A001

*Sphingorhabdus pulchriflava* sp. nov., Isolated from a River

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A facultative anaerobic and Gram-negative bacterium, strain GY_G⁹, was isolated from a river (Daedeock-cheon) in Daejeon, Republic of Korea. The isolate was catalase-positive and oxidase-positive and formed yellow colonies. The strain GY_G⁹ was phylogenetically classified in the genus *Sphingorhabdus* and other closely related strains were *Sphingorhabdus wooponensis* 03SU3-P⁹ (97.30% similarity) and *Sphingorhabdus contaminans* JC216⁹ (96.75% similarity) based on 16S rRNA gene sequences. The growth conditions for GY_G⁹ were temperatures ranging from 10°C to 45°C (optimal 25°C), pH 6–10 (optimum pH 7) and 0–6% NaCl (optimum 0.5–1.5%). GY_G⁹ could utilize D-turanose, D-fructose-6-phosphate, glucuronamide, α-keto-glutaric acid, and acetoacetic acid. The major fatty acids of GY_G⁹ were summed features 8 (C₁₈:1 ω7c/C₁₈:1 ω6c, 40.0%) and 3 (C₁₆:1 ω6c/C₁₆:1 ω7c, 27.6%). The major quinone required for respiration was Q-10. The polar lipids of GY_G⁹ consisted of diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylethanolamine (PE), and sphingolipid (SGL). The G+C content of the genome was 57.7%. The Average nucleotide identity (ANI) and Average amino acid identity (AAI) values between GY_G⁹ and 03SU3-P⁹ were 71.04% and 72.69%. Based on phylogenetic and phenotypic attributes, we suggest that strain GY_G⁹ is a novel species in the genus *Sphingorhabdus* and is named *Sphingorhabdus pulchriflava*. The type strain is GY_G⁹ (=KCTC 62791T =JCM 32855T).

[Supported by KIGAM (19-3413)]

A002

Potential Survival and Pathogenesis of a Novel Strain, *Vibrio parahaemolyticus* FORC_022, Isolated from a Soy Sauce Marinated Crab by Genome and Transcriptome Analyses

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*Vibrio parahaemolyticus* can cause gastrointestinal illness through consumption of seafood. In this study, a novel strain of *V. parahaemolyticus* FORC_022, was isolated from soy sauce marinated crabs, and its genome and transcriptome were analyzed. FORC_022 did not include major virulence factors of thermostable direct hemolysin and TDH-related hemolysin. However, FORC_022 showed high cytotoxicity and had several *V. parahaemolyticus* islands and other virulence factors, such as various secretion systems, in comparative genome analysis with CDC_K4557 and RIMD2210633. FORC_022 harbored additional virulence genes, including accessory cholera enterotoxin, zona occludens toxin, and tight adhesion locus. The expressions levels of genes involved in the virulence factors of type III secretion system, tad locus, and thermolabile hemolysin were overexpressed. Therefore, the risk of foodborne-illness may be high following consumption of FORC_022 contaminated crab. These results provided molecular information regarding the survival and pathogenesis of *V. parahaemolyticus* FORC_022 strain in contaminated crab and may have application in food safety.

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A003

*Pelagibacterium sediminicola* sp. nov., Isolated from Tidal Flat Sediment

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A Gram-stain-negative, aerobic, cream-coloured, non-gliding, motile with a single polar flagellum and rod-shaped bacterium, designated IMCC34151^T, was isolated from tidal flat sediment of the Yellow sea, Republic of Korea. Phylogenetic analysis based 16S rRNA gene sequences indicated that strain IMCC34151^T was affiliated with the genus *Pelagibacterium* in the family *Hyphomicrobiaceae* and shared 94.7-96.8 % sequence similarities with *Pelagibacterium* species. Whole genome sequencing of strain IMCC34151^T revealed genome size of 3.2 Mbp and the G+C content of 62.6 mol%. The ranges of average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) values between strain IMCC34151^T and other *Pelagibacterium* species were 75.4-74.0 % and 20.6-19.8 %, respectively. The strain contained summed feature 8 (C_{18:1} \omega 7c and/or C_{18:1} \omega 6c), C_{19:0} cyclo \omega 8c and C_{16:0} as the major fatty acids and ubiquinone-10 (UQ-10) as the major respiratory quinone. The polar lipids detected in the strain were phosphatidylglycerol, diphosphatidylglycerol, two unidentified glycolipids and twelve unidentified lipids. On the basis of phylogenetic and phenotypic characteristics, strain IMCC34151^T is considered to represent a novel species of the genus *Pelagibacterium*, for which the name *Pelagibacterium sediminicola* (type strain IMCC34151^T = KACC 19595^T = NBRC 113420^T) sp. nov., is proposed.

[Supported by a grant from the Collaborative Genome Program of the KIMST funded by the MOF (No. 20180430), Korea.]

A004

Characterization of Probiotic Properties of *Lactobacillus plantarum* SRCM101502 Isolated from Kimchi

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This study was aimed to isolate lactic acid bacteria having probiotics properties from Korean fermented food, Kimchi. 6 isolates were investigated for safety verification by biogenic amine, antimicrobial and antioxidant activities. Especially, SRCM101502 showed higher antioxidant activity (21.27%) than other strains. SRCM101502 was also evaluated to various antimicrobial spectrum and biogenic amines non-producing microorganisms. Finally, SRCM101502 was selected to confirm probability of probiotics strain, and named as *Lactobacillus plantarum* SRCM101502 by 16S rRNA sequencing analysis. Additionally, SRCM101502 was analyzed to their hemolytic, harmful substances and enzyme productivity, coagulation of milk protein, bile salt hydrolase, antibiotic resistance and survival ability of acidic and bile condition. As a result, SRCM101502 was confirmed as safe strain because of its non-hemolytic activity and non-production of harmful substances (Phenyl pyruvic acid and indole) and enzymes (β-glucuronidase and urase). And SRCM101502 showed survivability more than 10^2 CFU/ml in acidic condition at pH 2.0. Also, SRCM101502 has higher survival rate (97%) in 0.5% bile resistance. In addition, SRCM101502 has resistant to various antibiotics. These results suggest that SRCM101502 has potential for application as probiotic lactic acid bacteria.
**A005**

*Paracoccus intestinalis* sp. nov., from the Gut of a Blood Cockle, *Tegillarca granosa*

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A novel bacterial isolate, designated as strain BM15\(^T\), was isolated from the gastrointestinal tract of a blood cockle, *Tegillarca granosa*, which was collected from the foreshore of Beolgyo-eup in Korea. Strain BM15\(^T\) was Gram-negative, nonmotile, strictly aerobic and coccus-shaped. Optimum growth of the isolate occurred at 20°C, in the presence of 4% (w/v) NaCl and at pH 6. The 16S rRNA gene sequence analysis showed that strain BM15\(^T\) belonged to the genus Paracoccus in the family Rhodobacteraceae and had more than 97% 16S rRNA gene sequence similarity with *Paracoccus zhejiangensis* J6\(^T\) (97.40% similarity) and *P. lutimaris* HDM-25\(^T\) (97.04% similarity). The polar lipid profiles of strain BM15\(^T\) comprised phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, an unidentified glycolipid and an unidentified lipids. The predominant respiratory quinone was ubiquinone-10 (Q-10).

The major cellular fatty acids (>20%) was summed feature 8 (C\(_{18:1}\)ω7c and/or C\(_{18:1}\)ω6c). Complete genome sequence of strain BM15\(^T\) comprised 3,759,866 bp with 62.2 mol% G+C contents. The results of the phylogenetic, phenotypic and genotypic analyses indicated that strain BM15\(^T\) represents a novel species in the genus Paracoccus, for which the name *Paracoccus intestinalis* is proposed. The type strain is BM15\(^T\) (= KCTC 72032\(^T\) = JCM 33289\(^T\)).

