김영희, 이지은, 허진석, 박은정

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우리나라 해조류 양식 생산량은 2016년 기준으로 약 136만 톤, 생산금액은 6,505억 원으로 전체 수산양식에서 차지하는 비중은 생산량(185만 톤)의 73.9%, 생산금액(2조3,328억 원)의 27.9% 차지하고 있다.

최근에는 해조류 품종보호제도에 대응하기 위해 선발·교잡·돌연변이 육종법을 이용하여 신품종 개발과 산업화 품종의 양식현장 보급의 필요성이 증가하고 있다. 이에 본 연구는 저준위 감마선조사를 이용하여 방사무늬김 우량 계통주를 선발하는데 그 목적이 있다.

우리원에서 확보한 방사무늬김 “부산명지3” 이용하여 감마선 조사를 하였다. 감마선 조사는 선량별 0Gy(대조구), 50Gy, 100Gy, 300Gy, 500Gy로 처리하였으며, 5℃, 10℃, 15℃, 20℃, 25℃의 온도조건과 광도 80μ㏖.m-2.s-1, 광주기 10L:14D 조건 하에 배양하였으며, 각 조건별로 30개체씩 1주일 간격으로 측정하였다.

그 결과 10주차에 평균엽장이 가장 큰 구간은 100Gy, 10℃(평균엽장 260.2㎜)에서 나타났으며, 평균엽폭이 가장 큰 구간은 50Gy, 20℃(평균엽폭 19.7㎜)으로 측정되었다.

우량 계통주를 선발하기 위한 가장 큰 엽장을 나타난 조사 구간은 10주차 50Gy, 20℃구간으로 최대엽장 970.0㎜, 최대엽폭 26.7㎜, 엽장/엽폭 비는 36.3으로 측정되었으며, 가장 큰 엽폭을 나타낸 조사 구간은 10주차 50Gy, 15℃로 최대 엽장 524.6㎜, 최대엽폭 63.5㎜, 엽장/엽폭비 8.26으로 측정되었다.

본 실험에서 조사를 통해 나타난 우량 계통주(50Gy, 20℃)를 유전자원을 확보하였고, 특히 20℃에서 가장 큰 크기를 나타낸 본 계통주는 수온상승의 내성을 가지고 있어 수온 상승으로 인하여 피해를 입는 어민들에게 도움을 줄 것으로 사료되며, 선발한 방사무늬김 우량계통주는 형질과 특성을 보존하고, 산업화 품종의 양식현장 보급을 통해 안정적 생산 기반을 마련하고, 향후 김의 생산성 향상에도 기여할 수 있을 것으로 기대된다.

[PC-16]

Diatom-Based Paleoenvironmental Reconstruction in Upo Wetland, South Korea

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Upo Wetland is located east of Nakdong River and is made up of four smaller wetlands (Upo, Mokpo, Sajipo, Jiokjibeol). It covers about 850ha and a bit over the quarter of the site(220ha) is permanent surface water of a large oxbow lake. The rest is marshland. To reconstruct the paleo-environment based on diatom assemblages in Upo Wetland, we sampled long sediment cores at four sites(site 1 and 2 : 10m, site 3 and 4 : 9m). The sediment cores were divided into water environment part and terrestrial environment part based on analysis of the oxidized layer of sediment core. The results of distribution of diatom, diatoms found in the expected sections to water environment only. In the sections, the diatom assemblages were composed pennate freshwater species mainly. The distribution of fossil diatoms and analysis of geological time of sediment cores in Upo Wetland will be used important information for the reconstruction of paleo-environment in Upo Wetland.

[PC-17]

Combined effect of irradiance and temperature on egg discharge efficiency from female gametophytes of *Undaria peterseniana* (Phaeophyta)

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Undaria peterseniana (Phaeophyta) – an endemic brown alga in southern coastal area (Udo, Jeju Island) and around the Ulleung Island in East Sea, Korea. Recently, the economic value of *Undaria peterseniana* (Phaeophyta) which distribute in Ulleung Island has been increasing with the higher demand of seaweed products. Samples for current study were collected from the Gongam site at Ulleung Island in August, 2016. Oogonium formation from the vegetative cell, its maturation and finally egg discharge- all procedures need the optimum range of temperature and the threshold level of irradiance. We detected the optimum level of temperature and irradiance for initiating the gametogenesis and for egg discharge from the oogonium. Using similar type of female gametophytes material, Egg Discharge Rate (EDR) as a egg discharge efficiency was assessed under lower to higher temperature (10^0C, 15^0C, 20^0C, 25^0C) and irradiance level (30, 60, 90, 120 μmol photons m^{-2}s^{-1}). Results show that temperature and irradiance have effect on both of the oogonium formation and egg discharge process. Under lower temperature (10^0C) and irradiance level (30 μmol photons m^{-2}s^{-1}), only 20% eggs were discharged on 10 days of culture whereas under higher temperature (20^0C) with higher irradiance level (60 μmol photons m^{-2} s^{-1}), 75% eggs were discharged on the similar culture days. However, the higher temperature (25^0C) with any irradiance levels halted the egg discharge rate. So, it is to be stated that higher temperature (>20^0C) would be an inhibiting factor for egg discharge from oogonium cell and also higher irradiance level enhance this egg discharge process.

[PC-18]

Protoplast isolation and regeneration from the filamentous brown algae, *Hecatonema terminale* (Ectocarpales, Chordariaceae)

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Protoplasts are naked living plant cells devoid of cell wall that can be used for a wide range of applications. *Hecatonema terminale* is a widespread filamentous brown algae that may be compared with other similar species like the model organism, *Ectocarpus siliculosus*. This work reports for the isolation and regeneration of protoplasts from *H. terminale* in order to obtain more information about the factors affecting protoplast production and morphogenesis in brown algae. In this study, we obtain a maximum protoplast yield of 2 x 10^6 protoplast g^{-1} fresh weight with high viability (>97%) using a simple commercial mixture of 1% Cellulase RS and 3 U/ml alginate lyase with chelating pre-treatment. Growth phase, temperature, and presence of cellulase are critical factors during protoplast isolation. Most of the protoplasts (87%) present the regeneration pathway characterized by a first asymmetric cell division outside. The present regeneration pathway differs from ones previosly described from other filamentous brown algae.

[PC-19]

바다숲 복원을 위한 지충이와 꼬시래기의 생리·생태 및 종묘생산

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조간대에 서식하는 지충이와 꼬시래기의 생리 및 생태적 특징을 구명하고 종묘생산 및 양식기술을 개발하여 향후 바다숲 조성종이나 천연해조장 복원 및 유지를 위해 활용할 목적으로 연구가 수행되었다. 두 종의 계절별 길이생장 및 습중량을 측정한 결과, 지충이는 하계(27.93±1.30 cm, 21.30±2.94 g)에서 최대, 동계(14.87±1.08 cm, 10.25±1.25 g)에서 최소였으며, 꼬시래기는 춘계(23.02±1.49 cm, 14.44±0.78 g)에서 최대, 추계(9.15±0.55 cm, 1.12±0.17 g)에서 최소였다. 지충이의 생식시기는 하계와 추계로 확인되었으며, 꼬시래기의 과포자체도 하계(82.5±3.3 %)와 추계(33.3±6.7 %)에 높은 비율을 보였다. 두 종의 채묘를 위하여, 지충이는 생식기탁에서 방출된 접합자를 육안으로 확인한 후 붓질로 탈락시켜 확보(300 개/ml)하였으며, 꼬시래기의 과포자는 낭과를 가진 과포자체에 저온·건조충격(681.61±127.83 개/낭과/일)을 주어 대량으로 확보하였다. 이후 실내배양을 통하여 지충이 접합자와 꼬시래기 배아의 최적생장조건(25 ℃, 90 μmol photons m^{-2} s^{-1})을 확인하였다. 지충이의 종묘생산은 접합자 현탁액은 채묘틀에 직접 바르는 건식법을 활용하였으며, 꼬시래기는 성숙된 과포자체를 종사 위에 놓는 방법으로 채묘를 실시하였다. 이후 실내수조(22-25 ℃, 50-80 μmol photons m^{-2} s^{-1})에서 4주간 배양하여 가이식에 적합한 수준의 크기로 생장한 엽체를 획득 할 수 있었다.

