General Information

Registration

Place: Sejong University Convention Center, Gwang-Gae-To Building B2 Convention Hall Lobby
Registration fee:

(KRW)

	Regular	Student	Undergraduate
Pre-Registration	80,000	40,000	10,000
On-Site Registration	100,000	60,000	

Information for Poster Presentation

Poster Presentation

Date	Posting Time	Presentation Time
Oct 25 (Fri)	09:00~18:00	15:00~16:00

Poster Topics

A Systematics and Evolution / 계통 및 진화
B Environment and Ecology / 환경 및 생태
C Physiology and Biochemistry / 생리 및 생화학
D Fermentation and Metabolites / 발효 및 대사산물
E Genetics and Genome / 유전 및 유전체
F Infection and Pathogenesis / 감염 및 병인기전
G Immunology and Signal Transduction / 면역 및 신호전이
H Biotechnology / 생물공학
I Food Microbiology / 식품미생물학
J Others / 기타

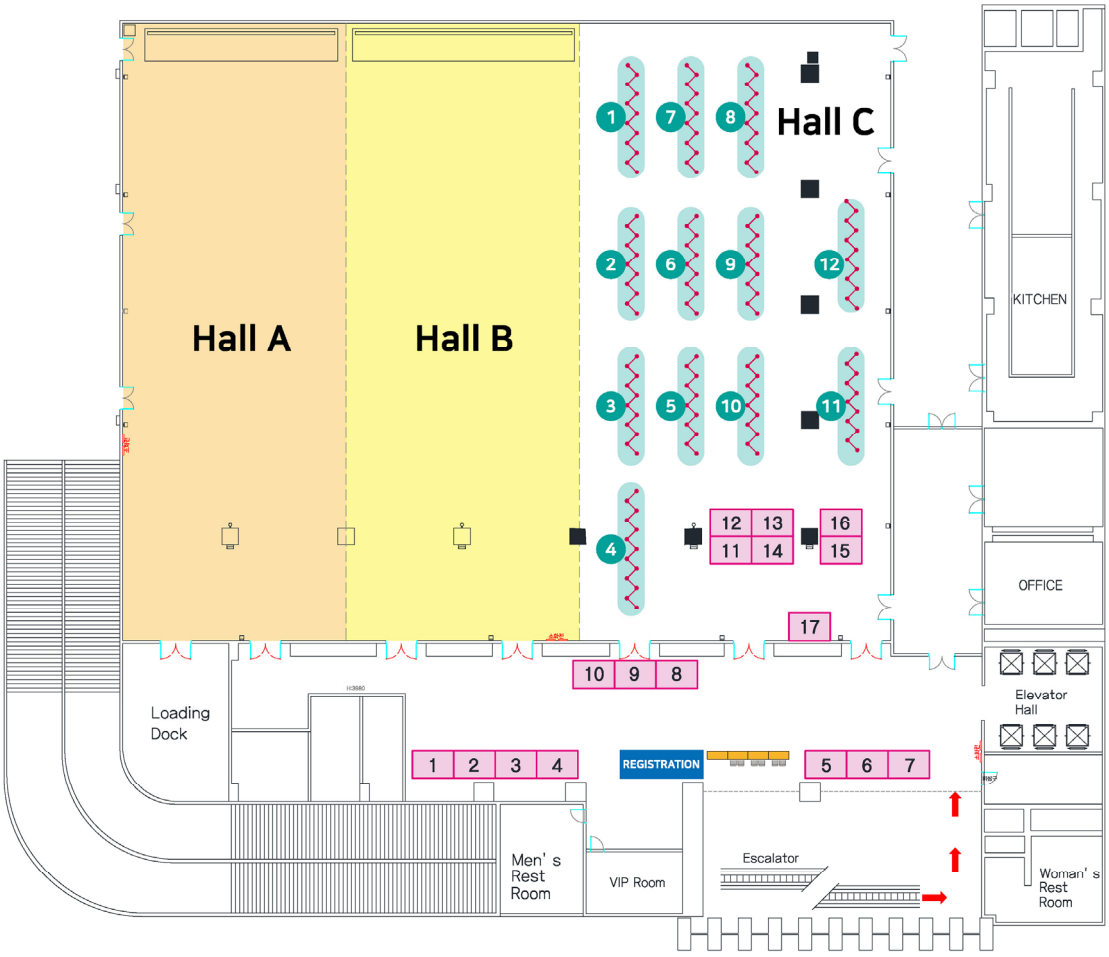
Poster Presentation Layout

Zone	Poster Number	Zone	Poster Number
1	A033-A042, F025 | B001-B011	7	D006-D012, E001-E004 | E005-E015
2	A023-A032 | B012-B021	8	H013-H023 | H024-H034
3	A013-A022 | B022-B032	9	H003-H012 | H035-H043, I001
4	A001-A012 | B033-B041, C001-C003	10	F018-F024, G001, H001-H002 | I002-I011
5	C004-C013 | F008-F017	11	I012-I019, J001-J002 | J023-J032
6	C014-C018, D001-D005 | E016-E018, F001-F007	12	J003-J012 | J013-J022

Timetable

10.25.(Fri)	Convention Hall A	Convention Hall B
08:50-09:00	Opening Address (Hall B)	
09:00-11:00		FKMS Session 1 Jaehyuk Choi (Incheon National University) Jin-Won Song (Korea University) You-Hee Cho (CHA University) Jong-Chan Chae (Chonbuk National University)
11:00-11:20	Break time	
11:20-12:00		Plenary Lecture Linda J. Kenney (National University of Singapore and University of Texas Medical Branch, USA)
12:00-13:30	Lunch	
	KSMy GM (한균 총회)	MSK GM (한미 총회)
13:30-15:00	Students' Presentation Session Dukyun Kim (Seoul National University) Min Ji Kim (Chungnam National University) Sewoong Kim (Korea University) June-Young Lee (Kyung Hee University) Jeong-Eun Kwak (KAIST) Kyeong Ryeol Shin (Korea University) Soo-Jin Oh (Korea University) Kwang-Min Yu (Chungbuk National University) Monmi Pangging (Chonnam National University) Yo-Han Ko (Chonbuk National University) Ki Hyeong Park (Seoul National University) Jong-Hwan Shin (Kangwon National University) Geeta Chhetri (Dongguk University) Donghyeun Kim (Chung-Ang University) Jin Ju Kim (Chung-Ang University) Seung-Dae Choi (Kyungpook National University)	FKMS Session 2 Jae-Ho Shin (Kyungpook National University) Sukhwan Yoon (KAIST) Junhyun Jeon (Yeungnam University)
15:00-16:00	Poster Presentation (Hall C)	
16:00-17:30		FKMS Session 3 Hosun Park (Yeungnam University) Sang Sun Yoon (Yonsei University) Won Hee Jung (Chung-Ang University)
17:30-18:00	Closing Ceremony (Hall B)	

Floor Plans



Convention Hall A	Students' Presentation Session
Convention Hall B	Opening Address, Plenary Lecture, Symposia, Closing Ceremony
Convention Hall C	Exhibition, Poster Session
Convention Hall Lobby	Registration Desk, Exhibition, Secretariat

Scientific Program

Plenary Lecture

PL Plenary Lecture

October 25 (Fri), Convention Hall B

Chair: You-Hee Cho (CHA University)

11:20-12:00

Imaging *Salmonella* Lifestyles

Linda J. Kenney (National University of Singapore and University of Texas Medical Branch, USA)

Symposium

S1 FKMS Session 1

October 25 (Fri), Convention Hall B

Chair: Jong-Chan Chae (Chonbuk Nat'l Univ.)

S1-1 09:00-09:30

Genetic Diversity and Dye-decolorizing Spectrum of the *Schizophyllum commune* Population

Jaehyuk Choi (Incheon National University)

S1-2 09:30-10:00

Active Surveillance and History of Hantaviruses, a New Family Hantaviridae in the Order Bunyavirales

Jin-Won Song (Korea University)

S1-3 10:00-10:30

New Insights into Phage Life Cycles through *Drosophila*-based Evaluation of Phage Therapy

You-Hee Cho (CHA University)

S1-4 10:30-11:00

From Microbial Degradation to Microbial Synthesis

Jong-Chan Chae (Chonbuk National University)

S2 FKMS Session 2

October 25 (Fri), Convention Hall B

Chair: Jae-Ho Shin (Kyungpook Nat'l Univ.) & Sukhwan Yoon (KAIST)

S2-1 13:30-14:00

Yes, Now We Know the Bacteria in Our Poop. How Do We Use It?