**A006**

*Salicibibacter halophilus* sp. nov., a Moderately Halophilic Bacterium Isolated from Kimchi

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A Gram-positive, rod-shaped, motile, and halophilic bacterium, designated strain NKC3-5\(^T\), was isolated from kimchi. Comparative phylogenetic analysis based on the 16S rRNA genes showed that the isolated strain was most closely related to the *Salicibibacter kimchii* NKC1-1\(^T\) with a similarity of 96.2–97.6%. The isolated strain NKC3-5\(^T\) was observed to grow at 0.0–20.0% (w/v) NaCl (optimum 10%), pH 6.5–10.0 (optimum pH 9.0), and 25–37°C (optimum 35°C). The polar lipids of strain NKC3-5\(^T\) consisted of phosphatidylglycerol and two unidentified lipids. This strain possessed anteiso-C\(_{15:0}\) and anteiso-C\(_{17:0}\) as the major cellular fatty acids and menaquinone-7 as the major isoprenoid quinone. The cell wall peptidoglycan of strain NKC3-5\(^T\) was determined as meso-diaminopimelic acid. The complete genome of strain NKC3-5\(^T\) was 3,754,174 bp long with a G+C content of 45.87 mol%. Strain NKC3-5\(^T\) genome contained 4,103 coding sequences, 16 rRNA genes (16S rRNA, six; 5S, five; and 23S, five) and 59 tRNA genes. Based on these data, strain NKC3-5\(^T\) is considered to represent a novel species belonging to the genus *Salicibibacter*, for which the name *Salicibibacter halophilus* sp. nov. is proposed. The type strain is NKC3-5\(^T\).

[This research was supported by a grant from the World Institute of Kimchi (KE1902-1), funded by the Ministry of Science and ICT, Republic of Korea.]
A007

Haloplanus rubicundus sp. nov., an Extremely Halophilic Archaeon Isolated from Solar Salt

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Two strains of extremely halophilic archaea, CBA1112ᵀ and CBA1113, were isolated from solar salt in Korea. The genome sizes and genomic G+C contents of strains CBA1112ᵀ and CBA1113 were 3,773,640 and 3,529,327 bp, and 66.0 and 66.5 mol%, respectively. Phylogenetic analysis based on 16S rRNA gene sequences and RNA polymerase subunit B’ gene sequences indicated that both strains CBA1112ᵀ and CBA1113 are distinct from other species of the genus Haloplanus and are most closely related to Haloplanus natans and Haloplanus salinus. OrthoANI and in silico DNA-DNA hybridization values were far below the species delineation threshold. Cells of both strains were Gram-negative and pleomorphic, and colonies were red-pigmented. The major polar lipids of both strains were phosphatidylglycerol, phosphatidylglycerol phosphate methyl ester, phosphatidylglycerol sulfate, and one glycolipid, sulfated mannosyl glucosyl diether. Based on genomic, phylogenetic, phenotypic, and chemotaxonomic features, strains CBA1112ᵀ and CBA1113 are described as members of a novel species of the genus Haloplanus, for which the name Haloplanus rubicundus sp. nov. is proposed. The type strain is CBA1112ᵀ (=KCCM 43224ᵀ =JCM 30475ᵀ).

A008

The Comparison of Characteristics of Soil Microbial Community at 4 Districts in Korea

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Soil biodiversity is worsening due to changes in climate and agricultural land use patterns. Therefore, appropriate soil management plan is needed. The objective of this study was to compare characteristics of soil microbial community in four areas: reclaimed land (Saemangeum Reclaimed Land), Alpine region (Pyeongchang), Miryang, and Suwon in Korea agriculture land. The analysis was carried out using the illumine Mseq system for DNA sequencing of the bacterial 16s rRNA genes in soil. Diversity index of 4 districts showed highest community richness in Alpine region (Pyeongchang), while reclaimed land (Saemangeum Reclaimed Land) showed lowest community richness. PCoA analysis was divided into three parts; reclaimed land (Saemangeum Reclaimed Land), Alpine region (Pyeongchang), Miryang, and Suwon. Our results suggest that it is necessary to observe how microbial diversity changes when agricultural cultivation techniques are applied to 4 districts in Korea.
A new species bacteria strain, named MS74 was isolated from soil in Itaewon road Seoul - Republic of Korea. MS74T is rod-shaped, endospore-forming, gram positive bacteria. The strain could grow well on R2A, nutrient agar, and tryptone soya agar. MS74T tolerated 3.5 % NaCl (w/v), pH 10.0 and also grew in optimal temperature 30°C. The phylogenetic sequence analysis based on the 16S rRNA gene from MS74T revealed that it was closely related to Paenibacillus vulneris CCUG 53270T with 96.41% sequence identity. Major polar lipids of strain MS74T were diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylethanolamine (PE), and phosphatidymonomethylethanolamine (PME). The major menaquinone was MK7. The fatty acids profile mainly consisted of C15:0 anteiso, C15:0 iso, C16:0 iso, and C16:0. The DNA G+C content of isolated strain was 51.6 mol%. Based on phenotypic, chemotypic and genotypic results, strain MS74T was identified as a novel species of the genus Paenibacillus, for which the name Paenibacillus itaewonii sp. nov.

A Gram-stain negative, yellow-coloured, rod-shaped bacterium, designated strain II4, was isolated from soil in Seongnam city, Gyeonggi-do, Republic of Korea using 6 well plate and cultured routinely on R2A agar at 28°C 3 days. The novel strain grew at R2A and TSA. Based on 16S rRNA gene sequence comparisons, strain II4 had close similarity with Lysobacter terrae THG-A13T (97.88%), Lysobacter niabensis GH34-4T (97.82%), Lysobacter oryzae YC6269T (97.74%), Lysobacter yangpyeongensis GH19-3T (97.53%), Lysobacter panacisoli CJ29T (97.24%), Lysobacter rhizosphaerae THG-DN8.3T (97.22%), Lysobacter tabacisoli C8-1T (97.14%). Chemotaxonomic data revealed that strain II4 possesses predominant quinone is Q8 and iso-C15:0, iso-C16:0 and iso-C17:1 v9c as the major fatty acids. The major polar lipids were phosphatidylethanolamine, phosphatidylglycerol) and diphosphatidylglycerol. Caseinase and dnase are hydrolysed. Catalase and oxidase activities positive.
A011

*Brachybacterium vulturis* sp. nov. and *Brachybacterium avium* sp. nov., Two Novel Species Isolated from Fecal Sample of an Andean Condor
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Two strains VM2412<sup>T</sup> and VR2415<sup>T</sup> were isolated from feces of an Andean condor (*Vultur gryphus*) in Seoul Grand Park, Gyeonggi-do, South Korea. They shared 99.3% 16S rRNA gene sequence similarities with each other, but they were identified as two distinct species according to 89.0-89.2% ANI<sub>b</sub>, 90.3% ANI<sub>m</sub>, 89.7% OrthoANI and 38.0% dDDH values using whole genome sequences. *Brachybacterium ginsengisol DCY80<sup>T</sup>* shared the highest 16S rRNA gene sequence similarities with strains VM2412<sup>T</sup> (98.7%) and VR2415<sup>T</sup> (98.4%) and showed the closest genomic relatedness with strains VM2412<sup>T</sup> (83.3-83.5% ANI<sub>b</sub>, 87.0% ANI<sub>m</sub>, 84.3% OrthoANI and 27.8% dDDH) and VR2415<sup>T</sup> (82.8-83.2% ANI<sub>b</sub>, 86.7% ANI<sub>m</sub>, 83.9% OrthoANI and 27.2% dDDH). Genome-based phylogenetic tree constructed by up-to-date bacterial core gene set (UBCG) showed that members of the genus *Brachybacterium* formed a clade with the isolated strains, supporting taxonomic classification of the strains into the genus *Brachybacterium*. Based on phenotypic and genotypic analyses in this study, strains VM2412<sup>T</sup> and VR2415<sup>T</sup> are considered to represent two novel species of the genus *Brachybacterium*.