[PC-20]

퇴적물의 양과 입자 크기가 갈조류 지충이 접합자의 부착률과 배아의 생존 및 생장에 미치는 영향

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인간활동에 의한 퇴적물의 증가는 바다숲의 감소의 중요한 요인이다. 실내배양에서 3종류의 퇴적물 입자 크기(small, 0~100; mid, 101~250; big, 251~600 μm)와 4종류의 양(No, 0; small, 2; mid, 4; high, 6 mg cm^{-2})이 갈조류 지충이 접합자 부착과 배아의 생존 및 생장에 미치는 영향을 조사하였다. 접합자의 부착율은 입자가 작을수록 퇴적물 양이 많을수록 감소하였으며, 입자가 작고(<600 μm), 퇴적물 양이 6 mg/cm^2 인 실험구에서 최소였으며, 퇴적물 미첨가인 대조구에 비해서 33% 정도였다. 정치 배양 15일 후, 접합자의 생존율은 퇴적물 크기가 크고(big, 251~600 μm)하고 농도가 소량(small, 2 mg/cm^2)인 실험구에서 22.13%로 최대였으며, 작은 크기(0-100 μm)와 농도가 대량(6 mg/cm^2)인 실험구에서 2.96 %로 최소였다. 배아 생장은 중간 입자크기(101~250 μm)와 소량(2 mg/cm^2)의 퇴적물 농도에서 최대(상대생장률, 12.37 % day^{-1})였으며, 작은 입자(0~100 μm)와 고농도(6 mg/cm^2)에서 최소(5.55 % day^{-1})를 보임으로써 접합자의 생존과 배아생장은 퇴적물 농도와 반비례하며, 퇴적물 입자의 크기에 비례하는 경향을 보였다. 본 연구 결과, 지충이의 초기 부착 및 생존과 배아 생장은 퇴적물 입자와 관련되며, 개체군 감소는 퇴적물 입자와 양이 증가하기 때문으로 사료된다.

[PC-21]

우리나라 양식종(방사무늬김, 모무늬돌김, 잇바디돌김)의 채묘 효율을 높이기 위한 최적 온도 및 조도조건 탐색

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우리나라 김 종묘산업은 2016년 기준 유리사상체 약 30kg, 패각사상체 약 280만 상자 약 87억원으로 산업의 규모는 커졌지만 대부분 굴패각을 수입하는 등 일본에 비하여 많은 패각 사용량을 보이고 있는 것으로 사료된다. 또한 우리나라 김 양식은 대부분 과거 일본양식방법에 의존하거나, 같은 환경조건에서 서로 다른 양식종을 배양하고 있는 실정이다. 따라서 우리나라 양식방법에 적합한 양식기술을 개발 할 필요성이 있다.

일정량의 김 사상체(방사무늬김, 모무늬돌김, 잇바디돌김)를 갈아 100배로 희석하여 10ml씩 패각에 잠입하여 다양한 온도(10,15,20,25,30), 조도(1,5,10,20,40,80μmol $m^{-2}s^{-1}$)에서 2주간 사상체 잠입실험을 하였다. 그 결과, 3개 양식종 모두 20~25℃, 40~80 μmol $m^{-2}s^{-1}$에서 단위면적)당 높은 잠입개체수를 보였다.

최적잠입조건(20℃, 40 μmol $m^{-2}s^{-1}$)에 2주간 잠입시킨 후 다양한 환경조건에서 패각사상체 생장실험을 실시한 결과, 20, 25℃, 조도가 높을수록(40~80 μmol $m^{-2}s^{-1}$) 높은 생장을 보였다. 하지만 고조도에서 종별 2~3주부터 각포자낭이 관찰되어 최적생장조건은 20℃, 20 μmol $m^{-2}s^{-1}$으로 확인되었다.

각포자낭 형성을 측정하기 위하여 각 사상체를 300,400,500배 희석하여 밀도 확인 후 400배(2.96~12.28 /cm^{2})로 하여 최적 잠입조건(20℃, 80 μmol $m^{-2}s^{-1}$) 2주, 생장조건(20℃, 20 μmol $m^{-2}s^{-1}$) 2주 배양한 후 다양한 환경조건에서 각포자낭 개수를 측정하였다. 그결과, 방사무늬김은 15~25℃, 80 μmol $m^{-2}s^{-1}$, 잇바디돌김은 모든 구간에서 각포자낭이 2.00개/cm^{2} 이하, 모무늬돌김은 30℃, 5~80 μmol $m^{-2}s^{-1}$로 각 종별로 각포자낭을 형성 할 때 필요로 하는 환경 조건이 다른 것을 확인 하였다

[PC-22]

유리배우체 채묘 효율 향상을 위한 최적 배우체 비율 및 고온자극이 아포체 형성에 미치는 영향

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미역 암·수배우체를 다양한 일장(8:16, 16:8LD), 온도(10, 15, 20, 25, 30℃)및 조도(10, 30, 50, 70 μmol photons m^{-2}s^{-1})에서 24일간 배양하여 최적 생장 조건을 확인하였다. 미역 암·수배우체의 상대생장률은 장일(16h), 20℃, 10 μmol photons m^{-2}s^{-1}의 조도에서 각각 8.86±0.21% day^{-1}과 9.14±0.01% day^{-1}로 가장 빠른 생장을 보였으며 조도의 증가와 함께 상대생장률이 감소하였다. 반면, 단일조건(8h)에서는 암배우체는 15℃, 10 μmol photons m^{-2}s^{-1}에서 최대생장(4.69±0.17% day^{-1})을 보였으며 수배우체는 25℃, 30 μmol photons m^{-2}s^{-1}에서 최대생장(6.61±0.10% day^{-1})을 나타내 최적 생장조건에 있어 차이를 보였다.

암·수 배우체의 밀도에 따른 혼합비를 달리(2:1, 1:1, 1:2 암:수)하여 배양하고 아포체 밀도를 측정하였다. 측정 결과, 배양 30일후 1:1, 2:1(암:수)비율조건에서 아포체가 형성되었으며 배양 33일 후 모든 조건에서 아포체의 형성이 확인되었다. 배양 45일 후, 각 비율조건별 아포체의 밀도는 1:1조건에서 15.00 indiv. cm^{-1}, 1:2조건에서 17.33 indiv. cm^{-1}, 2:1조건에서 27.67 indiv. cm^{-1}로 암배우체의 비율이 높을수록 아포체의 밀도가 증가하였다.

배우체의 아포체 형성에 고온자극이 미치는 영향을 확인하기 위해 미역 7개 계통주의 암·수배우체를 100~200μm 내외로 잘라 동일한 비율로 혼합하여 고온조건(27℃, 대조구 21℃)에서 일주일간 배양한 후 다양한 온도(15, 18, 21, 24, 27℃)조건으로 분주하여 아포체의 형성유무 및 밀도를 측정하였다. 측정 결과, 고온자극 시험구에서는 배양 15일 후 15~24℃온도조건에서 1계통주 이상이 아포체를 형성하였으며 온도가 낮아질수록 아포체 형성 계통주의 수가 증가 하였다. 또한 배양 22일 후에는 15℃와 18℃ 조건의 모든 계통주에서 아포체 형성이 확인되었다. 반면, 대조구에서는 배양 22일 후 18℃조건에서 1계통주만 아포체를 형성하였고 7개 계통주가 모두 아포체를 형성하기까지 15℃에서는 30일, 18℃에서는 50일, 21℃에서는 57일이 소요되어 고온자극이 미역 배우체의 아포체 형성을 촉진하는 것으로 확인되었다.

[PC-23]

Physiological effects of copper on the freshwater algae *Closterium ehrenbergii* and its potential use in toxicity assessments

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The freshwater green algae *Closterium* responds sensitively exposed to various environmental contaminants and it is considered as one of the algal toxicity testing models; however, little toxicity data of these algae are available to date. Here, we selected the freshwater green algae *Closterium ehrenbergii*, and assessed the acute toxicity of copper. Median effective concentration (EC_{50}) of copper sulfate based on dose response curve was calculated. After 6 h culture exposed to copper decreased the photosynthetic efficiency (*Fv/Fm* ratio) of the cells, whereas the value was significantly decreased after 48 h ($P < 0.01$). In addition, the production of reactive oxygen species (ROS) was significantly increased in the cells ($P < 0.01$) with the increasing of time, and damaged the intracellular organelles. These indicate that copper induce oxidative stress in the cellular metabolic process and leads to severe physiological damages in the cells, even cell death. From this it is sufficiently testified that *C. ehrenbergii* can be used as a potential testing model in aquatic toxicity assessment.

[PC-24]

Feasibility study on seed production and aquaculture of *Saccharina japonica* (Phaeophyta) in the middle coast of East Sea, Korea

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Saccharina japonica (Phaeophyta) is one of the major brown alga in the eastern coast of Korea. Natural population of this species has been decreasing since 2000. To compare the seed production and morphological characteristics between the native species and the cultured one, we collected the natural(Gwangjin port) and cultured (Yangyang offshore, seed from Baengnyeong Island) sample in underwater Yangyang coast. We compared the total length, total wet weight, blade length, blade weight, maximum blade width and stipe length. The average total length of cultured sample is 159.8cm and natural sample is 137.6cm. So, Yangyang cultured sample is 20cm longer than that of natural one. Average total wet weight of cultured sample is 183.7g and natural one is 127.2g. Cultured sample is 56g heavier than that of natural one. Also the average blade width of cultured one is 14.68cm whereas the natural one is 12.50cm; cultured sample is 2cm wider than that of natural one. However, this study covers very limited area in the East Sea region; so natural sample from wider area should also be collected and compared with the culture sample. Also zoospore was collected from the natural sample and gametophytes were cultured in the lab culture condition. Both male and female gametophytes were isolated and cultured to check optimum culture condition and to find the potential strain for aquaculture purposes in this region.