Jae-Ho Shin (Kyungpook National University)

S2-2 14:00-14:30

Multimodal Influence of Methanotrophic Community on Nitrous Oxide Emissions from Soil Denitrification

Sukhwan Yoon (KAIST)

S2-3 14:30-15:00

Epigenetic Regulation of Fungal Development and Pathogenicity in the Rice Blast Fungus

Junhyun Jeon (Yeungnam University)

S3 FKMS Session 3

October 25 (Fri), Convention Hall B

Chair: Sang Sun Yoon (Yonsei Univ.) & Won Hee Jung (Chung-Ang Univ.)

S3-1 16:00-16:30

Group B Coxsackievirus Induced Pregnant Loss and Infertility

Hosun Park (Yeungnam University)

S3-2 16:30-17:00

Bacterial Infection Controls Enabled by Neighboring Commensals

Sang Sun Yoon (Yonsei University)

S3-3 17:00-17:30

Genomic Analysis of Antifungal Resistance of *Malassezia restricta*

Won Hee Jung (Chung-Ang University)

Students' Presentation Session

SS Students' Presentation Session

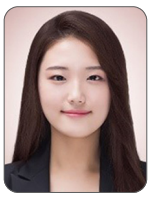
October 25 (Fri), Convention Hall A

Chair: Sung Ho Yoon (Konkuk Univ.) & Eun-Jin Lee (Korea Univ.)

SS-1 13:30-13:35

Transcriptomic Identification and Biochemical Characterization of HmpA, a Nitric Oxide Dioxygenase, Essential for Pathogenesis of *Vibrio vulnificus*

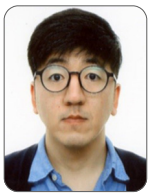
Dukyun Kim (Seoul National University)



SS-2 13:35-13:40

Taxonomy and Antimicrobial Potential of *Micromonospora* sp. Isolated from Riverside Soil

Min Ji Kim (Chungnam National University)



SS-3 13:40-13:45

Tor1 and Sch9 Coordinately Regulate Hyphae Specific Genes or Ribosomal Protein Genes in *Candida albicans*

Sewoong Kim (Korea University)

SS-4 13:45-13:50

Reshaping of the Gut Microbiota in Small Heterodimer Partner Deficient Mice

June-Young Lee (Kyung Hee University)

SS-5 13:50-13:55

Development of a DNA Vaccine for SFTSV that Confers Complete Protection against Lethal Infection in Ferrets

Jeong-Eun Kwak (KAIST)

SS-6 13:55-14:00

Development of Bivalent Vaccines for Poultry

Kyeong Ryeol Shin (Korea University)

SS-7 14:00-14:05

Whole Transcriptome Analyses Reveal Differential mRNA and microRNA Expression Profiles in Primary Human Dermal Fibroblasts Infected with Clinical or Vaccine Strains of Varicella Zoster Virus

Soo-Jin Oh (Korea University)

SS-8 14:05-14:10

Shedding and Transmission Modes of Severe Fever with Thrombocytopenia Syndrome Virus in a Ferret Model

Kwang-Min Yu (Chungbuk National University)

SS-9 14:10-14:15

Novel Fungal Species from Aquatic Environments in Korea

Monmi Pangging (Chonnam National University)

SS-10 14:15-14:20

Functional Analysis of DNA Methyltransferases from *Cryphonectria parasitica*

Yo-Han Ko (Chonbuk National University)

SS-11 14:20-14:25

Different Impact of Abiotic Factors on Fungal Communities in Arbuscular Mycorrhizal and Ectomycorrhizal Forests Soil (*Carpinus cordata* and *Fraxinus rhynchophylla*)

Ki Hyeong Park (Seoul National University)

SS-12 14:25-14:30

Secretome Analysis in Pepper Anthracnose Pathogen *Colletotrichum scovillei*

Jong-Hwan Shin (Kangwon National University)

SS-13 14:30-14:35

Pontibacter oryzae sp. nov., a Carotenoid-producing Species Isolated from a Rice Paddy Field

Geeta Chhetri (Dongguk University)

SS-14 14:35-14:40

Iron Uptake and Antifungal Susceptibility are Modulated by pH in *Cryptococcus neoformans*

Donghyeun Kim (Chung-Ang University)

SS-15 14:40-14:45

Dissemination of Antibiotic Resistance Genes in Freshwater from the Wastewater of Livestock and Aquaculture Farm

Jin Ju Kim (Chung-Ang University)

SS-16 14:45-14:50

The Imitative Cultivation of the Human Gut Microbiota in Single Batch and Its Potential Possibility as a Microbial Agent for FMT

Seung-Dae Choi (Kyungpook National University)

Plenary Lecture

PL

Imaging *Salmonella* Lifestyles

Linda J. Kenney

Mechanobiology Institute, National University of Singapore and University of Texas Medical Branch, Galveston, TX, USA

After ingestion of *Salmonella* from contaminated food or water, *Salmonella* transits through the stomach and then catalyzes its uptake across the intestinal epithelium. This process requires pathogen-stimulated changes in host actin and other pathways resulting from activation of genes located on *Salmonella* pathogenicity island 1 (SPI-1). *Salmonella* subsequently trafficks across the epithelium, and is phagocytosed by macrophages, where it resides in an acidic vacuole. The *Salmonella* cytoplasm acidifies to pH 5.6 in a process that involves non-canonical activation by OmpR/EnvZ and this acidification step is an important signal in activating genes on pathogenicity island 2 (SPI-2). SPI-2 encodes a type three secretion system that secretes effectors that modify the vacuole, preventing its degradation as well as endosomal tubulation. Using super-resolution imaging in single bacterial cells, we show that low pH induces expression of the SsrA/B two-component signaling system located on SPI-2. Single particle tracking identifies a pH-dependent stimulation of DNA binding by SsrB. The low level of SPI-2 injectisomes observed in single cells is not due to fluctuating SsrB levels in single cells. Super-resolution imaging enables us to visualize the emergence of *Salmonella*-secreted effectors into the host cytoplasm and follow the resulting endosomal tubulation. This work highlights the surprising role that acid pH plays in the virulence and intracellular lifestyle of *Salmonella*, and suggests that modification of acid survival pathways represents a potential target for inhibiting *Salmonella*. Our studies of infection in heterologous host models allow us to visualize many steps in the entire infection process, including biofilm formation *in vitro* and *in vivo* in *C. elegans*.

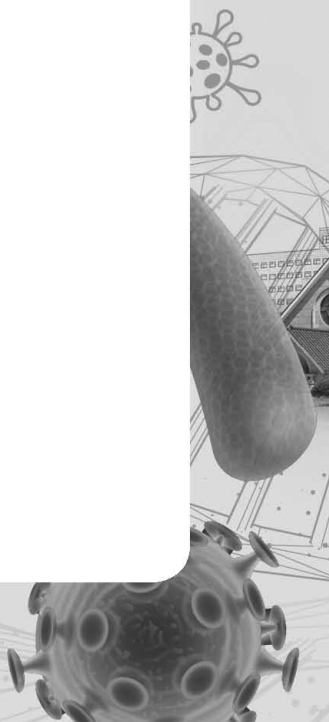
[Supported by the Research Center of Excellence in Mechanobiology from the Ministry of Education, Singapore, VA 5I01BX000372 and NIH AI123640.]

Keywords: Acidification, Super-resolution imaging, Single cells, Single particle tracking, SsrA/B two-component regulatory system, Heterologous host models, Biofilm formation

The Federation of Korean Microbiological Societies

Symposium [S1]

FKMS Session 1



S1-1

Genetic Diversity and Dye-decolorizing Spectrum of the *Schizophyllum commune* Population

Jaehyuk Choi*, Yongjun Choi, Jiwon Lee, Dawoon Kim, and Junhyeok Nam

Division of Life Sciences, College of Life Sciences and Bioengineering, Incheon National University, Incheon 22012, Republic of Korea

Schizophyllum commune, a basidiomycetes fungus, is distributed throughout the world. It has been used as a model of mushroom development study because it takes short time for fruiting body formation, its whole genome sequence is publicly available, and genetic tools for transformation is developed. This fungus is easily found on trees where it decomposes non-degradable lignin. First we investigated genetic diversity of *S. commune* population in Korea. A total of 79 Korean isolates were compared with 138 world population based on the ITS region. Some groups of local population forms their own clades, indicating they were evolutionally isolated from the others. Secondly, the decolorizing activities for four textile dyes were examined using 81 *S. commune* strains. Interestingly, the wide range of decolorization spectrum was shown in this population. The dye decolorizing activities were observed mostly in the methylene blue and crystal violet, whereas remazol brilliant blue R and Congo red were rarely degraded in most strains. Five strains showing decolorization in at least three dyes were selected for further analysis. One of the selected strains was IUM01114. From this parental strain, we obtained 64 monokaryon and mated them in combination. Additionally, 24 monokaryotic strains were screened for four dyes. Based on mating and dye decolorizing ability, monokaryotic SS01 and SS13 were chosen and prepared for whole genome sequencing. They will be useful genetic resources for studying gene involved in decomposition of non-degradable materials and for development of a new biodegradation technique.