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A012

*Undibacterium piscinae* sp. nov. and *Jeotgalibaca ciconiae* sp. nov., Two Novel Bacteria Isolated from Korean Indigenous Vertebrate
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Two putative novel species, strain S11R28<sup>T</sup> and H21T32<sup>T</sup>, were isolated from fecal samples of oriental stork (*Ciconia boyciana*) and a gut sample of Korean shiner (*Coreoleuciscus splendidus*) respectively. A Gram-negative, non-spore-forming, obligate aerobic, rod-shaped, flagellated bacterium, designated S11R28<sup>T</sup> grew optimally at 20° C, pH 8, in the absence of NaCl. The strain possessed ten polar lipids and ubiquinone Q-8. The strain showed high sequence similarity to the type strains of *Undibacterium parvum* DSM 23061<sup>T</sup> (97.99%) and ANI value between two strains was 78.66%. Strain H21T32<sup>T</sup> was Gram-positive, non-spore forming, facultative anaerobic, and grew optimally at 30°C, pH 8, in the presence of 0.5% NaCl. The strain possessed eight polar lipids and C<sub>16:1</sub>ω9c, C<sub>18:2</sub>ω9c, and C<sub>16:0</sub> as main fatty acids. Strain H21T32<sup>T</sup> formed a monophyletic clade with *Jeotgalibaca arthritidis* CECT 9157<sup>T</sup> (96.89%) and ANI value between two strains was 77.25%. Based on these phylogenetic, chemotaxonomic, and genotypic properties of two strains, strain S11R28<sup>T</sup> and H21T32<sup>T</sup> are considered to represent a novel species, for which the name *Undibacterium piscinae* sp. nov. and *Jeotgalibaca ciconiae* sp. nov. is proposed.

[This work was supported by a grant Collaborative Genome Program for Fostering New Post-Genome industry (NRF-2015M3C9A2054299) through the National Research Foundation (NRF) of Korea funded by the Ministry of Science ICT & Future Planning.]
A novel Gram-negative, aerobic, rod-shaped, reddish-orange coloured, motile bacterial strain designated L12M1\textsuperscript{T} was isolated from the gut of the Korean scallop. The phylogenetic analysis based on 16S rRNA sequences revealed that strain L12M1\textsuperscript{T} belonged to the genus \textit{Flammeovirga} and showed highest 16S rRNA gene sequence similarity with \textit{Flammeovirga kamogawensis} YS10\textsuperscript{T} (98.66\%). The optimal growth condition of strain L12M1\textsuperscript{T} was 25°C, pH 7 and 2% (w/v) NaCl. The major cellular fatty acids of strain L12M1\textsuperscript{T} were iso-C\textsubscript{15:0} and C\textsubscript{20:4} ω6,9,12,15c. The predominant isoprenoid quinone was MK-7. The DNA G + C content was 32.1 mol%. The polyphasic analyses indicated that strain L12M1\textsuperscript{T} represents a novel species of the genus \textit{Flammeovirga}, for which the name \textit{Flammeovirga pectinis} sp. nov. is proposed. The type strain is L12M1\textsuperscript{T} (=KCTC 62750\textsuperscript{T} = JCM 33169\textsuperscript{T}).

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A yellow pigmented, Gram-stain-negative, strictly aerobic, rod-shaped, non-flagellated, gliding motility, catalase and oxidase positive bacterium, designated as strain DS2-A\textsuperscript{T}, was isolated from soil. Growth was observed at 4-32°C (optimum, 30°C), pH 6-9 (optimum, 7.0) and with 0-0.25% (w/v) NaCl (optimum, 0%). Phylogenetic analysis 16S rRNA gene sequence revealed that strain DS2-A\textsuperscript{T} belonged to the genus \textit{Flavobacterium} and was most closely related to \textit{Flavobacterium aquatile} 7307\textsuperscript{T} (96.44\%), \textit{Flavobacterium inkyongense} IMCC27201\textsuperscript{T} (95.42\%) and \textit{Flavobacterium cucumis} R2A45-4\textsuperscript{T} (95.18\%). Strain DS2-A\textsuperscript{T} produce flexirubin-type pigments. The major fatty acids were iso-C\textsubscript{15:0}, iso-C\textsubscript{17:0}3OH and iso-C\textsubscript{15:0}3OH. The major respiratory quinone was menaquinine-6 (MK-6). The major polar lipid was phosphatidylethanolamine (PE). The DNA G+C content of stain DS2-A\textsuperscript{T} was 35.3 mol%. Based on the phylogenetic and phenotypic analyses, strain DS2-A\textsuperscript{T} is considered a novel species of the genus \textit{Flavobacterium}, for which the name \textit{Flavobacterium croceum} sp. nov., (type strain DS2-A\textsuperscript{T} = KACC 19715\textsuperscript{T} = JCM 32786\textsuperscript{T}) is proposed.

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A015

Lysobacter helvus sp. nov. and Lysobacter xanthus sp. nov., Isolated from Soil in South Korea

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Two bacterial strains, designated D10T and U8T, were isolated from soil samples from the Dong-angyeong cave and Geommeolle wharf sea-coast, Udo-Island, Jeju, South Korea. Both novel bacterial strains were yellow-pigmented, Gram-stain-negative, motile by means of monotrichous flagella, short-rod shaped, and strictly aerobic. A phylogenetic tree was reconstructed based on their 16S rRNA sequences, which indicated that these two strains belong to the genus Lysobacter within the family Xanthomonadaceae. The major polar lipids for both strains were diphosphatidylglycerol, phosphatidylethanolamine, and phosphatidylglycerol. The major cellular fatty acids for both strains were iso-C15:0, iso-C16:0, and summed feature 9 (iso-C17:1ω9c/C16:1ω10-methyl and ubiquinone (Q-8) as the only isoprenoid quinone for both strains. The DNA G+C contents of the strains D10T and U8T were 70.2 [mol% and 70.6 mol%. On the basis of phenotypic, genotypic, chemotaxonomic, and phylogenetic analysis, both strains D10T and U8T represent a novel member in the genus Lysobacter, for which the name Lysobacter helvus sp. nov. and Lysobacter xanthus sp. nov. are proposed, respectively. The type strain of Lysobacter helvus is D10T (= KCTC 62111T = JCM 32364T) and the type strain of Lysobacter xanthus is U8T (= KCTC 62112T = JCM 32365T).

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A016

Amnibacterium setariae sp. nov., an Endophytic Actinobacterium Isolated from Yellow Foxtail

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A Gram-stain-positive, short rod-shaped, aerobic, non-motile, non-spore-forming, yellow-pigmented actinobacterium, designated as strain DD4aT, was isolated from yellow foxtail in Republic of Korea. Phylogenetic analysis based on 16S rRNA gene sequence studies showed that strain DD4aT was most closely related to Amnibacterium soli MB78T (98.4%), Amnibacterium kyonggiense KSL51201-037T (98.2%), and Amnibacterium endophyticum 1T4Z-3T (97.43%). Strain DD4aT contained a peptidoglycan ε-2,4-diaminobutyric acid the diagnostic cell-wall diamino acid. The polar lipids of strain DD4aT were diphosphatidylglycerol, phosphatidylglycerol, seven unidentified glycolipids. The major cellular fatty acid for strain was anteiso-C15:0 42.9%, iso-C16:0 34.6% and MK-11, MK12 the major menaquinones. The DNA G + C content of strain DD4aT was 73.9 mol%. DNA-DNA relatedness of strain DD4aT with A. soli MB78T, A. kyonggiense KSL51201-037T, and A. endophyticum 1T4Z-3T were 53.34% (± 1.1%), 47.01% (± 0.5%), and 47.86% (± 0.9%). On the basis of phenotypic, genotypic, chemotaxonomic, and phylogenetic analysis, strain DD4aT represent a novel member in the genus Amnibacterium, for which the name Amnibacterium setariae sp. nov. are proposed respectively. The type strain of Amnibacterium setariae is DD4aT (= KACC 19817T = JCM 32878T).