[PC-25]

Sexual maturity of male and female gametophytes of *Undaria peterseniana* (Phaeophyta) in Ulleungdo island

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Development stages from releasing zoospore to mature gametophytes of a large brown alga, *Undaria peterseniana* (Phaeophyta) were studied. Samples were collected from its natural habitat located at the Gongnam site at Ulleung Island, East Sea in August, 2016. The mature fronds of the plant were cut into 0.3cm X 0.3cm sizes and incubated at 20^0C temperature with 30 μmol photons $m^{-2}s^{-1}$. After around 24 hours of incubation period, the zoospores were released. From 4-6 days, germination in the spores were occurred. From 10 days of culture, male gametophytes and female gametophytes were become identical by their different shapes. Female gametophyes were become thicker than the male one; and male gametohytes were started branching just after germination. More branching was prominent in both of the male and female gametophytes in the 3rd week of culture and they became matured gametophytes. In the 4th week of culture, the antheridia and oogonia were observed in the male and female gametophytes respectively, however, antheridia were more clearly visible than the oogonia in female gametophytes. Within 5th to 6th weeks of culture, eggs were discharged from oogonia, fertilization took place and fertilized zygote became juvenile sporophytes; also the unfertilized male and female gametophytes started more branching and became cluster. Male gametophytes growth (both in length and cell number) were higher than that of female one and it was more prominent after 3 weeks of culture.

[PC-26]

Outdoor cultivation of Korean domestic microalgae in large scale

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It has long been believed that covered greenhouse would be a necessity for microalgae outdoor mass cultivation in Korean geoclimate conditions due to summer monsoon seasons and sub-zero winter temperatures. To elucidate the efficiency of a covered and uncovered outdoor mass cultivation systems, we built two identical 675.0 m^2 open pond raceways with or without a semitransparent film cover in a central region of South Korea, and analyzed algal biomass productivity from June 2014 to January 2017. We also analyzed nitrogen and phosphorus consumption, transition of dominant microalgal species and influence of zooplankton predation. Year-round cultivation was possible in the semitransparent film-covered raceway, but the average seasonal biomass productivities were lower than those of the non-covered one, mainly due to the reduced solar radiation. The maximal productivity, 29.3 g dry weight/m^2-day with 15.0% lipid and a calorific value (CV) of 20.1 MJ/kg, was attained in the non-covered raceway during the summer months of 2016. The addition of a semitransparent cover did not confer advantages for the healthier production of microalgae, even though the production period was extended over sub-zero temperature winter seasons. In this study, the grazer-resistant microalgae were allowed to dominate in raceways rather than maintaining target strains and the results demonstrated the potential of naturally occurring microalgae as a biofuel source since the calorific values of the biomass were close to those of terrestrial energy crops. Also, the mass cultivation of the isolates could be applied for wastewater treatment due to their high capacity to assimilate nutrients.

PD. 응용조류 및 생명공학

[PD-01]

Cryopreservation of freshwater microalgae in Korea

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Freshwater microalgae are regarded as potential biomaterials in various research fields such as cosmetic ingredients, food supplement, and pharmaceuticals. Periodical subculture of algal strain is a very time-consuming and labor-intensive work. Compared to many studies in aboard, the cryopreservation of freshwater algae in Korea has not been investigated. In this study, we determined the optimum concentration of cryoprotectant (glycerol, dimethyl sulfoxide, and sucrose), cooling rate, and freezing process for 10 species of freshwater microalgae. The optimum concentrations were 10%, 20%, and 10% for dimethyl sulfoxide, glycerol, and sucrose, respectively. The maximum viabilities were found about 20-30% under 10% dimethyl sulfoxide, about 15-20% under 20% glycerol, and 10% under 10% sucrose, respectively. The 10% dimethyl sulfoxide was most effective when a single composition was used as a cryoprotectant. Furthermore, the algal viabilities were significantly enhanced up to 50% when the 10% sucrose was added into 10% dimethyl sulfoxide. Therefore, the mixed cryoprotectant composed of 10% dimethyl sulfoxide and 10% sucrose was suggested as the best cryoprotectant for the stable preservation of freshwater algae.

[PD-02]

Possible Application of the Polychaete-Assisted Integrated Culture for IMTA Development

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Aquaculture is growing rapidly all over the world and the increasing number of fish culture industries has begun to create serious environmental problems due to the impact caused by fish farming wastes. Based on the information on great potential of the polychaete worms for bioremediation and the successful seed production of the polychaete rockworm *Marphysa sanguinea* at Fisheries Science and Technology Center, PKNU, some trials have been conducted to test the water quality improvement by uptake organic substances in the rockworm settlement bottles receiving wastes both from olive flounder rearing tanks in land-based experiment systems and from marine fish farms in the southern coastal areas.

In comparison between culture systems in land-based experiments, the pure production of the worm was 1.5 times higher in flow-through system than in semi-recirculating system. Different effects on the removal efficiency were appeared both in culture systems and among treatments. In flow-through system, the highest removal efficiency showed in TN (56 %), TP (59%), TSS (86%), and COD (30%). In semi-recirculating system, the highest removal efficiency was in TN (63%), TP (53%), TSS (80%), and COD (21%). The results demonstrate that utilization of waste from the integrated fish culture system as a feed source for the rockworm polychate is highly efficient. Therefore, for bioremediation of organically enriched deposited sediment below fish farm, the potential for a survival and growth of the rockworm polychaete were examined by hanging or bottom settlement the polychaete boxes below an experimental fish farm in Punghwa-ri, Gyeongnam-do, Korea for 300 days from May 2015 to March 2016. Utilization of deposited materials was highly efficient by showing 85% of removal rate (from 10 cm to 1.5 cm in stock height) for 3 months from May to August 2015. At the end of experiments for 300 days, survival rate of the adult rockworm was 85.8% which showed 2.3 times higher than that of the juvenile rockworm showed 26%, but growth of the adult and juvenile worms showed markedly different effects on 9% and 488% increase in weight gain compared to their initial weight of 3.90 g and 0.69 g, respectively. These results suggest that the rockworm *M. sanguinea* is an excellent candidate for integrated aquaculture and waste recycling by organic nurient removal of aquaculture discharges for IMTA development.

[PD-03]

Effects of extracellular polymeric substances (EPS) components on the flocculation and adsorption behaviors of *Ettlia* sp.

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The cost and energy balance of microalgae-based biodiesel production depends largely on harvesting methods. Therefore, microalgal species with high lipid content, fast growth rate, and high sedimentation efficiency are more preferable. Our lab isolated *Ettlia* sp. YC001 possess all the above-mentioned characteristics and usually forms flocs during its cultivation periods that facilitate the harvesting process. In activated sludge, extracellular polymeric substances (EPS) are well-known as an important factor that contributes to the formation of bioaggregates but little is known in pure microalgae culture. In this work, two different fractions of loosely bound (LB)- and tightly bound (TB)-EPS were isolated from axenic and xenic *Ettlia* cultures at different growth phases. Both of the fractions were analyzed for total organic carbon and their specific components. The size distribution of the protein fraction was analyzed by SDS-PAGE. The results showed that protein is the main component and it presents mostly in LB-fraction whereas most of the polysaccharide presents in the inner TB-layer of the EPS matrix. Moreover, protein seems to play an important role in the turbidity adsorption capacity of *Ettlia*. SDS-PAGE data also confirmed the main presence of higher MW protein in the LB-fraction, suggesting their importance in the adsorption and flocculation behaviors of *Ettlia*.

[PD-04]

A new strain development of *Saccharina japonica* for stable abalone feed industry in Korea

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Cultivations of the brown seaweed, *Saccharina japonica* was developed, promoted, and industrialized in the 1970’s and is highly valued in Korea both for human consumption and as a feed for the rapidly developing abalone farming industry. Production has continually increased, and approximately 442,637 ton wet weight was harvested in Korea in 2015. Abalone is a highly sought-after delicacy in Korea, and the abalone farming industry has been developed based on a stable production of seaweed. Korean abalone farmers prefer to feed their stock on locally cultured *S. japonica*; however, between August and November the supply of farmed *S. japonica* declines because higher seawater temperatures reduce *S. japonica* productivity. In an attempt to overcome this temperature induced period of low production, cultivation trials with a strain of *S. japonica* selected to withstand higher cultivation temperatures were undertaken. Strain selection involved using individual parent thalli that were found to remain productive under high seawater temperature (26°C) at Wando. Male and female gametophytes were isolated through 3 cycles of free-living gametophyte culture to produce the F_3 strain used in the production trials. Production trials using the selected strain were initiated every month between December 2014 and March 2015. This delayed the initiation of culture beyond the latest initiation time currently used by farmers (December). Delaying initiation of cultivation resulted in delayed maximum growth compared to the control. Growth of the F_3 strain, continued for up to 3 months longer than normally achieved on farms for non-selected thalli. The mean length, growth rate and biomass were also greater than those achieved by the control strain. The use of the F_3 strain of *S. japonica* coupled with delayed initiation of culture can therefore be used to help to ensure a stable year round algal feed supply for abalone industry in Korea.