Keywords: Split-gill mushroom, Phylogenetic analysis, Dye degradation, Whole genome sequencing

S1-2

Active Surveillance and History of Hantaviruses, a New Family Hantaviridae in the Order Bunyavirales

Jin-Won Song

Dept. of Microbiology, College of Medicine, Korea University, Republic of Korea

Orthohantaviruses, enveloped negative-sense single-stranded RNA viruses, belong to the order *Bunyavirales*, family *Hantaviridae*. The genome of orthohantaviruses consists of tripartite RNA segments (Large, Medium, and Small) which encode the RNA-dependent RNA polymerase (RdRp), two surface glycoproteins (Gn and Gc), and nucleocapsid protein (N), respectively. The prototype virus species is *Hantaan orthohantavirus*. The family *Hantaviridae* is divided into four subfamilies including *Mammantavirinae, Repantavirinae, Actantavirinae* and *Agantavirinae*. The subfamily *Mammantavirinae* is divided into four genera including *Orthohantavirus*, *Loanvirus*, *Mobatvirus*, and *Thottimvirus*. The four Hantavirus species have been found in Korea including three Orthohantaviruses (*Hantaan orthohantavirus*, *Seoul orthohantavirus*, and *Jeju orthohantavirus*) and one Thottimvirus (*Imjin thottimvirus*). The targeted trapping system, incorporating the epidemiologic surveys, clinical data, and acquisition of whole genomic sequences from samples of HFRS patients and rodents using next-generation sequencing (NGS), enabled accurate and precise tracking of infection sites.

Keywords: *Hantaan orthohantavirus*, *Hantaviridae,* Thottimvirus, Next-generation sequencing

S1-3

New Insights into Phage Life Cycles through *Drosophila*-based Evaluation of Phage Therapy

Eun Sook Kim, In-Young Chung, Hee-Won Bae, Se-Jeong Ahn, Chanseop Park, and You-Hee Cho*

Department of Pharmacy, College of Pharmacy and Institute of Pharmaceutical Sciences, CHA University, Republic of Korea

Non-mammalian model hosts have been exploited to understand the various aspects of host-pathogen interactions and also provided small-scale research platforms for identification of virulence factors, screening for antimicrobial hits, and evaluation of antimicrobial efficacy. The fruit fly, *Drosophila melanogaster* is one of the model hosts for a variety of bacterial pathogens, in that the innate immunity pathways and tissue physiology are highly similar to those in mammals. Here we present the up-to-date information on the optimization of a *Drosophila* systemic infection model to assess the antibacterial efficacy of therapeutic bacteriophages (phages) toward the opportunistic human pathogen, *Pseudomonas aeruginosa*. Since phages, unlike antibacterial chemicals, can be easily and sensitively enumerated by simple assays, it is also possible to address the pharmacokinetic properties of administered phages even in this small-scale infection model. More importantly, we observed some discrepancy between the phage-mediated killing curves *in vitro* and the antibacterial efficacies in *Drosophila* infections, which is deemed attributed to the previously unknown phage lifecycles that hijack the bacterial virulence factors. Topics discussed will include our on-going studies to elucidate the mechanism of the phage-mediated mitigation of bacterial virulence, which leads to a new idea for the next-generation antibacterial strategies.

Keywords: Phage, *Pseudomonas aeruginosa*, *Drosophila*, Antibacterial, Virulence

S1-4

From Microbial Degradation to Microbial Synthesis

Jong-Chan Chae

Division of Biotechnology, Chonbuk National University, Republic of Korea

In many biorefinery processes, mono-aromatic compounds produced during the degradation of aromatic polymers remains as low-value wastes. We investigated chemical conversion of intermediate aromatic compounds using *Comamonas testosteroni* P19 as case studies. Bacterial genus *Comamonas* showing metabolic diversity and potential in bioremediation provided the impetus for functional genomic approach. The random plasposon mutagenesis explicated that the predicted gene clusters were essential in the metabolic pathways of aromatic compounds. Ferulic acid is a major component of lignin and has been used as a model substrate for lignin degradation. Among the mutant library of strain P19, we have isolated a mutant which showed no growth on ferulic acid and was deficient in putative esterase. When ferulic acid was incubated with the mutant strain, novel intermediate was accumulated. Its structure was assigned by NMR spectroscopy and LC-ESI-MS analysis. Subsequently the compound was a dimer form of vanillate suggesting a possibility of novel metabolic pathway in the strain. In addition, conversion of an aromatic compound, 4-methoxybenzoic acid (4-MBA), to poly-β-hydroxybutyrate (PHB) in strain P19 was observed. The strain showed growth and PHB production in mineral salts basal medium supplemented with 4-MBA as sole carbon source at different concentrations. Among different concentrations, P19 at 5 mM of 4-MBA exhibited highest PHB production, but production was low when compared with non-aromatic compound i.e., acetate. After optimization of substrate concentration, the concentration of nitrogen and phosphate was optimized. Optimization of those factors improved PHB production by over 5%. The functional groups, thermal, and physical properties of the produced PHB were also analyzed. The generation of PHB from aromatic hydrocarbons as a feedstock provides a route for converting hydrocarbon wastes into useful biological polyesters.

Keywords: *Comamonas*, Biodegradation, Genome, PHB

The Federation of Korean Microbiological Societies

Symposium [S2]

FKMS Session 2

S2-1

Yes, Now We Know the Bacteria in Our Poop. How Do We Use It?

Jae-Ho Shin

School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

We, all human beings (or at least microbiologists) were most interested in their poop throughout the history for last 15 years. The study of human gut microbiome has long been beyond the traditional interest in infectious diseases, and has now led to associations with autoimmune diseases, cancer, depression and degenerative diseases as well as obesity, diabetes and liver disease. As consequence, the healthy human's intestinal microflora is now considered a potential source of new therapeutics. Nevertheless, it is not yet clear whether the intestinal microbiome of humans are the cause or effect of diseases. My lab has not focused research on many academic pros and cons of human gut microbes. We are only interested in what we can do with information about such personal gut bugs. We are therefore interested in research on microbiome-based foods, medicine, probiotics, prebiotics, diagnostic tools, supplements and drugs for treatment. Through this symposium, we would like to present a series of efforts for the practical science of human intestinal microbiome and to collect positive and negative feedback.

Keywords: Microbiome, Microbiota, Gut

S2-2

Multimodal Influence of Methanotrophic Community on Nitrous Oxide Emissions from Soil Denitrification

Sukhwan Yoon[1*], Jin Chang[1], and Jeremy D. Semrau[2]

[1]Department of Civil and Environmental Engineering, KAIST, Republic of Korea
[2]Department of Civil and Environmental Engineering, University of Michigan, USA

The composition and the metabolic activity of the soil microbiome determine whether soil would function as the net source or sink of potent greenhouse gases methane (CH_4) and nitrous oxide (N_2O). Proteobacterial methanotrophs are important biological sinks of CH_4 at the oxic-anoxic interfaces, and *nosZ*-possessing organisms offset N_2O released from various biotic and abiotic sources. Proteobacterial methanotrophs require Cu for synthesizing functional particulate methane monooxygenase, the enzyme mediating CH_4 turnover to CH_3OH. Several distinct mechanisms for Cu scavenging have been identified in methanotrophs, including synthesis and utilization of the Cu-specific chelator methanobactin. Here, we report the recent finding that these Cu sequestration mechanisms may interfere with N_2O reduction of *nosZ*-possessing organisms and result in enhanced N_2O emissions from soil denitrification.

Initially, the effect of methanobactin exuded by alphaproteobacterial methanotrophs on N_2O emissions from denitrification was examined using *Methylosinus trichosporium* OB3b and axenic denitrifier cultures. Permanent N_2O production resulted from the denitrifiers incubated in O_2-depleted methanotroph cultures, while no significant N_2O accumulation was observed when the mutant strain with defunct methanobactin production pathway was used in place of the wildtype strain OB3b. Soil enrichments have also been examined for the effect of methanotrophs on N_2O production from denitrification. Methanotrophs enriched from rice paddy soils with both high (20% v/v) and low (0.5% v/v) CH_4 concentrations increased N_2O production when the enrichment was transitioned to anoxic condition despite the lack of methanobactin-producing alphaproteobacterial population, suggesting that gammaproteobacterial methanotrophs employ distinct Cu sequestration mechanism that interferes with the N_2O reduction activity of denitrifiers and non-denitrifying N_2O-reducers. The multimodal influence of methanotrophs on N_2O emissions was further demonstrated with soil enrichment experiments, where varying cell numbers of methanobactin-producing *M. trichosporium* OB3b was added to rice paddy soil suspensions before CH_4 enrichment. N_2O production was enhanced in both methanotroph enrichments, but to a greater extent in the *M. trichosporium*-dominant enrichments than in the Gammaproteobacteria-

dominant enrichments.