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A017

*Sphingomonas edaphi* sp. nov., a Novel Species Isolated from Cave Soil in South Korea

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A yellow color, Gram-negative, motile, strictly aerobic bacterial strain, designated strain DAC4⁷ was isolated from a soil sample collected at Ahnmok beach (Busan, South Korea). The cells of strain DAC4⁷ were rod-shaped, colonies were round and convex. The strain DAC4⁷ grew optimally at 30°C, pH 7.0 and 0% (w/v) NaCl on R2A agar. Phylogenetic analysis based on 16S rRNA gene sequence of strain DAC4⁷ revealed that the bacterium belonged to the genus *Sphingomonas*, the family of *Sphingomonadaceae*, and most closely related to *Sphingomonas jaspsi* DSM18422⁷ (98.01%), *Sphingomonas sedimincola* KCTC12629⁷ (97.37%) and *Sphingomonas orziterrae* KCTC22476⁷ (97.05%). The major respiratory quinone was Q-10, and the major cellular fatty acids were summed feature 8 (18:1 ω7c) and summed feature 3 (16:1 ω7c/ 16:1 ω6c). The whole genome sequence shown DNA G+C mol% of the strain DAC4⁷ was 62.16 mol%. Phosphatidylethanolamine, diphosphatidyglycerol, sphingoglycolipids, three undefined glycolipids, and two undefined lipids were detected in strain DAC4⁷. On the basis of phylogenetic, phenotypic and chemotaxonomic distinctiveness, strain DAC4⁷ is considered as a novel species of the genus *Sphingomonas*, for which the name *Sphingomonas edaphi* sp. nov. is proposed. The type strain is DAC4⁷ (=KCTC 62107⁷ =JCM 32377⁷).

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A018

*Tumebacillus avium* sp. nov., Isolated from the Gut of a Cinereous Vulture, *Aegypius monachus*

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A Gram-stain-positive, facultatively aerobic, spore-forming, rod-shaped, and motile bacterial strain, AR23208⁷, was isolated from the gut of a cinereous vulture (*Aegypius monachus*), collected at the Seoul Grand Park Zoo. Strain AR23208⁷ grew optimally at 25–30°C, at pH 7, in the absence of NaCl. The phylogenetic analysis revealed that the 16S rRNA gene of strain AR23208⁷ shared 98.2% and 97.1% sequence similarity with the corresponding sequences of *Tumebacillus algifaecis* THMBR28⁷ and *T. lipolyticus* NISO-510⁷, respectively. The predominant fatty acids (>10%) of strain AR23208⁷ were iso-C₁₅:₀ (46.5%), summed feature 4 (anteiso-C₁₇:₁ B and/or iso-C₁₇:₁ I, 11.7%) and anteiso-C₁₅:₀ (11.1%). The OrthoANI value based on the complete genome sequence of strain AR23208⁷ and the closest related strain, *T. algifaecis*, was 80.4%. The genomic DNA G+C content of strain AR23208⁷ was 56.0 mol%. In this study, strain AR23208⁷ is proposed to be a novel species candidate of the genus *Tumebacillus*, with the strain name *Tumebacillus avium* sp. nov. and strain AR23208⁷ as the type strain.

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A019

*Quadrisphaera setariae* sp. nov., Polyphosphate-accumulating Coccus in Tetrads or Aggregates Isolated from Yellow Foxtail

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A Gram-stain-positive, aerobic, round-shaped, non-spore-forming, non-motile, designated DD2A^T, was isolated from yellow foxtail in Republic of Korea. Phylogenetic analysis based on 16S rRNA gene sequence studies showed that strain DD2A^T was most closely related to the type strains of genus *Quadrisphaera*. Strain DD2A^T showed high 16S rRNA gene sequence similarities with *Quadrisphaera granulorum* AG019^T (98.5% similarity). Strain DD2A^T showed auto aggregation ability. The major polar lipids of strain DD2A^T were diphosphatydilglycerol, phosphatydilglycerol, two unidentified phosphoglycolipid. The major cellular fatty acid for strain DD2A^T were anteiso-C_{15:0}. The cell-wall peptidoglycan contained meso-diaminopimelic acid (type A1γ) and MK8(H2) was the major Menaquinone. Strain DD2A^T showed a low DNA-DNA relatedness to *Quadrisphaera granulorum* AG019^T 27.1%. The DNA G+C content of strain DD2A^T was 75.5 mol%. On the basis of phenotypic, genotypic, chemotaxonomic, and phylogenetic analysis, strain DD2A^T is considered to represent a novel member in the genus *Quadrisphaera*, for which the name *Quadrisphaera setariae* sp. nov. are proposed. The type strain of *Quadrisphaera setariae* is DD2A^T (= KACC 21165^T).

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A020

A New Starch-hydrolysing Bacterium Isolated from the West Sea, South Korea

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A Gram-negative, orange-pigmented, non-flagellated, non-gliding, rod-shaped and aerobic bacterium with the ability to degrade starch, designated F202Z8^T, was isolated from coastal seawater of the West Sea in Korea. Phylogenetic analyses based on 16S rRNA gene sequences indicated that the isolate was affiliated to the family *Flavobacteriaceae* and showed highest similarity to *Maribacter aestuarii* GY20^T (94.69%). Growth was observed at 15-33°C (optimum, 26°C), at pH 6.5-7.5 (optimum, 7.0) and with 2.5-4.5% (w/v) NaCl (optimum, 4.0%). The predominant cellular fatty acids were iso-C_{15:0}, iso-C_{15:1} G and iso-C_{17:0} 3-OH and the major respiratory quinone was MK-6. Polar lipids included phosphatidylethanolamine, five unidentified lipids, and two unidentified aminolipids. The DNA G+C content was 43.26 mol%. On the basis of the data from the present polyphasic taxonomic study, strain F202Z8^T is considered to represent a novel species of a new genus in the family *Flavobacteriaceae*. [This work was supported by the MABIK in-house program (2019M00700).]
A021

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

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An aerobic, Gram-stain-negative, non-motile, non-spore-forming, rod-shaped, pink-pigmented, carotenoid producing bacterium, designated strain KIRANT, was isolated from soil. Flexirubin-type pigments were absent. The 16S rRNA gene sequence analysis showed that strain KIRANT clustered together with *P. actiniarum* KMM 6156\(^T\), *P. korlensis* X14-1\(^T\), *P. odishensis* JC130\(^T\), *P. litorisediminis* YKTF-7\(^T\) and *P. aurantiacus* NP1\(^T\) (97.6, 97.5, 97.3, 97.3 and 96.7% sequence similarity, respectively). Genomic analyses, including average nucleotide identity and DNA–DNA hybridization, clearly separated strain KIRANT from reference strains with values below the thresholds for species delineation. The major cellular fatty acids included iso-C15:0, iso-C17:0 3-OH, summed feature 3 and summed feature 4. The DNA G+C contents of strains X14-1\(^T\) and X19-1 were 48.2 mol%. The predominant menaquinone was MK-7. The polar lipid profile consisted of phosphatidylethanolamine. Strain KIRANT could be clearly distinguished from the related species of the genus *Pontibacter* by its physiological and biochemical characteristics as well as by its phylogenetic position and DNA–DNA relatedness. Therefore, the strain represents a novel species of the genus *Pontibacter*, for which the name *Pontibacter oryzae* sp. nov. (type strain KIRANT\(^T\)=KACC 19815\(^T\)=JCM 32880\(^T\)).