[PD-05]

Development of molecule delivery system by using cell-penetrating peptides in red alga *Pyropia tenera*

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Cell penetrating peptides (CPPs) are effective molecular tools that can deliver various molecular materials into different types of cells. However, there is no study about molecular material delivery system by using CPPs into cells of red algae, especially *Pyropia*. In this study, we attempted to develop a delivery system of molecular materials into cells of *Pyropia tenera* by using CPPs. Well-known CPPs which were previously reported in other organisms were selected for introducing molecules into cells, and were classified by their physical-chemical properties like hydrophobicity, charge etc. Then, their cell penetration activities were calculated by *in silico* method. CPPs were synthesized with fluorescein isothiocyanate (FITC) for convenient screening of CPPs. We treated FITC-labeled CPPs into PES medium with *P. tenera*, and selected CPPs which have high cell penetration activity by using fluorescence microscope. The cell penetration patterns of selected CPPs were observed by using confocal microscope. These results may provide basic knowledge of molecule delivery tool for algal research.

Cell penetrating peptides (CPPs) are effective molecular tools that can deliver various molecular materials into different types of cells. However, there is no study about molecular material delivery system by using CPPs into cells of macroalgae, especially *Pyropia*.

In this study, we attempted to develop a delivery system of molecular materials into *P. tenera* by using CPPs. Well-known CPPs, previously reported in other organism system, were selected for introducing molecules into cells, and were classified by their physical-chemical property like hydrophobicity, charge etc. Then their cell penetration activities were calculated by *in silico* method. CPPs were synthesized with fluorescein isothiocyanate (FITC) for easy observation. We treated FITC-labeled CPPs into PES medium with *P. tenera*, and selected high cell penetration activity by using fluorescence microscope. The cell penetration pattern of selected CPPs were observed by using confocal microscope.

[PD-06]

Comparative transcriptomics of thermal responses in red-tide algae *Cochlodinium polykrikoides*

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Cochlodinium polykrikoides causes a Harmful Algal Bloom (HAB) known as red-tide in worldwide and disturbs the balance of marine ecosystem recent decades (Howard *et al.*, 2012). On the fishery industry, massive fish kills was impacted by *C.polykrikoides* and created an economic loss (Gobler *et al.*, 2008). To avoid HAB damage, many ecological and physiological interpretation for *C. polykrikoides* blooms have been attempted, and among distinct explanation related to *C. polykrikoides* blooming mechanism, temperature effect has been widely discussed as one of the major key factors (Griffith & Gobler, 2016, Kim *et al.*, 2004). However, due to the absence of genome information and limited functional genomics studies to *C. polykrikoides*, molecular mechanisms of responses to fluctuant temperature have been not wholly resolved at the current stage. To understand the genomic responses to thermal changes, we first set culture conditions with three options at 23℃ as well-growth condition (Kim et al., 2004, Kudela & Gobler, 2012) and 5℃ up and down (18℃, 23℃, 28℃). We performed *de novo* transcriptome assembly from next-generation sequencing data in each cultured sample at three temperatures. As a result of *de novo* assembly, a *C.polykrikoides* transcriptome database consisting of 97,505 transcripts with 1,086 bp average length was generated. For the downstream analyses, we also conducted gene annotation, abundance estimation of expressed genes, and Differentially Expressed Gene (DEG) analysis. 6,041, 6,065 and 5,788 transcripts were expressed ($\geq$ 1 FPKM [*F*ragments *P*er transcript *K*ilobase per *M*illion fragments mapped]) under 18℃, 23℃ and 28℃ respectively. Among them, 5,455 transcripts were commonly expressed in three temperatures. Moreover, we identified 568 DEGs (< 0.05 false discovery rate (FDR)) through pairwise comparison as valuable candidates for further investigation. Although further studies are still needed, our initial experimental results will define a novel gene set responding to temperature, and will help us to understand the blooms of *C. polykrikoides*.

[PD-07]

The discovery of novel stage-specific biomarkers for early detection of harmful marine organisms using transcriptome profiling analysis

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With the increase in worldwide traffic of marine vessels and ocean fishing, harmful marine organisms are increasing. These marine organisms are disturbing the domestic coastal ecosystem by invading the habitats of native marine life and destroying the food chain. This not only causes physical damage to aquaculture and fishery, but also destroys domestic coastal ecosystems and reduces the number of native species (Carver C and Mallet AL, 2003; Carver C and Vercaemer B, 2006; Januario S and Lima M, 2015). To cope with invasion of these harmful marine organisms, early detection of harmful marine organisms is a very important issue for ecosystem conservation and environmental protection in the coast. Together with conventional detection techniques including sonic wave, ultrasonic wave, biosensor, and DNA biomarker (Bok TH and Kang D, 2010; Kim E and Kang D, 2010; Scholin CA and Anderson DM, 1994), a detection method using DNA biomarkers has been known as one of the most efficient methods. However, the molecular biomarker-based method is difficult to detect in advance before the blooming of harmful organisms, and false detection may occur due to the dead debris flowing from the nearby sea.

In this study, we design a pipeline to find biomarkers that could detect harmful marine organisms early, by comparing and analyzing the transcriptome data at the stage of development, and used them to find candidates for biomarkers. By using RNA biomarkers through transcriptome analysis, it is possible to prevent the detection of fragments or DNA from the dead debris flowing in the vicinity. Also, it is possible to design stage-specific biomarkers of interest through the gene expression profiles of developing embryos and adult tissues.

In order to validate our proposed method, *Ciona intestinalis*, that is one of the global harmful marine organisms (Januario S and Lima M, 2015) and has large-scale developmental and adult transcriptome data sets (Matsuoka T and Satou Y, 2013; Ikeda T and Satou Y, 2013; Romiguier, Gayral et al., 2014), was tested. First, 56 and 23 transcriptome profiling datasets were collected from 12 different developmental stages and embryonic and 4 specific adult tissue types of *C. intestinalis*, respectively (Ikeda, Matsuoka et al. 2013). Two integrated data sets from each stage (embryonic vs. adult) were used to be classified into either embryonic-specific, adult-specific, and whole stages. As a result, we found 332 embryonic-specific transcripts and 102 adult-specific transcripts, which were uniquely expressed in each stage. In addition, 355 transcripts were found in the whole stage. Among them, we designed a primer for verification by randomly extracting two transcripts from embryonic-specific data for the early detection of harmful marine organisms. As a comparative group, we used two transcripts expressed in whole stage. cDNA was extracted from embryonic, planktonic, and adult stages of C. intestinalis and PCR was performed. Consequently, biomarkers selected from the embryonic-stage were correctly detected embryonic and planktonic cDNA, and biomarkers designed as transcripts expressed in the whole stage could be detected adult cDNA.

In this study, we have established a novel method for early detection of harmful marine organisms by using RNA, but not DNA biomarkers at each developmental stage. This method will be very helpful for early detection of harmful marine life and prevent damage. In the long run, this will help to stabilize the ecosystem of the oceans, thereby enhancing environmental, cultural and economic value.

[PD-08]

Loss of CpSRP components affected LHCP transport and assembly of thylakoid membranes in *Chlamydomonas reinhardtii*

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In chloroplast, photosynthetic apparatus in the thylakoid membranes converts light energy into chemical energy to perform various physiological processes. Therefore, proper arrangement of photosynthetic apparatus is critical factor for sustaining life of photosynthetic organism. Among the thylakoid membrane proteins, light harvesting chlorophyll-carotenoid binding protein (LHCP) takes a role in absorbing and transferring light energy for photosynthesis. Since genetic information of LHCP is located in nuclear genome, peptide of LHCP is synthesized in the cytosol and transferred into the chloroplast. After LHCP enters the chloroplast, LHCP takes a chloroplast signal recognition particle (CpSRP) pathway to reach its final destination, the thylakoid membranes. In higher plants, several proteins involved in CpSRP pathway were identified, including CpFTSY, CpSRP43 and CpSRP54. These proteins form a transit complex with LHCP to maintain solubility of the hydrophobic region of LHCP, then transports LHCP to the thylakoid membranes. However, in green microalgal *Chlamydomonas reinhardtii*, the function of CpSRP54 is unrevealed. Here, we investigated specific gene knockout mutants of proteins involved in CpSRP pathway [1]. The mutants were generated by random mutagenesis or currently developed methodology, RNA-guided engineered nucleases (RGENs) CRISPR-Cas9 [2]. Biochemical and physiological analyses of these mutants showed that *Chlamydomonas* CpSRP components are involved in LHCP transport and assembly, but may have different in vivo functions as compared to their higher plant counterparts. These characteristics may help to elucidate the evolution of the CpSRP system from green algae to higher plants.