These observations suggest that involuntary inhibition of N_2O reduction is a plausible mechanism of N_2O emissions at oxic-anoxic interfaces in the environments where methanotrophy and denitrification may simultaneously take place.

Keywords: Methanotrophs, Denitrification, Methanobactin, Nitrous oxide, Copper

S2-3

Epigenetic Regulation of Fungal Development and Pathogenicity in the Rice Blast Fungus

Junhyun Jeon*, Jaejoon Lee, Jongjoon Lee, Taehyun Kim, and Gnanendra Shanmugam

Department of Biotechnology, College of Life and Applied Sciences, Yeungnam University, Gyeongsan 38541, Republic of Korea

Fungal pathogens have huge impact on health and economic wellbeing of human by causing life-threatening mycoses in immune-compromised patients or by destroying crop plants. A key determinant of fungal pathogenesis is their ability to undergo developmental changes in response to host or environmental factors. Here we set out to investigate contribution of one of the most important epigenetic modifications, histone acetylation/deacetylation to this morphogenetic process, using a model plant pathogenic fungus, *Magnaporthe oryzae*. Based on a web-based database (dbHiMo), which had been constructed first to archive and analyze histone modifying enzymes from eukaryotic species, we carried out functional analysis of genes encoding histone acetyltransferases (HAT) and deacetylases (HDAC). Gene deletion or silencing approaches showed that disruption of histone acetylation status generally leads to defect in vegetative growth and asexual sporulation. RNA-seq analysis on one of the HAT mutants (△*Mosas3*) indicated that such growth defect is related to down-regulation of a whole array of genes involved in nitrogen and carbon metabolisms. For HDAC, our data suggest that Class I HDACs have great impact on fungal biology. In particular, we revealed that *MoHOS2* is required for asexual reproduction through stage-specific regulation of some of the conidiogenesis-related genes. Interestingly, in △*Mohos*2, it appears that reduced pathogenicity is attributed to mis-regulation of genes encoding effector proteins. Furthermore, we showed that lack of deacetylase activity alone is able to recapitulate most of phenotypic defect in △*Mohos*2. Together with our preliminary data on H3K4 methylation, our results indicate that histone modification is an important regulatory layer for gene expression and appears to be required for establishing and maintaining identity of fungal cells.

Keywords: Rice blast fungus, Epigenetic factor, Histone modifications, Fungal development, Pathogenicity

The Federation of Korean Microbiological Societies

Symposium [S3]

FKMS Session 3

S3-1

Group B Coxsackievirus Induced Pregnant Loss and Infertility

Hosun Park[1,2*], Sivilay Xayaheuang[1], Byung-Kwan Lim[3], Yunhwa Kim[1], Kyung Min Lee[1], and Ji Young Hwang[1]

[1]Department of Microbiology, College of Medicine, Yeungnam University, Republic of Korea
[2]Immunogenicity Evaluation Laboratory, Yeungnam University Medical Center, Daegu, Republic of Korea
[3]Department of Biomedical Science, Jungwon University, Goesan-gun, Chungbuk, Republic of Korea

Group B coxsackieviruses (CVB) are a member of enterovirus and they use coxsackievirus-adenovirus receptor (CAR) as a major receptor for entry. We found that CAR is highly expressed not only in developing brain and heart but also in uterus and ovary. The infection of CVB during pregnancy induced pregnant loss, such as miscarriage or fetal anomaly. Furthermore, CVB3 infection also induced infertility in female mice. The CVB3-infected infertile female mice had lower level of serum estradiol and showed severe osteoporosis compared to mock-infected mice. To understand the role of CAR in ovary, we made ovary-specific conditional CAR knock-out mice. The body weight and gross phenotypes of CAR KO mutant mice were not significantly different with wild type. However, their fertility rate was decreased significantly and atretic follicles in ovary were increased. Therefore, CAR might be very important molecule in pregnancy. However, further studies are necessary to understand the detailed mechanisms of CAR in pregnancy.

Keywords: Coxsackievirus-adenovirus receptor, Coxsackievirus B3, CAR knock-out mice, Infertility

S3-2

Bacterial Infection Controls Enabled by Neighboring Commensals

Sang Sun Yoon

Department of Microbiology and Immunology and Brain Korea 21 PLUS Project for Medical Sciences, Yonsei University College of Medicine, Seoul 03722, Republic of Korea

Due to the presence of indigenous microbes maintaining a complex self-regulating community inside the host tissues, infections are outcomes of multi-layered interactions between commensal microbes and pathogenic invaders. However, it remains unclear how modulations of the commensal microbiota composition affect host infection resistance. Here, we reveal that two commensal microbes, *Bacteroides vulgatus* and *Staphylococcus epidermidis* can exert protective effects against pathogenic infections in host intestine or airway, respectively. *Bacteroides vulgatus*, a dominant species of the Bacteroidetes phylum in mouse intestine, suppresses infection by *Vibrio cholerae*, an important human pathogen. The Bacteroidetes-depleted adult mice developed severe cholera-like symptoms, when infected with *V. cholerae*. Germ-free mice mono-associated with *B. vulgatus* became resistant to *V. cholerae* infection. Among forty nine *S. epidermidis* isolates from healthy human nasal cavity, one strain, named SE5, specifically and robustly inhibited airway infection by *Pseudomonas aeruginosa*, an important human airway pathogen *in vivo*. SE5 was found to produce a secretome, whose composition is distinct from other isolates of the same species. Detailed mechanisms of infection controls by these symbiotic microbes will be presented.

Keywords: Microbiome, Infection, Metabolites, Airway infection and intestinal infection

S3-3

Genomic Analysis of Antifungal Resistance of *Malassezia restricta*

Minji Park[1], Yong-Joon Cho[2], Yang Won Lee[3,4], and Won Hee Jung[1]*

[1]*Department of Systems Biotechnology, Chung-Ang University, Anseong, Republic of Korea*

[2]*Korea Polar Research Institute, Incheon, Republic of Korea*

[3]*Department of Dermatology, School of Medicine, Konkuk University, Seoul, Republic of Korea*

[4]*Research Institute of Medicine, Konkuk University, Seoul, Republic of Korea*

Malassezia restricta is an opportunistic fungal pathogen on human skin and is associated with various skin diseases including seborrheic dermatitis, dandruff and atopic dermatitis, which are commonly treated with the azole antifungal drug ketoconazole. In this study, we clinically isolated ketoconazole resistant *M. restricta* strains, designated as KCTC 27529 and KCTC 27550, from dandruff patients. To understand the ketoconazole resistance, the genome and transcriptome of the isolated strains were sequenced and compared with that of the susceptible reference strain *M. restricta* KCTC 27527. With our genomic approaches, we identified multiplications of the genomic locus encoding the homolog of Atm1 in *M. restricta* KCTC 27529, the result of which was supported by our transcriptome analysis showing an increased expression of the *ATM1* homolog in the same strain. Atm1 is a mitochondrial iron exporter and is involved in Fe-S cluster transport as well as azole sensitivity in fungi implicating that the protein also contributes azole resistance in *M. restricta*. Furthermore, transcriptome analysis suggested that the homolog encoding the *PDR5* homolog is significantly up-regulated in *M. restricta* KCTC 27529 implying that, in addition to the genomic multiplication of the *ATM1* homolog, an increased drug efflux influences the ketoconazole resistance of the strain. The mechanism of ketoconazole resistance in the other resistant isolate *M. restricta* KCTC 27550 is different from KCTC 27529. The comparative genome and transcriptome analyses revealed that there is a genomic multiplication of the locus encoding homologs of *ERG11* in *M. restricta* KCTC 27550 which are highly expressed compared to the reference strain. Overall, our data suggest genomic rearrangement, for example, multiplication of the locus encoding genes involved in drug resistance, is a common mechanism of ketoconazole resistance in *M. restricta*. In addition, *PDR5* has an important role in the azole resistance of *M. restricta*.