[This research was supported by a National Research Foundation of Korea (NRF) grant by the Korean government (MIST) (NRF-2017R1A2B4009448)].

A022

**Tabrizicola piscis** sp. nov., Isolated from the Intestinal Tract of a Korean Indigenous Freshwater Fish, *Acheilognathus koreensis*

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A novel Gram-stain-negative, facultative aerobic, rod-shaped and non-motile bacterium, designated strain K13M18\(^T\), was isolated from intestinal tract of a Korean Indigenous fish, oily bitterling (*Acheilognathus koreensis*). Strain K13M18\(^T\), was grown on marine agar plate and had creamy-pink colonies. A phylogenetic analysis based on 16S rRNA gene sequence similarity showed that strain K13M18\(^T\) was most closely related to *Tabrizicola aquatica* RCR19\(^T\) with 97.41% similarity. Strain K13M18\(^T\) was a part of the genus *Tabrizicola* which shaped a monophyletic clade with *Tabrizicola aquatica* RCR19\(^T\) on a 16S rRNA sequences based phylogenetic tree. Strain K13M18\(^T\) grew optimally on 0% (w/v) NaCl, pH of 7 and 30°C in marine broth medium. The predominant cellular fatty acids were C\(_{18:1}\) ω7c and C\(_{18:1}\) ω6c. The major respiratory isoprenoid quinone was ubiquinone Q-10. Phosphatidylcholine (PC), phosphatidylethanolamine and unidentified lipid were the component of the polar lipids. According to the genome sequencing, the DNA G+C content was 64.08 mol% and the ANI value, calculated from comparative genomic analysis between strain K13M18\(^T\) and *T. aquatica* RCR19\(^T\) was 79.75%. Based on the phylogenetic, genotypic and phenotypic information, strain K13M18\(^T\) is suggested as a novel species of the genus *Tabrizicola*. The type strain is K13M18\(^T\)(=KCTC 62659\(^T\)=JCM 33230\(^T\)).

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A023

Iodobacter ciconiae sp. nov., a Bacterium Isolated from Faces of Oriental Stork, Ciconia boyciana

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A novel Gram-negative, facultatively anaerobic, non-motile, non-violet-pigmented, rod-shaped bacterium, designated strain H11R3^T, was isolated from the feces of Oriental stork, Ciconia boyciana, collected from Seoul Grand Park zoo, Republic of Korea. Phylogenetic analysis of the 16S rRNA gene sequence revealed that strain H11R3^T formed a monophyletic clade with Iodobacter fluviatilis DSM 3764^T, Iodobacter arcticus DSM 100243^T, and Iodobacter limnosediminis DSM 103822^T, with sequence similarities of 98.80%, 98.63%, and 98.36%, respectively. Strain H11R3^T grew optimally at 15°C, pH 8, with 0.5% (w/v) NaCl. The predominant isoprenoid quinone is ubiquinone-8 (Q-8), and polar lipids include three unidentified lipids, four unidentified phospholipids, one unidentified aminolipid, and two unidentified aminophospholipids. The major fatty acids are summed feature 3 and C16:0, and the G+C content of the genome is 48.04 mol%. The average nucleotide identity (ANI) value between strains H11R3^T and I. fluviatilis NCTC 11159^T (=DSM 3764^T) is 83.73%. Based on phenotypic, genotypic, phylogenetic, and chemotaxonomic characteristics, strain H11R3^T represents a novel species of the genus Iodobacter for which the name Iodobacter ciconiae sp. nov. is proposed. The type strain is H11R3^T (=KCTC 62666^T =JCM 33283).

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A024

Taibaiella lutea sp. nov., a Flexirubin-type Pigment Producing Bacterium Isolated from Setaria viridis near Dongguk University, South Korea

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A yellow-coloured bacterial strain, designated KVB11T, was isolated from a grass sample collected in Goyang, South Korea. Strain KVB11T was Gram-stain-negative, strictly aerobic, rod-shaped, non-motile and non-spore-forming. Flexirubin-type pigments were produced. Growth occurred at 20–35°C (optimum, 30°C), at pH 6.0–8.0 (pH 7.0) and with 0–1.0% (w/v) NaCl (0%). Phylogenetic analysis based on 16S rRNA gene sequences showed that strain KVB11T belonged to the genus Taibaiella and was related to Taibaiella smilacinae PTJT-5^T (96.4%) and Taibaiella yonginensis THG-SC4T (96.3%). The predominant respiratory quinine was MK-7, with MK-8 as a minor component. The major polar lipids were phosphatidylethanolamine, two unidentified phosphoglycolipids, one unidentified aminophosphoglycolipid and one unidentified aminoglycolipid. The major cellular fatty acids were iso-C15:0, iso-C15:1 G and iso-C17:0. The G+C content of the genomic DNA based on total genome calculations was 51.3 mol%. On the basis of the genotypic and phenotypic data presented here, strain KVB11T represents a novel species of the genus Taibaiella, for which the name Taibaiella lutea sp. nov. is proposed. The type strain is KVB11T (=KCTC 62442^T =JCM 33679^T).

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A025

*Adhaeribacter aurantiacus* sp. nov, Isolated from Soil of Paddy Field

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Strain DK36\(^T\) was isolated from a soil sample collected at Ilsan, Gyeonggi-do, Republic of Korea. Cells of this strain were observed to be Gram-stain-negative, rod-shaped. Colonies were orange-red in colour. Phylogenetic analysis based on 16S rRNA gene sequences indicated that the closest relative of strain DK36\(^T\) was *Adhaeribacter aerophilus* 64245-25\(^T\) with 96.3% sequence similarity. The strain showed the typical chemotaxonomic characteristics of the genus *Adhaeribacter*, with the presence of menaquinone MK-7 as the respiratory quinone, and summed feature 4 (composed of iso-C\(_{17:1}\) \(\beta\)/anteiso-C\(_{17:1}\) \(\beta\)), iso-C\(_{15:0}\) and C\(_{16:1}\) \(\omega5c\) as the major fatty acids. The major polar lipid was phosphatidylethanolamine. The DNA G+C content was 48.1 mol%. Based on its phenotypic and genotypic properties, together with its phylogenetic distinctiveness, strain DK36\(^T\) should be considered a representative of a novel species in the genus *Adhaeribacter*, for which the name *Adhaeribacter terrae* sp. nov. is proposed. The type strain is DK36\(^T\) (=KCTC 52512\(^T\)=JCM 31652\(^T\)).

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A026

*Hymenobacter aurantiacus* sp. nov., Isolated from Dry Grass Called Foxtail

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A non-motile, rough, rod-shaped and dark-red-pigmented bacterium, designated strain Fur-1\(^T\), was isolated from green foxtail, near hospital of Dongguk University, Republic of Korea. The 16S rRNA gene sequence of strain Fur-1\(^T\) exhibited highest similarities to *Hymenobacter metalli* A2-91\(^T\) (97.4%) and *Hymenobacter marinus* KJ035\(^T\) (97.0%). The major fatty acids of strain T-3T were iso-C\(_{15:0}\) (27.66%), summed feature 4 (iso-C\(_{17:1}\) \(\beta\) and/or anteiso-C\(_{17:1}\) \(\beta\), 15.84%), anteiso-C\(_{15:0}\) (14.08%) and summed feature 3 (C\(_{16:1}\) \(\omega7c\) and/or C\(_{16:1}\) \(\omega6c\), 12.38%). The major menaquinone of strain Fur-1\(^T\) was MK-7. Phosphatidylethanolamine (PE) was predominant in the polar lipid profile. The G+C content of the DNA of strain Fur-1\(^T\) was 69.17 mol%. The DNA–DNA relatedness of strain Fur-1\(^T\) with respect to *Hymenobacter metalli* A2-91\(^T\) and *Hymenobacter marinus* KJ035\(^T\) was less than 42%. On the basis of the phylogenetic inference and phenotypic data, strain Fur-1\(^T\) represents a novel species of the genus *Hymenobacter*, for which the name *Hymenobacter aurantiacus* sp. nov. is proposed. The type strain is Fur-1\(^T\) (=KCTC 32637\(^T\)=JCM32899\(^T\)).