[PD-09]

Study of the screening method of *H.pluvialis* mutants for enhancing the astaxanthin yield

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The keto carotenoid astaxanthin (3, 3’- dihydroxy - β, β – carotene - 4, 4’- dione) is a biologically active material useful for many applications and also exhibits higher antioxidant activity than that of β -carotene or vitamin E. *Haematococcus sp.*, the green alga, is known for its ability to accumulate keto carotenoid, astaxanthin in high concentrations under stress conditions. But in Korea, it is not easy to cultivate due to various climatic conditions. *Haematococcus pluvilais* be mutated by γ-ray irradiation to promte the astaxanthin yield and change to character for suitible culturing in korea. However, it is very difficult to screening the higher astaxanthin synthesis mutant. In this study *H. pluvilais* screened under herbicide, sodium chloride and peracetic acid conditions and also, screened under temperature conditions as like winter and summer. Herbicide resistant mutants are regarded as mutated at a specific of carotenoid biosynthesis gene. Sodium chloride and peracetic acid resistant mutants are used to protect *H. pluvilais* from other microalgae in outdoor culture. And mutant that can be culturable at 10 and 30℃ is for culturing at various weather conditions in Korea. Followed all above methods, several mutants were isolated.

[PD-10]

The methods for increasing Astaxanthin and DHA contents from *Schizochytrium* SHG 104

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Schizochytrium has been producing DHA (docosahexaenoic acid) and EPA (eicosapentaenoic acid). DHA and EPA is used to improve human cardiovascular disease such as high blood pressure, coronary artery diease, irregular pulse. So, many people ingests DHA and EPA from external colored fish like a sardine. However, fish has much heavy metals and then leads to take another disease. Spotlight of astaxanthin have been increased because of their anti-oxidative and anti-aging effects. Furthermore, this pigment has various function as immunity intensification, anti-diabetic effect and solved cardiovascular problems. Although synthetic anti-oxidative pigments are exist, natural sources astaxanthin is the best pigment for human. Extracted astaxanthin from this microalgal cell is 6,000 times stronger than Vitamin C and 550 times stronger than Vit. E. Astaxanthin reduce reactive oxygen species (ROS) which play a crucial role mentioned various disease at human body, skin, and other animals. We focus on the increasing astaxanthin contents in the microalgal cell, and then find various stress to microalgae for gaining higher pigment. Krill shrimp has astaxanthin in their body (approximately 0.01%) by intaking their environment. Nowadays, many people have been knowing krill oil and eating it for protecting anti-oxidative disease. However, krill oil is limited by Convention for the conservation of Antarctic marine living resources agreement (CCAMLR). Our research has been finding alternate materials to producing krill oil involve omega-3 and astaxanthin. At the result of this experiments, we have got high content of DHA (32.5%) and lipid accumulation (31.8%). Also, we can get 0.03% natural astaxanthin from Schizochytrium SHG 104. Astaxanthin is known for extremely anti-oxidant materials. Base on the results, we will try to conduct studies about increasing microalgal biomass and industrialization.

[PD-11]

Isolation and Characterization of high temperature tolerant strain in *Pyropia yezoensis*

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High temperature stress related to the global warming reduces growth and productivity of seaweeds and hence new strain development is urgently required for maintaining or even enhancing productivities of useful seedweeds such as *P. yezoenesis* against warming sea environment. To develop competitive high temperature tolerant strain in *P. yezoensis* (Sugwawon No. 104), we screened gamma-ray induced mutant libraries and identified high temperature resistant (HTR) mutants. Mutant strain HTR-1 and HTR-2 grew well at high temperature, at which wild type could not grow. Efficiency of conchosporangium maturation and conchospores release of HTR-1 was similar or higher compared to wild type. Performance of thallus growth, pigments contents, photosynthetic efficiency, and monospores release from the growing thallus in HTR-1 were highly maintained even at high temperature (20℃). Taken together, newly isolated high temperature tolerant strain showed better growth performance under high temperature growth condition. These results will be useful for strain development and cultivation of *P. yezoensis* and related species against sea warming environment.

[PD-12]

해양심층수를 활용한 스피룰리나 (*Arthrospira platensis*)의 광합성 색소와 항산화능 연구

김미성, 김용찬, 김영라, 김종현, 이정석, 한영석

㈜ 네오엔비즈 바이오사업부

해양 미세조류 스피룰리나 (*Arthrospira platensis*)는 50-70%의 많은 단백질과 각종 무기질, 비타민 등을 함유하고 있으며, 특히, 카로티노이드 (Carotenoids), 피코시아닌(Phycocyanin) 등의 유용색소가 풍부하여 항산화능이 뛰어난 건강기능식품 소재로 알려져 있다. 본 연구에서는 스피룰리나 배양액에 해양심층수소금과 미네랄농축수를 각각 첨가하여, 대조군 대비 광합성 색소와 항산화능을 비교하였다. 스피룰리나의 Chlorophyll *a* 색소함량은 심층수소금 > 미네랄농축수 > 대조군 순으로 나타났으며, Carotenoids 색소는 미네랄농축수 > 심층수소금 > 대조군 순으로 나타났다. c-Phycocyanin 색소는 심층수소금 > 미네랄농축수 > 대조군 순으로 높게 나타났다. 스피룰리나의 Total polypheonol 함량은 미네랄농축수, 심층수소금 > 대조군 순으로 높게 나타났으며, DPPH 라디칼 소거능 또한 미네랄농축수 > 심층수소금 > 대조군 순으로 나타났다. 종합해볼 때, 미네랄농축수를 첨가한 배지에서 자란 스피룰리나의 Carotenoids 색소가 가장 높게 증가하였으며, DPPH 라디칼 소거능 또한 높게 나타났는데, 이는 스피룰리나의 유용색소가 증가하면서 이에 따라 항산화능도 증진된 것이라 사료된다.

[PD-13]

Development of Efficient Transformation and Selection Methods for Microalgae

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Although microalgae including Chlorella are a very attractive organism for the expression of foreign protein to overcome some limitation of *Escherichia coli* expression system such as the lack of post-translational modification, microalgae expression system has some drawbacks. One of the limitations is the natural resistance of microalgae to antibiotics commonly used as selection makers. A new method for the efficient transformation and selection of the transformed chlorella was developed. The target gene, the VHSV glycoprotein with the cauliflower mosaic virus 35S promoter and *Chlamydomonas* rbcs gene terminator was flanked by DNA fragments form the nitrate reductase (NR) gene of Chlorella vulgaris. After introduction into *Chlorella vulgaris* by electroporation, the target DNA can be integrated into the *Chlorella vulgaris* chromosome by double homologous recombination, which confers resistance against $KClO_3$ which is converted into toxic ClO_2^- by NR. Transformants were successfully selected on a plate containing 150mM of $KClO_3$ and integration of the target gene and expression of the VHSV G protein was confirmed by PCR and western blot, respectively.

[PD-14]

신품종 심사를 위한 나문재의 특성조사요령

김승오, 김경환, 황일기, 이채길, 황미숙

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품종보호제도는 국제적으로 식물 신품종의 지식재산권을 보호함으로써 신품종 개발을 촉진하고 우수품종 이용을 확대하여 농림수산업의 생산성 증대와 농어업인의 소득을 증대시킬 수 있는 긍정적인 효과가 기대되면서 전 세계 76개국에서 확대 시행되고 있다. 특히 세계 각국이 공통의 기본 원칙에 따라 신품종을 보호하기 위하여 1968년 국제기구인 국제식물신품종보호동맹(UPOV)이 결성되었고, WTO (세계무역기구) TRIPs협정(지식재산권협정)에 따라 모든 가입 국가에게 그 실시를 의무화하고 있다. 염생식물은 염분 농도가 높은 토양에 적응하여 자라는 식물로 전 세계에 1,500여 종이 생육하고 있으며, 국내에는 134종이 분포한다. 염생식물은 법령상 광의의 해양식물(해조류, 해초류, 염생식물)로 분류되고 있으며, 최근에는 혈압조절, 혈당개선, 다이어트, 변비 등에 효과가 있는 것으로 알려지면서 건강식품으로 수요가 증가하고 있다. 따라서, 국내에서 재배되고 있는 염생식물의 신품종 심사에 필요한 특성조사요령 제정이 필요하다. 이에 본 연구에서는 염생식물 나문재를 대상으로 2014년부터 2015년까지 자생지와 재배지에서 분류학적 형질특성 자료를 확보하여 나문재의 특성조사요령을 제정하였다. 특성조사요령은 신품종 출원 및 출원품종 재배심사 시 필요한 조사형질과 이에 대한 조사시기, 조사방법 등을 제시하고 있다. 조사형질은 지상부 높이, 지상부 너비, 뿌리의 측근 발달 정도, 줄기의 분지 횟수, 줄기의 직경, 잎의 색, 열매의 크기 등 15개 형질이다.