Students' Presentation Session

The Federation of Korean Microbiological Societies

SS-1

Transcriptomic Identification and Biochemical Characterization of HmpA, a Nitric Oxide Dioxygenase, Essential for Pathogenesis of *Vibrio vulnificus*

Dukyun Kim[1,2], Eun Jung Na[1,2], and Sang Ho Choi[1,2*]

[1]*National Research Laboratory of Molecular Microbiology and Toxicology, Seoul National University, Seoul, Republic of Korea*

[2]*Department of Agricultural Biotechnology and Center for Food Safety and Toxicology, Seoul National University, Seoul, Republic of Korea*

Nitric oxide (NO) and its derivatives are important effectors of host innate immunity, disrupting cellular function of infecting pathogens. Transcriptome analysis of *Vibrio vulnificus*, an opportunistic human pathogen, identified a set of genes induced upon exposure to NO. Among them, *VvhmpA* (*V. vulnificus hmpA*), encoding a multidomain NO dioxygenase, was the most greatly induced upon exposure to NO and was thus further characterized. Absorption spectra demonstrated that *Vv*HmpA is a heme protein in which the heme iron can exist in either reduced, NO-bound, or oxidized state. Biochemical studies revealed that *Vv*HmpA is a flavohemoglobin containing equimolar amounts of heme and FAD as cofactors. The K_M and k_{cat} values of *Vv*HmpA for NO at 37°C, the temperature encountered by *V. vulnificus* in the host, were greater than those at 30°C, indicating that *Vv*HmpA detoxifies high levels of NO effectively during infection. Compared with the wild type, the *VvhmpA* mutant exhibited a lower NO-decomposition activity and impaired growth in the presence of NO *in vitro*. Also, the cytotoxicity and survival of the *VvhmpA* mutant infecting the NO-producing murine macrophage cells were lower than those of the wild type. Furthermore, the mouse lethality of the *VvhmpA* mutant was reduced compared to that of the parental wild type. The combined results revealed that *Vv*HmpA is a potent virulence factor that is induced upon exposure to NO and important for the survival and pathogenesis of *V. vulnificus* during infection.

Keywords: *Vibrio vulnificus*, Gene expression profiling, Nitric oxide, Flavohemoglobins, Virulence factors

SS-2

Taxonomy and Antimicrobial Potential of *Micromonospora* sp. Isolated from Riverside Soil

Min Ji Kim, Ji Hye Lee, Yeon Jeong Ryu, and Seung Bum Kim*

Department of Microbiology and Molecular Biology, College of Bioscience and Biotechnology, Chungnam National University, Daejeon 34134, Republic of Korea

The genus *Micromonospora* is one of the promising genera for the potential to produce secondary metabolites. Following the survey on the taxonomic diversity and antimicrobial potential of the genus *Micromonospora*, an isolate designated *Micromonospora* sp. R_77 exhibited an outstanding anti-microbial activity, and was thus subjected to further analysis. Based on the 16S rRNA gene sequence analysis, the strain R_77 was mostly related to the type strains of *M. avicenniae* and *M. echinospora* with the sequence similarity of 99.00 and 98.93%, respectively. Strain R_77 could grow well on ISP7 medium at 30°C and possessed optimal culture condition in pH 6 and 1% salt concentration. The strain utilized monosaccharides and disaccharides as a sole carbon sources and aliphatic and aromatic amino acids as a sole nitrogen sources. The strain had polymer degrading activity such as starch, lipid and carboxy-methylcellulose. Furthermore, the strain was active against Gram-positive bacteria and yeasts, whereas little activity was observed against Gram negative bacteria or filamentous fungi. The PCR based screening of biosynthetic genes also yielded positive results for polyketides synthetase type I, II and non-ribosomal peptide synthetase. The ongoing analysis includes search for optimal culture conditions for antimicrobial activity, detection of antimicrobial compounds using high performance liquid chromatography-mass spectrometry (HPLC-MS), and also extraction and purification of the compounds as well as chemo-taxonomic characterization.

Keywords: *Micromonospora*, Taxonomic characterization, Antimicrobial activity, Antimicrobial compound, HPLC-MS

SS-3

Tor1 and Sch9 Coordinately Regulate Hyphae Specific Genes or Ribosomal Protein Genes in *Candida albicans*

Se Woong Kim[1,2], Young Kwang Park[1], and Joon Kim[1,2*]

[1]*Laboratory of Biochemistry, Division of Life Sciences, Korea University, Seoul 02841, Republic of Korea*
[2]*HAEL Lab, TechnoComplex, Korea University, Seoul 02841, Republic of Korea*

Candida albicans is an opportunistic fungal pathogen. In immunocompromised individuals, it can cause bloodstream infections with high mortality rates. *C. albicans* reversibly switches between yeast and hyphal morphologies, with hyphae being associated with virulence. Here, we present the first evidence showing that the transcription of RP genes in *C. albicans* is associated with hyphae formation via the Tor1 and Sch9 signaling pathways. We have observed a decrease in gene transcription of ribosomal proteins (RP) during hyphae formation. Also, morphogenesis-dependent reduction of RP genes transcription was confirmed in constitutive yeast or filamentous growing strains. We also observed that Tor1 and Sch9 kinase activity was reduced in hyphae growing cells compared with in yeast growing cells. Five residues in c-terminus of Sch9 play a role in the regulation of RPG and HSG expression and cell–cell adhesion. Interestingly, the major portions of hyphae are composed of vacuoles and we showed that the filamentous growth of *C. albicans* requires vacuolar H^+-ATPase function. Based on these findings, Vma4 and Vma10 are not only involved in vacuole biogenesis and hyphal formation, but also are good targets for antifungal drug development in *C. albicans*. Our new findings provide evidence to show that the Tor1-Sch9 kinase cascade stimulates RP transcription, and V-ATPase activity plays an important role in morphological changes of *C. albicans*.

SS-4

Reshaping of the Gut Microbiota in Small Heterodimer Partner Deficient Mice

June-Young Lee[1], Na-Ri Shin[1], Tae Sung Kim[2], Eun-Kyeong Jo[2], and Jin-Woo Bae[1]*

[1]Department of Life and Nanopharmaceutical Sciences and Department of Biology, Kyung Hee University, Seoul 02447, Republic of Korea

[2]Department of Microbiology, Chungnam National University School of Medicine, Daejeon 35015, Republic of Korea

The small heterodimer partner (SHP) is an orphan nuclear receptor that can interact with various nuclear receptors and transcription factors related to lipids and bile acids metabolism. SHP is activated by farnesoid X receptor (FXR) and regulates bile acid biosynthesis by inhibiting cytochrome P450 7A1 (CYP7A1), which is the rate-limiting enzyme in synthesis of bile acid from cholesterols. Gut microbiota has profound effects on bile acid metabolism by promoting deconjugation of taurine and glycine, dehydrogenation and dihydroxylation of primary bile acids.

We investigated how SHP deficiency in mice affects gut microbiota profile through 16S rRNA gene amplicon sequencing. We found that microbial diversity (α-diversity) was significantly increased in SHP KO mice compared to WT mice ($p < 0.002$). Community structures of gut microbiota from WT and SHP KO were significantly different and clustered separately ($p < 0.001$). In detail, compared to SHP WT, the bacterial genera *Bacteroides*, *Butyricimonas* and *Rikenella* were decreased and *Lactobacillus*, *Allobaculum* and unclassified Peptostreptococcaceae were increased in SHP KO mice. As a result of dysbiosis in SHP KO mice, mice were more susceptible to dextran sulfate sodium (DSS)-induced colitis. We investigated specific taxa that differently represented in WT and SHP KO mice before DSS treatment. Especially, *Lactobacillus* increased in SHP KO mice before DSS treatment.

From these data, we conclude that SHP deficiency can modify the host gut bacterial community and regulate host sensitivity to DSS induced colitis. Through further study, we will figure out interaction of the genus *Lactobacillus* with SHP KO and DSS sensitivity.