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**A027**

**Lysobacter caseinilyticus**, sp. nov., a Casein Hydrolyzing Bacterium Isolated from Sea-water

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A novel bacterial strain, designated KVB24\(^T\), was isolated from sea-water of Busan Harbor in South Korea. Cells of strain KVB24\(^T\) were Gram-stain-negative, aerobic, rod shaped and non-motile. Strain KVB24\(^T\) grew optimally at 25-28\(^\circ\)C and pH 6.5-7.0. Based on 16S rRNA gene sequence analysis, strain KVB24\(^T\) was shown to belong to the genus *Lysobacter* within the class *Gammaproteobacteria* and was most closely related to *Lysobacter dokdonensis* DS-58\(^T\), *Lysobacter hankyongensis* KTce-2\(^T\) and *Lysobacter niastensis* GH41-7\(^T\). DNA-DNA relatedness between strain KVB24\(^T\) and its closest relative was below 70%. The predominant fatty acids of strain KVB24\(^T\) were iso-C\(_{11:0}\), iso-C\(_{11:0}\) 3-OH, iso-C\(_{14:0}\), iso-C\(_{15:0}\), anteiso-C\(_{15:0}\), iso-C\(_{16:0}\) and summed feature 9 comprising (iso-C\(_{17:1}\) ω9c and/or 10 methyl C\(_{16:0}\)); their prominent isoprenoid was Q-8 and their major polar lipids were dihexadecylglycerol, phosphatidylglycerol and phosphatidylethanolamine. The G+C content of genomic DNA from the strain KVB24\(^T\) was determined to be 67.5 mol%. Based on the phenotypic, genotypic and chemotaxonomic analyses, strain KVB24\(^T\) represents a novel species of the genus *Lysobacter*, for which the name *Lysobacter caseinilyticus* sp. nov. is proposed. The type strain is KVB24\(^T\) (= KACC19816\(^T\) = JCM32879\(^T\)).

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**A028**

**Runella soli** sp. nov., a Member of the Genus *Runella* Isolated from Garden Soil

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A Gram-stain-negative, aerobic, salmon-pink, non-motile and rod-shaped bacteria, designated as 15J11-1\(^T\), was isolated from soil sample collected from university garden in Nowongu, South Korea. The 16S rRNA gene sequence analysis showed that the strain 15J11-1\(^T\) was phylogenetically related to *Runella slithyformis* DSM 19594\(^T\) and *Runella palustris* HMF3829\(^T\) (96.9% and 95.4% sequence similarity, respectively). The major fatty acids of the strain 15J11-1\(^T\) were identified as iso-C\(_{15:0}\), iso-C\(_{17:0}\) 3-OH, C\(_{16:1}\)ω5c and summed feature 3 (C\(_{16:1}\) ω7c and/or C\(_{16:1}\) ω6c). The predominant respiratory quinone was identified as MK-7. The polar lipid comprised of phosphatidylethanolamine, three unidentified aminolipids, five unidentified glycolipids, two unidentified aminoglycolipids, one unidentified phospholipid and one unidentified polar lipid. The G+C content in the genomic DNA of the strain 15J11-1\(^T\) was determined to be 49.9 mol%. Based on the results of genotypic, phenotypic and chemotaxonomic analyses, the strain 15J11-1\(^T\) represents a novel species of the genus *Runella*, for which the name *Runella soli* sp. nov. (type strain 15J11-1\(^T\) = KCTC 52021\(^T\) = NBRC 112817\(^T\)) is proposed.

[This research was supported by a National Research Foundation of Korea (NRF) grant by the Korean government (MIST) (NRF-2017R1A2B4009448)]
A029

**Acromobacter aestuarii** sp. nov., Isolated from Estuary in South Korea

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A Gram-staining-negative, strictly aerobic bacterium, designated KS-M25^T^, was isolated from an estuary, in Korea and its cells were oxidase-positive and catalase-weak positive motile rods by a double lateral flagellum. Growth of strain KS-M25^T^ was observed at 10–25°C (optimum, 20 °C), pH 5.5–9.0 (optimum, pH 7.5) and in the presence of 0–6.0% (w/v) NaCl (optimum, 1 %). Strain KS-M25T contained C₁₆:₀, C₁₇:₀ cyclo and sum in feature 3 (comprising C₁₆:₁ ω7c and/or C₁₆:₁ ω6c). Ubiquinone-8 were identified as the sole isoprenoid quinone. The G+C content of the genomic DNA was 63.2 mol%. Strain KS-M25^T^ was most closely related to *Achromobacter anxifer* LMG 26857^T^, *Achromobacter dolens* LMG 26840^T^ and *Achromobacter xylosoxidans* LMG 1863^T^ with 97.79%, 97.79% and 97.66% 16S rRNA gene sequence similarities, respectively, but it formed a distinct phylogenetic lineage within the genus *Achromobacter*. Based on phenotypic, chemotaxonomic and molecular properties, strain KS-M25^T^ represents a novel species of the genus *Achromobacter*, for which the name *Acromobacter aestuarii* sp. nov. is proposed. The type strain is KS-M25^T^.

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A030

**A Novel Aliirhodobacter LPB0142^T^ gen. nov. sp. nov. Isolated from Seawater**

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A Gram-stain-negative, rod-shaped, facultatively anaerobic bacterial strain designated LPB0142^T^ was isolated from the seawater. The 16S rRNA gene sequence was found to share the highest sequence similarity with *Rhodobacter maris* AM745438^T^ (97.0%), *Rhodobacter lacus* JA826^T^ (97.0%), *Paenirhodobacter enshiensis* DW2-9^T^ (96.8%), *Sinorhodobacter ferrireredens* Sg2-3^T^ (96.7%), and *Thioclava atlantica* 13D2W-2^T^ (96.7%). Strain LPB0142^T^ has a circular chromosome of 3.46 Mb with DNA G+C content of 67.4 mol% and three plasmids (264 kb, 29 kb, 24 kb). The genome includes 2,604 protein-coding genes and three copies of rRNA operons. Strain LPB0142^T^ contained ubiquinone 10 (Q-10) and possessed C₁₈:₁ ω7c/C₁₈:₁ ω6c (75.8%) as the major fatty acids. The major polar lipids of strain LPB0142^T^ were phosphatidylethanolamine, phosphatidylglycerol, and phosphatidylcholine. Strain LPB142^T^ does not have the known photosynthetic gene clusters other than species of the genus *Rhodobacter*. In addition to the differences in phylogenetic position, many biochemical and physiological characteristics also distinguished the isolate from species within the genus *Paenirhodobacter* and *Sinorhodobacter*. On the basis of polyphasic taxonomic data obtained here, we propose strain LPB0142^T^ as a novel genus and species, for which the name *Aliirhodobacter maris* sp. nov. is proposed.
A031

Taxonomic Characterization of Novel Species Isolated from *Hemibarbus labeo*

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Gram-stain-negative, non-spore-forming, motile by means of flagellum, rod shaped bacterial strain designated S1-19⁷ was isolated from intestine of freshwater fish (*Hemibarbus labeo*) collected from Nakdong River. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain S1-19⁷ was formed an evolutionary independent lineage within the family Neisseriaceae. Strain S1-19⁷ was most closely related to *Aquitalea mangnusonii* TRO-001DR8¹ with 93.9% sequence similarity and exhibited 16S rRNA gene sequence similarity values between 92.2-93.4% to the type strains of the other recognized species within the family Neisseriaceae. Growth occurred at 4-30°C (optimum 20-25°C), at pH 6.0-8.0 (optimum pH 7.0) and with 0-2.0% NaCl (optimum 0%). They contained Q-8 as the predominant menaquinone and summed feature 3 (comprising C₁₆:₁ ω₇c and/or C₁₆:₁ ω₆c) and C₁₆:₀ as the major fatty acids. G+C contents of strain S1-19⁷ was 59.19%. Differential phenotypic properties and phylogenetic distinctiveness suggested that strain S1-19⁷ represent a novel species of a new genus in the family Neisseriaceae.