[PD-15]

Rapid transformation of *Chlamydomonas reinhardtii* using Subtilisin (Alcalase)

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The algal cell wall is a potent barrier for the delivery of protein-gRNA complexes needed for CRISPR/Cas-based targeted gene editing. Conventional methods developed for higher plant systems are often unable to penetrate or remove algal cell walls owing to their unique physical and chemical properties. We developed a simple transformation method for *Chlamydomonas reinhardtii* using commercially available enzymes. Of seven enzymes screened for cell wall disruption, Subtilisin (Alcalase) was most effective at a low concentration (0.3 Anson units/mL). The efficiency was comparable to that of gamete lytic enzyme, a protease commonly used for the genetic transformation of *C. reinhardtii*. The transformation efficiency of our non-invasive method was similar to that of methods using Autolysin as a cell wall-degrading enzyme in conjunction with glass bead transformation. Subtilisin shared approximately 35% sequence identity with sporangin, a hatching enzyme of *C. reinhardtii*, and shared conserved active domains, which may explain the effective cell wall degradation by Subtilisin. Our transformation method using Subtilisin may be useful for the non-invasive delivery of protein-gRNA complexes into algal cells.

[PD-16]

Effect of nutrient limitation on lipid production by *Chlamydomonas reinhardtii*

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Both lipid and free fatty acid are regulated by nutrient sources in microalgae. In this study, newly developed mutant *Chlamydomonas reinhardtii* Cr-4013 was investigated for the effect of nutrient limitation. Nitrogen NO_3^- and phosphate PO_4^{3-} were respectively limited during the cultivation. By the nutrient limitation, the cell growth was retarded, but the content of lipid was increased. Under nutrient starvation condition, total lipid content level was increased to 27~33% and C16:0 fatty acid content constituted over 31~43% of total fatty acid.

[PD-17]

Anti-ulcer effect of polysaccharides from *Undaria* sp.

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In this study, the effects of polysaccharides from *Undaria* sp. was evaluated on biochemical (aspartate and alanine transaminases, creatinine, blood urea nitrogen (BUN), total cholesterol and triglyceride) and immunological parameters such as cytokines (INFγ, IL-6 & IL-10) on aspirin-induced ulcer in rats. The status of stomach tissue glycogen storage and histological changes were also examined. Examination of basic biochemical parameters using auto analyzer showed significant ($p < 0.01$) alterations in aspartate and alanine transaminase (AST & ALT) in ulcer induced animals. Analysis of aspirin treated rats serum cytokines using enzyme linked immunosorbent assay showed a moderate decrease in IL-10 with considerable increase of IL-6 and INF-γ as compared to control. Histopathological examination showed neutrophil infiltration, inflammation in oxyntic cells with altered glycogen storage (Periodic acid Schiff's staining). Administration of polysaccharides from *Undaria* sp. showed considerable ($p < 0.05$) protection against ulceration by inhibiting the acute alterations of AST, ALT, cytokines and stomach glycogen. The effect of molecular weight of polysaccharides was also considered. Rats that received lower molecular weight polysaccharides (0.02 g/kg body weight, for two weeks p.o) also showed moderate inhibition on altered parameters as compared with ulcerated rats. These findings suggest the anti-ulcer property of polysaccharides from *Undaria* sp.

[PD-18]

Optimized process for the sequential production of lipid and carotenoids from *Ettlia* sp.

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The main problem with microalgae-based biodiesel production is higher production costs than petroleum-based fuels. Microalgae produce not only lipid for biodiesel, but also lutein and β-carotene which can be used as colorants and antioxidants. Nitrogen starvation stress is more suitable to produce lipids for biodiesel due to the increase of neutral lipids than membrane lipids. In this study, a two-stage process was operated and each stage was optimized for the production of three materials: lipids, lutein, and beta-carotene. In the first stage, temperature and light quality stress were applied. The highest biomass was obtained with white light at 25°C. However, the maximum lutein content in cells was achieved with blue light at 10°C. Lipid contents were similar regardless of light quality. In the second stage, UV-A and nitrogen starvation were applied. UV stress increased chlorophyll-*a* and β-carotene content. Oleic acid and β-carotene were increased under nitrogen starvation and the color of *Ettlia* sp. turned from green to brownish orange. Lutein was the main carotenoid in the first stage, but β-carotene in the second stage. This study proved that *Ettlia* sp. as an ideal feedstock for commercial production of lutein, β-carotene, and biodiesel is qualified.

[PD-19]

세포분열능이 우수한 *Haematococcus pluvialis* B0103의 Astaxanthin 생산 방식 개선에 관한 연구

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Astaxanthin은 강력한 천연 항산화물질로 여러 산업에 활용되고 있다. Astaxanthin은 새우나 가재 같은 갑각류에서 주로 추출할 수 있지만 항산화 성능이 낮고 사람에게 적용하기가 어려워 Haematococcus pluvilis에서 대량생산을 하는 연구가 많이 진행되고 있다. 일반적으로 아스타잔틴을 합성할 때, 세포에 광 및 영양염 스트레스를 주어 생합성을 유도하는데, 이때 많은 세포가 사멸하게 된다. 이러한 문제를 해결하기 위해 감마레이 조사를 통해서 광 스트레스 내성이 높은 종균을 개발하였다. 일반적인 종균은 광 자극 시 세포벽이 두꺼워지고, 세포가 커지면서 세포수가 지속적으로 줄어드는데 반면, B0103의 경우 250umom2s-1 이상의 높은 광에서도 편모가 있는 유동세포가 많고 우수한 분열능을 보이며 꾸준히 세포수가 증가하는 것을 볼 수 있다. 특히 B0103은 적색세포단계에서 편모가 있는 유동세포를 가졌기 때문에 아스타잔틴 추출에 유리할 것으로 판단된다. 실험결과 감마레이를 통해 선별된 돌연변이 B0102, B0103, B0104, B0105 균체중 B0103이 녹색세포단계에서 바이오매스 성장률, 영양염 섭취는 비슷하지만 높은 광량에서 최종 세포의 생존율이 높고, 세포당 아스타잔틴 함량이 3.5% 수준으로 나타나 아스타잔틴 생산에 가장 유리한 것으로 나타났다

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[PD-20]

The anti-cancer compounds Saringosterol acetate from Hizikia fusiforme inhibit cancer cell growth and PIK3/AKT/mTORpathway on Hep3B and Du145 cancer cell lines.

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Hizikia fusiforme, an edible brown alga, is widely consumed in Korea, Japan, and China and possesses a number of potentially beneficial biological functionalities, including anti-oxidants, anti-coagulant, anti-cancer, and anti-inflammation. In this study, we isolated a Saringosterol from the brown alga and examined whether it could inhibit cell growth against cancer cell lines. Therefore, the potent anti-cancer effects of saringostrol acetate (SSA) isolated from 70% EtOH extraction of H. fusiforme was investigated for its inhibitory effects on liver and prostate cancer in Hep3B and Du145 cell lines. The SSA markedly inhibited cancer cell growth and increased the population of cells in sub-G1 compared to the control. Furthermore, we confirmed that the mechanism involved in this process occurs through PI3K/Akt/mTOR pathway an important regulator of cell growth, metabolism, survival, metastasis, and resistance to chemotherapy. Therefore, SSA significantly reduced the expression of PI3K, Akt, mTOR protein levels in both cells. These results indicated that the SSA has the potential to be used in applications related with nutraceuticals or functional foods to reduce carcinogenic effects.

[PD-21]

Functional expression and characterization of GlcNAc specific marine algal lectin, BPL3

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당결합단백질인 렉틴은 탄수화물과 결합하는 특성으로 인해, 의학•학술적 용도로서 잠재적 활용가치가 높으나, 활성을 갖는 재조합 렉틴의 생산은 일부 렉틴에 한정되어 보고되고 있다. 참깃털말로부터 유래된 *Bryopsis plumosa* lectin (BPL3)는 GlcNAc와 GalNAc에 특이성을 가지는 렉틴으로 분자탐침 등의 소재로서 활용 가능성이 제시되었다. 본 연구에서는 반복된 서열을 갖는 렉틴의 서열 구조를 모방하여 높은 활성을 가지는 렉틴을 생산하는 방법을 제시하였다. Recombinant BPL3 (rBPL3)는 pET28a(+) system과 BL21(DE3)를 이용하였을 때 높은 발현율을 나타냈다. 발현된 rBPL3는 Ni-NTA 친화크로마토그래피를 이용하여 정제하였으며. rBPL3의 단백질 서열은 LC-MS/MS spectrometry를 이용하여 분석하였다. 짧은 Spacer를 이용하여 연결된 연쇄반복 구조의 BPL3는 천연의 BPL3와 동일한 혈구 응집 활성을 가지고 있었으나, 단일 copy의 BPL3는 혈구 응집 활성을 나타내지 않았다. rBPL3는 단당류인 GlcNAc와 GalNAc에 의해 활성이 저해 되었다. rBPL3는 2가 양이온에 의해 활성에 영향을 받지 않으며, 70°C에서 온도 안정성을 나타내었다. 이러한 결과는 BPL3의 재조합단백질이 기존의 천연물과 동일한 생화학적 특성을 가짐을 알 수 있다. 당결합특성을 규명하기 위해 Glycan array를 수행하였으며, 잠재적인 산업적 가치에 대해 논하였다.