Keywords: shp, Gut microbiota, Colitis, *Lactobacillus*, Bile acid

SS-5

Development of a DNA Vaccine for SFTSV that Confers Complete Protection Against Lethal Infection in Ferrets

Jeong-Eun Kwak[1], Young-Il Kim[2], Su-Jin Park[2], Moonsup Jeong[3], Joel N. Maslow[3], Min-Suk Song[2], Jae U. Jung[4], Eui-Cheol Shin[1], Young Ki Choi[2], and Su-Hyung Park[1]*

[1]Graduate School of Medical Science and Engineering, KAIST, Republic of Korea

[2]College of Medicine & Medical Research Institute, Chungbuk National University, Republic of Korea

[3]GeneOne Life Science, Inc., Seoul 06060, Republic of Korea

[4]Department of Molecular Microbiology and Immunology, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033, USA

Severe fever with thrombocytopenia syndrome (SFTS) is a newly emerging tick-borne infectious disease caused by the SFTS virus (SFTSV) belonging to the *Phenuiviridae* family. The majority of SFTS cases have been identified in East Asia, primarily in China, Korea, and Japan. The incidence of SFTSV infection has increased from its discovery with a mortality rate of 10–20% and the major clinical symptoms of SFTSV infection are fever, vomiting, diarrhea, thrombocytopenia, leukopenia and multiple organ failure. However, no effective vaccines are currently available for SFTSV. Here, we describe the development of a SFTSV vaccine using DNA vaccine-based platform, its immunogenicity, and its protective efficacy. Vaccine candidates induced both a neutralizing antibody response and multifunctional SFTSV-specific T cell response in mice and ferrets. To investigate the vaccine efficacy *in vivo*, we applied a recently developed ferret model of lethal infection that can accurately mimic SFTS progression in humans. Immunization of ferrets with SFTS vaccine candidates conferred complete protection against lethal-dose SFTSV challenge without any clinical symptoms. Moreover, we found that anti-envelope antibodies play an important role in protective immunity and non-envelope-specific T cell responses also can contribute to protection against SFTSV infection. This study provides a valuable insight to the design of preventive vaccines for SFTSV, as well as corresponding immune parameters, to control SFTSV infection.

Keywords: Severe fever with thrombocytopenia syndrome (SFTS), SFTS virus (SFTSV), DNA vaccine, Protective immunity

SS-6

Development of Bivalent Vaccines for Poultry

Kyeong Ryeol Shin, Joon-Yong Bae, Jeong Hun Kim, Jin Il Kim, and Man-Seong Park*

Department of Microbiology and Institute for Viral Diseases, College of Medicine, Korea University

Although public health measures and drug interventions are absolutely necessary tools in our efforts to combat virus outbreaks, vaccines are equally crucial to countering such threats. In fact, vaccination has proven to be the single best weapon against infectious diseases in animals. It is thus believed that vaccination is a rational and important strategy for protecting the animal against infectious diseases. Even though current animal vaccines are effective in hampering the spread of disease, they need to be improved for the preparation of unpredicted virus outbreaks by technology such as reverse genetics system. This system can allow company to shorten the lengthy process of preparing vaccine seed viruses since the rapid development of new and better vaccines against future virus outbreak appears to be imperative. Live attenuated-vaccines have proven to be effective against a variety of viral diseases, and they have been shown to induce strong and long lasting immunity. By using reverse genetics system, we can rapidly develop live-attenuated vaccines that would be safer, optimized against unexpected viral outbreak. In recent years, outbreaks of high pathogenicity avian influenza have been reported in Asia, Africa, and Europe. These outbreaks involving H5N1 or H7N7 influenza viruses resulted in lethal infections in domestic poultry, and the death of a limited number of human cases. Vaccination against avian influenza in poultry can play an important role in the reduction of virus shedding and in raising the threshold for infection and transmission. Therefore, poultry vaccination with a high quality vaccine against avian influenza virus can be part of an effective control program. For this, a recombinant bivalent vaccine was constructed by reverse genetics system generating lentogenic Newcastle disease virus strain with insertion of the hemagglutinin gene from avian influenza virus.

Keywords: Newcastle disease virus (NDV), Avian influenza virus (AIV), Bivalent vaccine

SS-7

Whole Transcriptome Analyses Reveal Differential mRNA and microRNA Expression Profiles in Primary Human Dermal Fibroblasts Infected with Clinical or Vaccine Strains of Varicella Zoster Virus

Soo-Jin Oh[1], Soo-Yeon Lim[1], Moon Jung Song[2], Jin Hyun Ahn[3], Chan Hee Lee[4], and Ok Sarah Shin[1]*

[1]Bk21 PLUS Program, College of Medicine, Korea University Guro Hospital, Seoul 136-701 Republic of Korea

[2]Department of Biosystems and Biotechnology, Division of Biotechnology, College of Life Sciences and Biotechnology, Korea University, Seoul, Republic of Korea

[3]Department of Molecular Cell Biology, Sungkyunkwan University School of Medicine, Suwon, Republic of Korea

[4]Department of Microbiology, Chungbuk National University, Cheongju, Republic of Korea

Licensed live attenuated vaccines have been developed to prevent Varicella zoster virus (VZV) infection, which causes chickenpox and shingles. The genomic sequences of both clinical- and vaccine-derived VZV strains have been analyzed previously. To further characterize the molecular signatures and complexity of virulent (clinical) versus nonvirulent (vaccine-derived) VZV-mediated host cellular responses, we performed high-throughput next generation sequencing to quantify and compare the expression patterns of mRNAs and microRNAs (miRNAs) in primary human dermal fibroblasts (HDF) infected with virulent (*YC01-low*) and nonvirulent (*YC01-high, SuduVax, VarilRix*) VZV strains. 3D multidimensional scaling of the differentially expressed genes demonstrated the distinct grouping of virulent and nonvirulent strains. In particular, we observed that HDFs infected with nonvirulent strains had an elevated expression of DEGs involved in retinoic acid inducible gene–I-like receptor and interferon-mediated signaling pathways compared with virulent strains. Additionally, miRNA expression patterns were profiled following the infection of HDFs with VZV. Small RNA sequencing identified that several miRNAs were upregulated, including miR-146a-5p which has been associated with other herpes virus infections, whereas let-7a-3p was downregulated in both virulent and nonvirulent VZV-infected cells. This study identified genes and miRNAs that may be essential in VZV pathogenesis.

Keywords: Varicella zoster virus, *SuduVax*, RNA-seq, miRNA

SS-8

Shedding and Transmission Modes of Severe Fever with Thrombocytopenia Syndrome Virus in a Ferret Model

Kwang-Min Yu[1,2], Hye-Won Jeong[1], Su-Jin Park[1,2], Young-Il Kim[1,2], Eun-Ha Kim[1,2], Se-Mi Kim[1,2], Seung-Hun Lee[1,2], Seong-Gyu Kim[1,2], Jae-Hyung Chang[1,2], Eun-Ji Kim[1,2], and Young-Ki Choi[1,2]*

[1]College of Medicine and Medical Research Institute, Chungbuk National University, Cheongju, Republic of Korea

[2]Zoonotic Infectious Diseases Research Center, Chungbuk National University, Cheongju, Republic of Korea

Background. Although human-to-human transmission of severe fever with thrombocytopenia syndrome virus (SFTSV) via direct contact with body fluids has been reported, the role of specific body fluids from SFTSV-infected hosts has not been investigated in detail.

Methods. To demonstrate the virus transmission kinetics in SFTSV-infected hosts, we adapted the ferret infection model and evaluated the virus shedding periods, virus titers, and transmission modes from various specimens of infected ferrets.

Results. Large amounts of infectious SFTSV are shed through nasal discharge, saliva, and urine from SFTSV-infected ferrets. Virus could be detected from 2 dpi and persisted until 12 dpi in these specimens, compared with the relatively short virus-shedding period in sera. Further, transmission studies revealed that SFTSV can be transmitted to close direct and indirect contact naive animals through various mediums, especially through contact with serum and urine. Further, ferrets contacted with human urine specimens from SFTSV-positive patients were successfully infected with SFTSV, suggesting that urine specimens could be a source of SFTSV infection in humans.

Conclusions. Our results demonstrate that the SFTSV can be shed in various body fluids for more than 12 days and that these specimens could be a source for direct or indirect transmission through close personal contact.

Keywords: Body fluids, Ferret, Indirect transmission, SFTSV, Virus shedding

SS-9

Novel Fungal Species from Aquatic Environments in Korea

Monmi Pangging and Hyang Burm Lee*

Department of Food Technology, Biotechnology & Agrochemistry, College of Agricultural & Life Sciences, Chonnam National University, Gwangju 61186, Republic of Korea

Fungi thriving in terrestrial environment play important roles in nutrient cycling and food webs and can shape microorganisms communities as parasites and mutualists. Only less than 10% of fungal species have been identified from 1.5 to over 5 million estimation of fungal species. To date, a relatively small percentage of species have been described from aquatic environments in comparison to terrestrial domain. Aquatic fungal communities are a diverse group of organisms and fulfill important functions in the food web dynamics of surface water ecosystems. They help in leaf litter breakdown in rivers and creeks, nutrient cycling and contributing food for detritus feeders. This study represents diversity of freshwater-derived fungi from Korea based on their molecular phylogenetic and morphological analyses. Knowledge on the geographic distribution of freshwater-derived ascomycetes and their asexual morphs in the Korean peninsula is limited. Freshwater samples were collected from Damyang, Yeosu, Hwangyong, Yocheon and Woncheoncheon streams, Korea. Our findings provide diversity of fungal community derived from freshwater niche in Korea.