A032

Microbial Diversity in the Onnuri Vent Field of Mid Indian Ocean Ridge and Their Identification

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Deep-sea hydrothermal vent is a fissure on the sea floor from which heated water by underlying magma. It forms an ecosystem for microbes and animals, such as tubeworms, giant clams, and blind shrimp that can withstand the hostile environment. Through 2018 Indian Ocean hydrothermal vent exploration, we obtained samples from the previously known as hydrothermal vent areas, Edmond and Solitaire, and from the newly discovered OVF (Onnuri Vent Field) site. Microbial diversity near suspected hydrothermal vent area had been analyzed from above sites through the amplicon sequencing approach. The communities found in Edmond site were dominated by *Thermodesulfovibrio* and *Campylonacterales* order. In Solitaire site, *Thiotricales* and *Campylonacterales* order were abundant. The newly discovered OVF area showed high proportion of *Chromatiales* and *Actinomarinales* order. In addition, enrichment cultures for isolation of chemolithoautotrophs and hyperthermophiles under mesophilic, thermophilic and hyperthermophilic condition has been progress. We have isolated sulfur-oxidizing, autotrophic microorganisms, *Sulfurimonas* and *Sulfurovum* species. Also, we have obtained 5 strains belonging to the hyperthermophilic archaeon, *Thermococcus* genus. Currently, we are analyzing the physiological characteristics of the obtained strains.

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A033

Paracoccus jeotgali sp. nov., Isolated from Korean Salted and Fermented Shrimp

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A Gram-stain-negative and facultatively aerobic bacterium, designated as strain CBA4604T, was isolated from a traditional Korean salted and fermented shrimp food (saeu-jeot). Strain CBA4604T was the most closely related to Paracoccus koreensis Ch05T (97.5% 16S rRNA gene sequence similarity) and other type strains (≤ 97.0%). The genome comprised a chromosome and two plasmids of 3,299,166 bp with 66.5% G+C content. The DNA-DNA relatedness values between strain CBA4604T and P. koreensis Ch05T, P. alcaliphilus DSM 8512T, and P. stylophorae KTW-16T were 30.5%, 22.9%, and 16.7%, respectively. Cells of the strain were short rod-shaped and oxidase- and catalase-positive. The growth of strain CBA4604T was observed at 10–40°C (optimum, 37°C), pH 6.0–10.0 (optimum, pH 7.0), and in the presence of 0–8.0% (w/v) NaCl (optimum, 0–2.0%). Strain CBA4604T contained ubiquinone 10 as the sole isoprenoid quinone and summed feature 8 (C18:1ω7c/C18:1ω6c) and C18:0 as the major cellular fatty acids. The polar lipids consisted of phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, phospholipid, an unidentified aminolipid, an unidentified glycolipid, and three unidentified lipids. Based on its phylogenetic, genomic, phenotypic, and chemotaxonomic features, we concluded that strain CBA4604T represents a novel species in the genus Paracoccus and we propose the name Paracoccus jeotgali sp. nov. The type strain is CBA4604T (= KACC 19579T = JCM 32510T).

A034

Nonlabens amylolyticus sp. nov. Isolated from Seawater

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A Gram-stain-negative, orange-pigmented, non-spore-forming, non-motile, aerobic, rod-shaped bacterial strain, designated, MJ115T, was isolated from seawater. Strain MJ115T grew at 4–35°C, pH 6.0–7.0 and 0–8% (w/v) NaCl. Phylogenetic trees based on 16S rRNA gene sequences revealed that strain MJ115T was grouped into the genus Nonlabens, and was closely related to Nonlabens agnitus JC2678T (96.34% identity). In silico DNA-DNA hybridization (DDH) of genome sequences determined 13.3–15.9% DDH values between strain MJ115T and type strains of Nonlabens species. The strain possessed MK-6 as the predominant menaquinone and iso-C15:0, anteiso-C15:0, C17:0 3-OH and iso-C17:0 3-OH as the major cellular fatty acids. The major polar lipids detected in strain MJ115T were phosphatidylethanolamine, 2 unidentified aminolipids, and 4 unidentified lipids. The DNA G+C content was 40.7 mol%. Differential biochemical and phenotypic properties along with phylogenetic and genetic distinctiveness, revealed that strain MJ115T is separated from recognized species of the genus Nonlabens. On the basis of the data presented, strain MJ 115T represents a novel species of the genus Nonlabens, for which the name Nonlabens amylolyticus sp. nov. is proposed.
A035

*Altibacter aquimarinus* sp. nov., a Marine Bacterium Isolated from Magma Seawater at Jeju Island, Republic of Korea

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A Gram-negative, aerobic, rod-shaped (1.1-1.9 µm × 0.3-0.5 µm) and non-motile marine bacterium, designated as ALE3EI³ was isolated from Magma Seawater at Jeju Island, Republic of Korea. The 16S rRNA gene sequence analysis revealed that strain ALE3EI³ showed high similarity with the *Altibacter lentus* JLT2010³ (96.7%). Growth was observed at 10-41°C (optimum 30°C), at pH 6.0-8.5 (optimum pH 7.5) and with 0.5-8% (optimum 4.0%) NaCl. The predominant cellular fatty acids were iso-C₁₅:₀ (23.5%), iso-C₁₆:₀ (10.2%), iso-C₁₆:₀ 3OH (10.5%), iso-C₁₇:₀ 3OH (16.8%) and summed feature 3 (comprised of C₁₆:₁ω₆c and/or C₁₆:₀ 7c: 9.6%). The DNA G+C contents is 40.9 mol%. The major respiratory quinone is MK-6. Several phenotypic characteristics such as production of acetoin, arginine dihydrolase and enzyme activities of acid phosphatase differentiate strain ALE3EI³ from *Altibacter lentus* JLT2010³. Major polar lipids were phosphatidylethanolamine, two unidentified glycolipids and two unidentified aminolipids. On the basis of this polyphasic taxonomic data, strain ALE3EI³ should be classified as a novel species in the genus *Altibacter* and it is proposed as *Altibacter aquimarinus* sp. nov. The type strain is ALE3EI³ (=KCCM 43303³ =JCM 33022³).

[Supported grants from KIOST (PE99722) & 2017043 from MOF].