[PD-22]

Inhibition of inflammatory responses elicited by urban fine dust particles in keratinocytes and macrophages by diphlorethohydroxy-carmalol isolated from a brown alga *Ishige okamurae*

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Fine dust (FD) particles have become a major contributor to air pollution causing detrimental effects on the respiratory system and skin. Although some studies have investigated the effects of FD on the respiratory system, their possible effects on the skin remain under-explored. We investigated the FD mediated inflammatory responses in keratinocytes, present in the outer layers of skin tissues and the transfer of inflammatory potential to macrophages. We further evaluated the anti-inflammatory effects of the polyphenolic derivative, diphlorethohydroxycarmalol (DPHC) isolated from *Ishige okamurae* against FD-induced inflammation. Size distribution of FD particles was analyzed by scanning electron microscopy. FD particles induced the production of cyclooxygenase-2, prostaglandin E2 (PGE2), interleukin (IL)-1β, and IL-6 in HaCaT keratinocytes and the expression of nitric oxide (NO), inducible nitric oxide synthases (iNOS), PGE2, tumor necrosis factor-α expression in RAW 264.7 macrophages. Further, we evaluated the inflammatory potential of the culture medium of inflammation-induced HaCaT cells in RAW 264.7 macrophages and observed a marked increase in the expression of NO, iNOS, PGE2, and proinflammatory cytokines. DPHC treatment markedly attenuated the inflammatory responses, indicating its effectiveness in suppressing a broad range of inflammatory responses. It also showed anti-inflammatory potential in *in-vivo* experiments using FD-stimulated zebrafish embryos by decreasing NO and reactive oxygen species production, while eventing cell death caused by inflammation.

[PD-23]

Anti-inflammatory effects of a sulfated polysaccharide isolated from an enzymatic digest of brown seaweed *Sargassum horneri*

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The present study was performed to evaluate the anti-inflammatory activities of crude polysaccharides (CPs) extracted from *S. horneri* in lipopolysaccharide (LPS)-stimulated RAW 264.7 cells. CPs were precipitated from *S. horneri* digests prepared by enzyme assistant extraction using four food-grade enzymes (AMG, Celluclast, Viscozyme, and Alcalase). The production levels of nitric oxide (NO) and pro-inflammatory cytokines, including tumor necrosis factor (TNF)-α and interleukin (IL)-1β were measured by Griess assay and enzyme-linked immunosorbent assay, respectively. The levels of inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2), nuclear factor (NF)-κB, and mitogen-activated protein kinases (MAPKs) were measured by using western blot. The polysaccharides from the Celluclast enzyme digest (CCP) showed the highest inhibition of NO production in LPS-stimulated RAW 264.7 cells (IC_{50} value: 95.7 μg/ml). Also, CCP dose-dependently down-regulated the protein expression levels of iNOS and COX-2 as well as the production of inflammatory cytokines, including TNF-α and IL-1β, compared to the only LPS-treated cells. In addition, CCP inhibited the activation of NF-κB p50 and p65 and the phosphorylation of MAPKs, including p38 and extracellular signal-regulated kinase (ERK), in LPS-stimulated RAW 264.7 cells. Furthermore, FT-IR analysis showed that the FT-IR spectrum of CCP is similar to that of commercial fucoidan. Our results suggest that CCP has anti-inflammatory activities and is a potential candidate for the formulation of a functional food ingredient or/and drug to treat inflammatory diseases.

[PD-24]

Protective effect of a novel antioxidative peptide purified from a marine *Chlorella ellipsoidea* protein against oxidative stress induced by free radicals

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The imbalance of reactive oxygen species (ROS) level in human body generally induces a variety of pathological conditions. The cellular defense mechanisms play an important role in preventing harmful effects caused by ROS. Synthetic antioxidants are used to prevent damage by ROS and these antioxidants are associated with adverse effects in human. Thus there is a greater demand for the natural antioxidants; therefore researchers pay their attention toward the isolation of compounds from natural resources. Marine ecological system is rich with large biodiversity and still it is not explore completely. This study is based isolation of peptide from marine micro alga *Chlorella ellipsoidea*. Protein derived the marine *Chlorella ellipsoidea* was hydrolyzed using different proteases for production of antioxidative peptide, and the antioxidant activities of their hydrolysates were investigated using free radical scavenging assay by electron spin resonance spin-trapping technique. Among the hydrolysates, the peptic hydrolysate exhibited the highest antioxi-dant activity compared to other hydrolysates. To identify antioxidant peptide, the peptic hydrolysate was purified using consecutive chromatographic methods, and the antioxidant peptide was identified by Q-TOF ESI mass spectroscopy. The antioxidant peptide scavenged peroxyl, DPPH and hydroxyl radicals at the IC_{50} values of 0.02, 0.92 and 1.42 mM, respectively. The purified peptide enhanced cell viability against AAPH-induced cytotoxicity on normal cells. Furthermore, the purified peptide reduced the proportion of apoptotic and necrotic cells induced by AAPH, as demon-strated by decreased sub-G_1 hypodiploid cells and decreased apoptotic body formation by flow cytometry.

[PD-25]

Marine algal polyphenols stimulate muscle growth in C2C12 muscle cells through myogenesis pathways

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Skeletal muscle is very important organ in energy metabolism and athletic performance. Synthetic muscle growth effective supplements and drugs have been shown to exhibit various side effects. Moreover, it is regulated by doping when athletes take. Therefore, we evaluated the muscle growth effect of substances that can act like synthetic supplements from edible seaweeds. First, we isolated 6 marine algal polyphenols like phlorotannins [dieckol (DK), 6,6’-bieckol (6,6-BK), 2,7’- phloroglucinol-6,6”-bieckol (PHB), phlorofucofuroeckol A (PFFA), phloroglucinol-6,6’-bieckol (PBK), and phloroglucinol (PG)] from an edible brown alga, *Ecklnoia cava* and evaluated C2C12 myoblasts proliferation and differentiation activities. Among 6 phlorotannins, DK and PHB exhibited proliferation of C2C12 myoblasts. In addition, DK and PHB regulates myogenesis through down-regulating the Smad signaling, a negative regulator, and up-regulating the IGF-1 (insulin-like growth factor-1) signaling, a positive regulator. Interestingly, DK and PHB strongly bind to myostatin, which is Smad signaling upstream protein. Moreover, they bind to IGF-1 receptor. Therefore, we suggest that DK and PHB would be new muscle growth materials in functional resources instead of synthetic drugs.

[PD-26]

Green TD- A New Environment-Friendly Algicidal Compound

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지구온난화와 수자원 부영양화가 심화됨에 따라 세계적으로 강과 호수, 그리고 바다에 유해조류 대발생의 빈도 및 그에 의한 피해 규모가 매년 증가하고 있다. 국내에서는 이에 더하여 4대강에 16개보 설치 이후 담수자원의 *Microcystis sp.*같은 유해녹조류의 대발생이 큰 사회문제가 되고 있으나, 녹조류를 제거 및 예방하는데 있어 현재까지 뚜렷한 해결책이 없는 상황이다. 본 연구진은 이러한 문제점을 해결하기 위해 지금까지 연구를 수행한 결과 유해녹조류 제거에 탁월한 효과가 있는 Green TD를 개발하였다. Green TD는 0.5 ppm 이하의 매우 낮은 농도에서 유해종인 *Microcystis sp.*에 대해 24시간 만에 약 70%의 살조능을 보였으며, 1주일 이내에 약 95% 이상의 살조능을 보였다. 또한, 실제 녹조 대발생이 일어난 경기도 수원시 서호, 경기도 의왕시 왕송호수, 경남 김해시 상동면 낙동강 지역 녹조수를 직접 채취하여 Green TD의 살조능을 시험한 결과, 24시간 이내에 뚜렷한 녹조 제거 효과를 관찰할 수 있었다. Green TD의 물벼룩과 송사리에 대한 독성 시험결과, 50% 개체수가 치명적 영향을 받는 48시간 EC_{50} 값과 LC_{50} 값이 각각 9.6 ppm과 54.6 ppm으로 낮은 독성을 보였으며, 전혀 영향을 받지 않는 48시간 EC_{50} 값과 LC_{50} 값은 각각 3.13 ppm과 25 ppm으로 나타나, Green TD의 처리농도인 0.5 ppm에서는 전혀 환경독성이 나타나지 않는 것으로 나타났다. 이러한 실험결과를 바탕으로 현재 "화학물질 등록 및 평가에 관한 법률"에 근거한 물질등록을 위한 다양한 안전성 시험을 진행하고 있다.

[PD-27]

Seaweed beer: an application of seaweed biomass

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Seaweed biomass has been used for various applications, including human food, animal feed, fertilizer, beauty, household and medical products, biofuel, etc. In Korea, the uses of seaweed biomass have been rather limited to human food and animal feeds. In America and Europe, seaweed has also been used for an ingredient for beer during the past decade. In Korea, however, very few attempts have been made to utilize seaweed to brew beer. In the present study, four seaweed species, *Pyropia*, *Saccharina*, *Undaria* and *Ulva* were added during the brewing process to make *seaweed beer*. Three types of seaweeds were used during the fermentation process, including seaweed extract, seaweed powder and dried seaweed. As a control, no seaweed was added. Blind taste tests were conducted and the test results will be presented.