Keywords: Ascomycete, Aquatic fungi, Ecology, Phylogeny, Morphology

SS-10

Functional Analysis of DNA Methyltransferases from *Cryphonectria parasitica*

Yo-Han Ko, Kum-Kang So, Jeesun Chun, and Dae-Hyuk Kim*

Department of Molecular Biology, Department of Bioactive Material Sciences, Institute for Molecular Biology and Genetics, Chonbuk National University, Jeonju, Chonbuk 54896, Republic of Korea

Two representative fungal DNA methyltransferases (DNMTase) genes from *Cryphonectria parasitica* had been identified as *CpDmt1* and *CpDmt2*, which were orthologous to repeat-induced point mutation (RIP) and RIP defective (RID) in DNA methylation of *N. crassa*, respectively. The *CpDmt1* but not the *CpDmt2* was proved to be implicated in sporadic occurrence of sectorization. Although both mutants showed no significant differences from the wild type in responses to stress such as temperature, high osmolarity, reactive oxygen species (ROS), and cell wall disturbing agents, both mutants showed significant changes in virulence but in opposite direction, i.e., the *CpDmt1*-null mutant showed increased virulence while the *CpDmt2*-null mutant showed decreased virulence. These results clearly indicated that each gene has a functional specificity. In addition, both mutants showed severe growth retardation after the hypovirus infection, suggesting epigenetic regulation in fungal responses to the hypovirus infection. Moreover, spontaneous viral clearance was occurred from hypovirus-infected hyphae of both mutants, which resulted in robust colonial growth showing the virus-free colonial characteristics such as pigmentation and conidiation. Compared to the virus-infected isogenic strain, drastically enhanced up-regulation of two key antiviral genes *dcl-2* and *agl-2* were observed in both mutants when the hypovirus infected. These results suggested the epigenetic regulation of the host responses to the hypovirus infection via antiviral RNA silencing pathway.

This study demonstrated that DNA methylation is important for the fungal virulence and hypovirus infection. Each fungal DNMTase affects fungal biology in a common as well as specific ways. These will help to understand epigenetic regulation of fungal virulence and responses to the virus infection.

Keywords: *Cryphonectria parasitica*, DNA methylation, Hypovirus, Virulence, RNA silensing

SS-11

Different Impact of Abiotic Factors on Fungal Communities in Arbuscular Mycorrhizal and Ectomycorrhizal Forests Soil (*Carpinus cordata* and *Fraxinus rhynchophylla*)

Ki Hyeong Park[1], Seung Yoon Oh[2], Myung Soo Park[1], Shinnam Yoo[1], Chang Sun Kim[3], and Young Woon Lim[1]*

[1]*School of Biological Sciences and Institute of Microbiology, Seoul National University*
[2]*Korean Lichen Research Institute, Sunchon National University*
[3]*Forest Biodiversity Division, Korea National Arboretum*

Arbuscular mycorrhizal (AM) and ectomycorrhizal (ECM) forests are known to have different nutrient foraging strategies and soil properties, but their effect on soil fungal communities during seasonal change is less understood. Here, we examined the effect of a biotic factor (tree species) and abiotic factors (season, soil property) on fungal communities in soil of adjacent *Carpinus cordata* (ECM) and *Fraxinus rhynchophylla* (AM) forests in Mt. Jeombong (South Korea) with high-throughput Illumina MiSeq sequencing. Our analyses showed that effect of environmental factors on both fungal community composition and their ecological guilds were significantly different between AM and ECM forests. In *C. cordata* forest, ECM fungi such as *Inocybe*, *Sebacina*, or *Russula* were dominant, but in *F. rhynchophylla* forest, saprotrophic or pathogenic fungi such as *Mortierlla*, *Leohumicola*, or *Chaetomium* were mainly found. Overall, while seasonal and soil property effects were mostly significant in fungal communities in *F. rhynchophylla* forest soil, fungal communities in *C. cordata* forest were not distinguished by these factors. Collectively, our data provides an additional insight into fungal phylogeny, functionality and interactions in forests with different mycorrhizal associations.

Keywords: Arbuscular mycorrhizal (AM) fungi, Ectomycorrhizal (ECM) fungi, Plant-soil interactions, Mycorrhizal associations, Fungi

SS-12

Secretome Analysis in Pepper Anthracnose Pathogen *Colletotrichum scovillei*

Jong-Hwan Shin and Kyoung Su Kim*

Division of Bio-Resource Sciences and BioHerb Research Institute, Kangwon National University, Chuncheon 24341, Republic of Korea

The occurrence of *Colletotrichum* sp. on pepper (*Capsicum annuum* L.) is a major problem in many countries over the world. *C. acutatum* is a species complex causing anthracnose disease in a wide range of host plants. We isolated a *Colletotrichum* sp. from an infected pepper fruit in Gangwon Province of South Korea and it was identified as *C. scovillei* by combined sequence analysis. Isolated *C. scovillei* KC05 developed appressorium on pepper fruit and penetrated cuticle layer of pepper fruit surface through penetration peg. From the penetration peg, a highly branched dendroid structure was formed in the cuticle layer of pepper fruit. Thin and branched hypha was observed inside dendroid structure and the hyphagrew along with dendroid structure toward the wall of the infected cell. Swollen biotrophic hyphae were formed in the neighboring cells. We hypothesized that small secreted proteins participate in *C. scovillei* infection on pepper fruit. We found a total of 39 proteins as *C. scovillei*-secreted protein candidates by SignalP4.1 and small secreted protein prediction pipeline. Targeted gene deletion was carried out on some genes among the candidates and we found *SSP16* (CSP_001584) is related to the disease development of *S. scovillei*. We constructed a SSP16:dsRED fusion construct and SSP16:dsRED proteins were localized inside dendroid structure. Collectively, our results indicate that *SSP16* might play an important role in *C. scovillei* infection on pepper fruit.

Keywords: *Colletotrichum scovillei*, Pepper anthracnose, Plant-fungal interactions, Secretome analysis

SS-13

Pontibacter oryzae sp. nov., a Carotenoid-producing Species Isolated from a Rice Paddy Field

Geeta Chhetri, Jiyoun Kim, Hyungdong Kim, Inhyup Kim, and Taegun Seo*

Department of Life Science, Dongguk University

A taxonomic study using a polyphasic approach was performed on a Gram-stain negative, red-pink, aerobic, non-motile, asporogenous, rod-shaped bacterium, designated strain KIRAN^T, isolated from soil collected from a rice paddy field. The 16S rRNA gene sequence analysis showed that strain KIRAN^T is phylogenetically related to *Pontibacter actiniarum* KMM 6156^T, *Pontibacter korlensis* X14-1^T, *Pontibacter odishensis* JC130^T, *Pontibacter litorisediminis* YKTF-7^T and *Pontibacter aurantiacus* NP1^T (97.6, 97.5, 97.3, 97.3 and 96.7% sequence similarity, respectively). The major fatty acids of strain KIRAN^T were identified as iso-$C_{15:0}$, iso-$C_{15:0}$ 3-OH and summed feature 4. The predominant menaquinone was identified as MK-7. The polar lipid profile was found to be consist of phosphatidylethanolamine, four unidentified phospholipids, an unidentified glycolipid, an unidentified aminolipid and four unidentified lipids. The genome of strain KIRAN^T has a G+C content of 48.3 mol%. The *in silico* DNA-DNA hybridization and average nucleotide identity values between strain KIRAN^T and the closely related strains *P. actiniarum* KMM 6156^T and *P. korlensis* X14-1^T, were 21.2%/ 21.8% and 76.4%/75.1%, respectively. On the basis of the data from phenotypic tests and genotypic differences between strain KIRAN^T and its close phylogenetic relatives, strain KIRAN^T is concluded to represent a new species belonging to the genus *Pontibacter*, for which the name *Pontibacter oryzae* sp. nov. is proposed. The type strain is KIRAN^T (=KACC 19815^T =JCM 32880^T).

Keywords: Paddy field, Carotenoid, Phylogenetic analysis, Cell morphology, New taxa

SS-14

Iron Uptake and Antifungal Susceptibility are Modulated by pH in *Cryptococcus neoformans*

Donghyeun Kim and Wonhee Jung*

Department of Systembiotechnology, Chung-Ang University

Cryptococcus neoformans is an opportunistic fungal pathogen which causes fatal meningitis in immunocompromised hosts. *C. neoformans* can invade by inhalation, but host's immune system militates against infection of the pathogen by phagocytosis. In that process, phagocytosed *C. neoformans* resides in phagosome which matures to form phagolysosome that results in acidification. However, in *Candida albicans* which is a fungal pathogen, it was showed that susceptibility of *C. albicans* against to fluconazole was reduced at acidic pH while it was high susceptible at neutral pH. In *C. neoformans*, deletion of *CFO1* and *CFT1*, which encode ferroxidase and iron transporter, respectively, each mutant showed reduced susceptibility at acidic pH. Based on this discovery, we investigated the interaction of pH, antifungal susceptibility and iron metabolism. To investigate relations of pH and iron uptake, western blotting, phenotypic analysis and growth curve analysis were performed. MICs analysis and phenotypic analysis were carried out to investigate interaction of pH and antifungal susceptibility. The results showed antifungal susceptibility of *C. neoformans* against to fluconazole were more reduced at acidic pH than neutral pH. Additionally, *cfo1*⊿ and *cft1*⊿ recovered growth defect in low iron media at acidic pH while each mutant showed growth defect at neutral pH. It suggested that iron uptake mechanism was altered by pH. Overall, our results suggested pH of media modulated survival mechanisms of *C. neoformans* such as cell wall integrity, antifungal susceptibility and iron uptake.

Keywords: *C. neoformans*, pH, Antifungal, Fluconazole, Iron

SS-15

Dissemination of Antibiotic Resistance Genes in Freshwater from the Wastewater of Livestock and Aquaculture Farm

Jin Ju Kim[1], Hoon Je Seong[1], Tae-Yune Kim[1], Woo Jun Sul[1], and Jong-Chan Chae[2]*

[1]Department of Systems Biotechnology, Chung-Ang University, Anseong, Republic of Korea
[2]Division of Biotechnology, Chonbuk National University, Iksan 54596, Republic of Korea

Antibiotics used in livestock and aquaculture farm are released into the environment and affect the accumulation of antibiotic resistance genes (ARGs) and antibiotic resistant bacteria (ARB). This study identified the bacteial community and ARGs in the upstream, effluent and downstream of the 6 rivers in Korea. Total of 57 samples were obtained from the treated waste water of 10 livestock and waste water of 3 aquaculturefarm. A total of 476 subtypes within 19 ARG types were detected and the most common types were Beta-lactam, Sulfonamide, Aminoglycoside, and Tetracycline. Metagenome-assembled genomes (MAGs) were reconstructed from co-assembled contigs. Total 1086 bacterial and 5 alcheal MAGs were obtained and 1018 of bacterial MAGs had ARGs in their genomes. Patescibacteria mainly had beta-lactamase class A, and Actinobacteria had class B. In Proteobacteria, class B was dominant but class A was also detected. 129 bacterial MAGs, including Patescibacteria, Bacteroidota, Proteobacteria, and Actinobacteria, were found to remain downstream under the influence of effluents. These results indicate that the key bacteria, that have ARGs from the wastewater can affect the diffusion and accumulation of ARBs and ARGs in the downstream environment. We suggest that the intensive use of antibiotics would lead a continuous influx of ARGs from wastewater into the environment, which would have a significant impact on aquatic environmental contamination and further on human health.

Keywords: Antibiotic resistance genes, Metagenome, Metagenome assembled-genome, Wastewater

SS-16

The Imitative Cultivation of the Human Gut Microbiota in Single Batch and Its Potential Possibility as a Microbial Agent for FMT

Seung-Dae Choi[1], Yu-Jeong Lee[3], Raja Gopal Kammara[1,2], Yeon Gyun Jung[1], YoungJae Jo[1], Chang Eon Park[1], HyunWoo Son[1], Eun Soo Kim[3*], and Jae-Ho Shin[1*]

[1]School of Applied Biosciences, College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41556, Republic of Korea

[2]AcSIR Faculty, Department of Protein Chemistry and Technology, CSIR-CFTRI, Mysuru, India

[3]Division of Gastroenterology, Department of Internal Medicine, School of Medicine, Kyungpook National University, Daegu 41944, Republic of Korea

Fecal microbiota transplantation (FMT) can be applied to induce changes in the metabolism of recipients to treat gut-related diseases such as ulcerative colitis (UC), Crohn's disease, and *Clostridium difficile* infection (CDI). In some cases, FMT is required several times for patient recovery. A dilemma is that the stool is collected from the donor whenever needed and difficult storage. Moreover, reproducibility of microbial composition from donor stool is challenging due to various environmental factors like diet, disease, stress, etc. There have been attempts to encapsulate a small amount of raw materials to improve the current method. However, until now, there are no developed standardized methods in the form of medicines and well-defined gut microbial composition. In addition, it is not easy to reveal the mechanism of interactions between the hosts and gut microbiota due to its complexity and compositional characteristics. Also, the desire to fully understand how the gut microbiota works synergistically and how its benefits humankind, there is an increasing need to culture the gut microbiota *in vitro*. The objectives of this study were to prove that the gut microbiota could be imitatively cultured in a single batch and that the cultured gut microbiota could have the same therapeutic effect when compared to the original stool as an FMT material.

Stool samples were collected from healthy persons (HG) and immediately stored at -80°C. For gut microbial composition screening, fecal DNA extraction and 16S rRNA amplicon sequencing (V4-V5 region) was done. The sample showing the closest composition to the averaged relative abundance of

the HG was selected. The gut microbiota of the selected original stool sample (SOS) was cultured under the complete anaerobic condition at 37°C.

The relative abundance, alpha and beta diversities of the cultured microbiota in several media (Brain Heart Infusion; BHI, Tryptic Soy Broth; TSB, Reinforced *Clostridium* Media; RCM and Fastidious Anaerobe Broth; FAB) from different time points were compared with SOS and samples from HG. Although Shannon and Simpson's index (Alpha diversity) showed that the cultured gut microbiota from 12 hours in both media dramatically decreased, the cultured gut microbiota in BHI from 72 hours shows recovery for both indices. On the other hand, cultured gut microbiota in the other media did not show the recovery of alpha diversities even when the culture time was extended. Meanwhile, the PCoA plot produced using the weighted unifrac (Beta diversity) revealed that the gut microbiota cultured in BHI from different time points except for 12 hours were found near the cluster of the HG. In the beta diversity as well, it showed that the longer the incubation time in TSB, the more separated from the SOS and HG.

The therapeutic effect of cultured gut microbiota was confirmed using the dextran sulfate sodium (DSS) induced IBD mouse model. The mice group introduced cultured microbiota transplantation after DSS treatment, was not different when it compared to the other FMT groups. Moreover, the cultured gut microbiota shows similar therapeutic effect when introduced to the IBD mice in not only the histological observation, but also the cytokine level compared to the other FMT groups.

Based on the above consequences, it is expected that this simple culture method may provide a breakthrough for the limitations of current FMT by reproducibility, industrial scale production and well-defined microbial composition. In addition, it may be established as an *in vitro* gut microbial model for research purpose.

References

1. Lagier, Jean-Christophe, et al. “Culture of previously uncultured members of the human gut microbiota by culturomics.” *Nature microbiology* 1.12 (2016): 16203.
2. Hungate, R. E. “A roll tube method for cultivation of strict anaerobes. 117–132. JR Norris and DW Ribbons (ed.) *Methods in microbiology*, vol. 3B.” (1969).
3. Payne, Amanda N., et al. “Advances and perspectives in *in vitro* human gut fermentation modeling.” *Trends in biotechnology* 30.1 (2012): 17-25.
4. von Martels, Julius ZH, et al. “The role of gut microbiota in health and disease: *in vitro* modeling of host-microbe interactions at the aerobe-anaerobe interphase of the human gut.” *Anaerobe* 44 (2017): 3-12.
5. Burrello, Claudia, et al. “Therapeutic faecal microbiota transplantation controls intestinal inflammation through IL10 secretion by immune cells.” *Nature communications* 9.1 (2018): 5184.

6. Yousi, Fu, et al. "Evaluation of the effects of four media on human intestinal microbiota culture *in vitro*." *AMB Express* 9.1 (2019): 69.
7. Takagi, Risa, et al. "A single-batch fermentation system to simulate human colonic microbiota for high-throughput evaluation of prebiotics." *PLoS One* 11.8 (2016): e0160533.
8. Le Bastard, Quentin, et al. "Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice." *Scientific reports* 8.1 (2018): 6219.
9. Kondepudi, Kanthi Kiran, et al. "A novel multi-strain probiotic and synbiotic supplement for prevention of Clostridium difficile infection in a murine model." *Microbiology and immunology* 58.10 (2014): 552-558.
10. Chassaing, Benoit, et al. "Dextran sulfate sodium (DSS)-induced colitis in mice." *Current protocols in immunology* 104.1 (2014): 15-25.

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