[PD-28]

Identification and Characterization of an Isoform Antifreeze Protein from the Antarctic Marine Diatom, *Chaetoceros neogracile* and Suggestion of the Core Region

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Antifreeze proteins (AFPs) protecting the cells against freezing are produced in response to extremely low temperatures in diverse psychrophilic organisms, and they are encoded by multiple gene families. The AFP of Antarctic marine diatom *Chaetoceros neogracile* is reported in our previous research, but like other microalgae, was considered to probably have additional genes coding AFPs. In this paper, we reported the cloning and characterization of additional AFP gene from *C. neogracile* (*Cn-isoAFP*). Cn-isoAFP protein is 74.6% identical to the previously reported Cn-AFP. The promoter sequence of *Cn-isoAFP* contains environmental stress responsive elements for cold, thermal, and high light conditions. *Cn-isoAFP* transcription levels increased dramatically when cells were exposed to freezing (−20 °C), thermal (10 °C), or high light (600 μmol photon $m^{-2}s^{-1}$) stresses. The thermal hysteresis (TH) activity of recombinant Cn-isoAFP was 0.8 ℃ at a protein concentration of 5 mg/mL. Results from homology modeling and TH activity analysis of site-directed mutant proteins elucidated AFP mechanism to be a result of flatness of B-face maintained via hydrophobic interactions.

[PD-29]

Control of zooplankton populations using CO2 asphyxiation: from laboratory cultures to a wastewater treatment High Rate Algal Pond

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High Rate Algal Ponds (HRAPs) with addition of CO2 are open pond wastewater treatment systems that recover nutrients as microalgal biomass. Such ponds are vulnerable to contamination by opportunistic zooplankton species able to survive the wastewater HRAP environment. The high food availability and a near neutral pH can promote the rapid development of high densities of zooplankton that can reduce treatment performance by consuming microalgae, particularly when they are easily ingestible by cladocerans and rotifers. CO2 asphyxiation is a promising treatment to control zooplankton density, and here we assessed its potential at three different scales. In controlled laboratory experiments, water CO2 concentrations between 320 mg/l and 2,000 mg/L caused mortality of the rotifers Brachionus calyciflorus and Brachionus rubens in time periods ranging from 3 min to 80 min; of the cladoceran Moina tenuicornis between 3 min and 30 min, and of the ciliate Paramecium spp. between 2 min and 5 min. In outdoor mesocosms with physicochemical and operational conditions similar to those of full scale HRAPs, a constant CO2 concentration of ~100 mg/L both during summer and winter periods maintained low pond water zooplankton densities, while a constant concentration of ~180 mg/L killed all microcrustaceans and rotifers present. CO2 treatments were associated with algal biomass (VSS), productivity, and chlorophyll-a concentration up to 147.2%, 154.4%, and 178.9%, respectively, compared to the control, during summer time. In an 8 m3 wastewater HRAP, night CO2 asphyxiation controlled zooplankton densities over 14 months. Pure CO2 flow rates between 2 L/min and 6 L/min promoted maximum CO2 concentrations between 167 mg/l and 420 mg/L, minimum pH between ~5 and ~6, and reduced the population densities of the cladoceran M. tenuicornis, the rotifers B. calyciflorus, F. longiseta, and Cephalodella catellina to ≤10% of that before treatment, in periods of time between 1 and 12 nights. Moreover, the cladoceran Daphnia thomsoni and the rotifer Brachionus urceolaris established only in the control HRAP. Zooplankton control by CO2 asphyxiation improved the overall performance of the treated WW HRAP compared to the control in several ways, including increasing algal biomass (VSS) (150.8%), productivity (151.4%), chlorophyll-a concentration (161.8%), and average settleability efficiency (189.2%). Both permanent and overnight CO2 asphyxiation showed the potential to control zooplankton and to promote better WW HRAPs performance.

후원사

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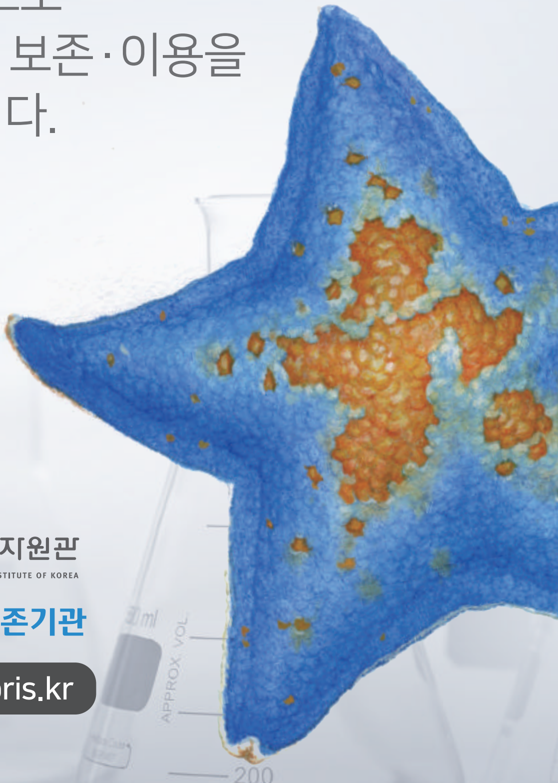

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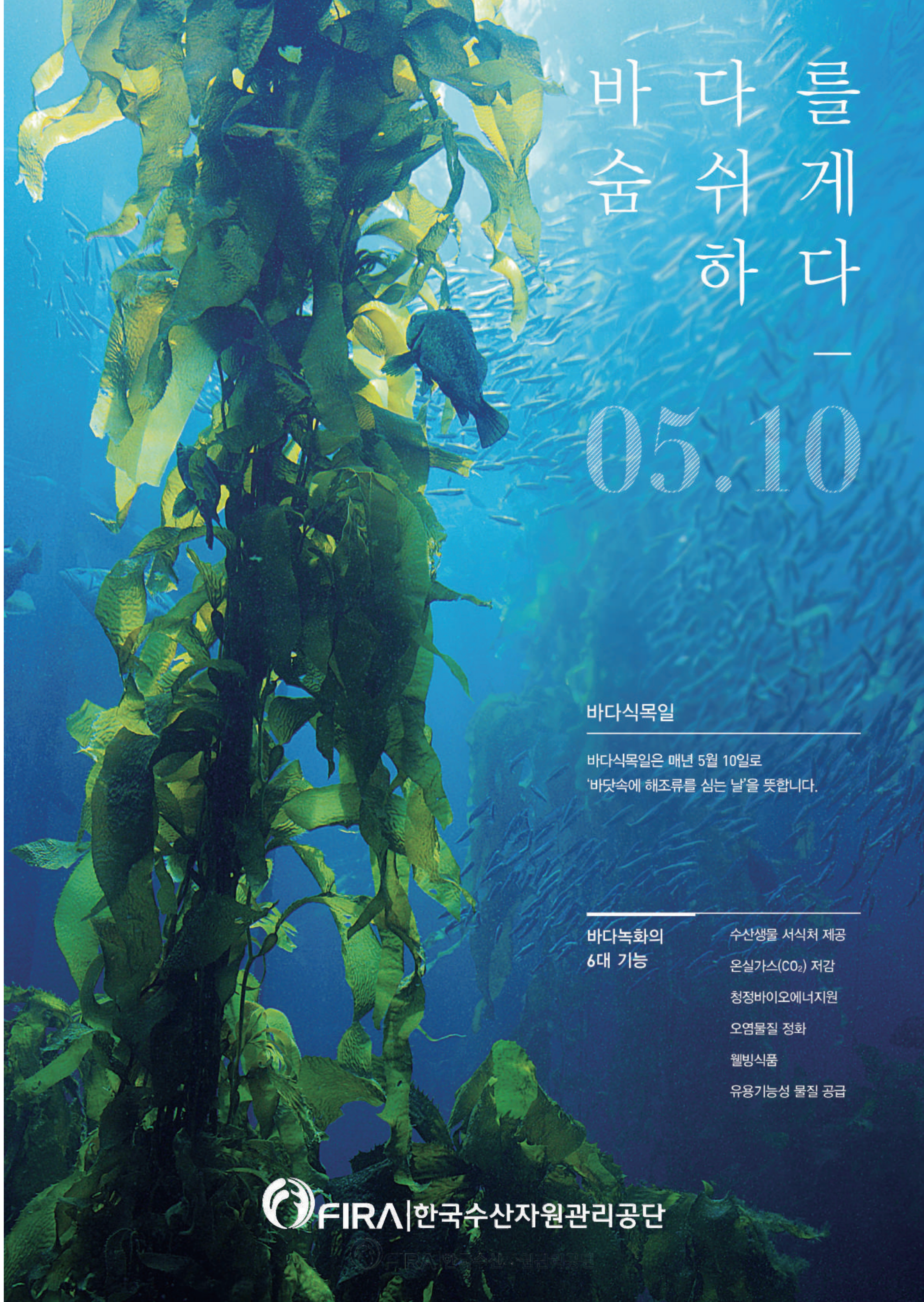

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