A036

*Sphingomonas gilva* sp. nov., a Novel Species Isolated from Soil in South Korea

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A novel light-yellow color, motile, Gram-stain-negative, rod-shaped, strictly aerobic bacterial strain, designated strain AE3¹, was isolated from a soil sample collected from Ahnmok beach (Busan, South Korea). Colonies were round, convex, and smooth. Strain AE3¹ grew optimally at 37°C, at pH 7.0 and at 0% (w/v) NaCl on R2A plate. Phylogenetic analysis based on 16S rRNA gene sequence of strain AE3¹ formed a lineage within the family *Sphingomonadaceae*, and it is closely related to members of the genus *Sphingomonas*, with *S. oryziterrae* KCTC 22477¹ being its closest relative (97.94% sequence similarity). The DNA G+C content of strain AE3¹ was 61.7 ± 3.1 mol%. Strain AE3¹ contained Q-10 as the predominant respiratory quinone, and the major fatty acids were C₁₇:₁ ω6c, summed feature 8 (C₁₈:₁ ω7c) and summed feature 3 (C₁₆:₁ ω7c and/or C₁₆:₁ ω6c). Strain AE3¹ contained a sphaingoglycolipid, phospholipid and phosphatidylethanolamine as the major polar lipids. DNA-DNA hybridization values of strain AE3¹ with *S. oryziterrae* KCTC 22477¹, and *S. jaspsi* DSM 18422¹ were 36.5 ± 1.6%, and 47.6 ± 3.7% respectively. On the basis of phenotypic, genotypic and phylogenetic analysis, the strain AE3¹ (= KCTC 62106¹ = JCM 33022¹) represents a novel species of the genus *Sphingomonas* for which the name *Sphingomonas gilva* sp. nov. is proposed.

[This research was supported by a National Research Foundation of Korea (NRF) grant by the Korean government (MIST) (NRF-2017R1A2B4009448).]
A037

**Shewanella maritimus** sp. nov., a Facultatively Anaerobic, Marine Bacterium Isolated from Sea Water in Korea
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National Marine Biodiversity Institute of Korea

A Gram-negative, motile, rod-shaped, facultatively anaerobic, marine bacterium, designated D4-2\(^T\), was isolated from sea water sample collected from the East Sea in Korea. Phylogenetic analysis based on the 16S rRNA gene sequences showed that strain D4-2\(^T\) was affiliated with members of genus *Shewanella* belonging to the class *Gammaproteobacteria* and was most closely related to *S. intestini* XMDDZSB0408\(^T\) (97.4%), followed by *S. gelidii* RZB5-4\(^T\) (96.7%) and *S. inventionis* KX275\(^T\) (96.1%). Growth was observed at 10-36°C (optimum 29-32°C), at pH 6-9 (optimum pH 7), and with 1-6% NaCl (optimum 2). The major cellular fatty acids (5% >) of strain D4-2\(^T\) were iso-C\(_{13:0}\), C\(_{16:0}\), iso-C\(_{15:0}\), C\(_{17:1}\)ω8c, summed feature 3 (iso-C\(_{15:1}\) H and/or C\(_{13:0}\)-OH) and summed feature 8 (C\(_{18:1}\)ω7c). The respiratory quinones were Q-7, Q-8, MK-7 and MMK-7. The polar lipids were phosphatidylethanolamine, phosphatidylglycerol, one unidentified aminophospholipid, one unidentified aminolipid and four unidentified lipids. The strain D4-2\(^T\) has a single circular chromosome of 4.72 Mbp with a DNA G+C content of 44.5 mol%. On the basis of polyphasic analyses, D4-2\(^T\) represents a novel species of the genus *Shewanella*, for which the name *Shewanella maritimus* sp. nov. is proposed with D4-2\(^T\) as the type strain.

[This work was supported by a grant from MABIK in-house program (2019M00700).]

A038

**Genome-based Reclassification of Marinobacter adhaerens as a Later Heterotypic Synonym of Marinobacter flavimaris**
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The genus *Marinobacter* belongs to the order *Alteromonadales* in the class *Gammaproteobacteria*. Until now, more than forty *Marinobacter* species have been reported. *Marinobacter adhaerens* HP15\(^T\) proposed as novel species mainly based on DNA-DNA hybridization relatedness (63.6 and 68.7%) with *Marinobacter flavimaris* SW-145\(^T\) in spite of high similarity of the 16S rRNA gene sequences (99.3%). We determined high quality whole genome sequencing of the type strain of *Marinobacter flavimaris*, which were then compared with that of *M. adhaerens*. The average nucleotide identity (ANI) value between two type strains of *M. adhaerens* and *M. flavimaris* was 96.5%, which is above 95-96%, the generally recognized cutoff value for bacterial species boundaries. Along with the ANI value, the phylogenetic analysis among highly related species based on the bacterial core genes indicated that the two strains should be the same species. Therefore, we propose that *Marinobacter adhaerens* is assigned to be later heterotypic synonyms of *Marinobacter flavimaris* (= SW-145\(^T\) = KCTC 12185\(^T\)).

[This study was supported by the Strategic Initiative for Microbiomes in Agriculture and Food, Ministry of Agriculture, Food and Rural Affairs, Republic of Korea (Project No. 914008-04).]
A Novel *Urechisicola croceus* gen. sp. Isolated from a Marine Spoon Worm
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A novel Gram-reaction-negative, aerobic, rod-shaped bacterium, designated strain LPB0138T, was isolated from a marine spoon worm. Cell growth occurred aerobically at 4–30°C (optimum 20°C), at pH 5.5–8.5 and in the presence of 1-5% NaCl. The complete genome sequence determined in this study revealed that strain LPB0136T possessed a circular chromosome with a total length of 3,426,122 bp. The genome had a 30.4 mol% G+C content and contained 2,987 protein-coding genes and 49 RNA genes. Phylogenetic analysis based on its 16S rRNA gene sequence indicated strain LPB0136T belongs to the Family Flavobacteriaceae and is most closely related to Lutibacter profundi LP1T (94.3% 16S rRNA gene sequence similarity) and *Lutibacter litoralis* CI-TF09T (93.1%). The respiratory quinone, major fatty acids were menaquinone-6 and iso-C15:0, iso-C15:0 3-OH, iso-C15:1 G and iso-C17:0 3-OH. The major polar lipids are phosphatidylethanolamine, unidentified three aminophospholipids, two aminolipids, two phospholipids, and four unidentified lipids. The size of genome, chemotaxonomic features, and physiological characteristics supported the assignment of strain LPB0138T in the genus *Urechisicola*. On the basis of polyphasic taxonomic data, strain LPB0138T should be proposed as a novel genus of the family Flavobacteriaceae.

[This study was supported by the Survey of Korean Indigenous Species Program through the National Institute of Biological Resources (NIBR) funded by the Korean Ministry of Environment.]

A040
Strain LPB0137T sp. nov. Belonging to the Genus *Arcobacter*
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Strain LPB0137T, a Gram-staining-negative, aerobic, motile, yellow-colored, catalase- and oxidase-negative bacterium, was isolated from a squid in Jumunjin in Korea. Best growth condition was observed at 25°C and pH 7 on marine agar. In the 16S rRNA gene sequence trees, strain LPB0137T was belonging to the genus *Arcobacter*. The highest sequence similarity was observed with *Arcobacter lekithochrous* (95.8%), and followed by *Arcobacter caeni* (94.9%), *Arcobacter venerupis* (94.7%), *Arcobacter acticola* (94.6%), and *Arcobacter suis* (94.2%). The low sequence similarity and tree topology demonstrated the taxonomic independence of the strain at species-level. The isolate possessed summed feature 3 (C16:1 ω7c/C16:1 ω6c), summed feature 2 (C12:0 aldehyde/unknown 10.928), and summed feature 8 (C18:1 ω7c and/or C18:1 ω6c) as the major cellular fatty acids. Strain LPB0137T has a circular chromosome of 2.87 Mb with DNA G+C content of 27.7 mol%. The genome includes 2,698 protein-coding genes and 85 RNA genes. Based on phylogenetic, genomic, and phenotypic data presented in this study, strain LPB0137T should be classified as a novel species in the genus *Arcobacter*. 
A041

Strain HYN0086\textsuperscript{T}, a Novel Member of the Genus *Flavobacterium*

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A Gram-staining-negative, yellow-pigmented, aerobic bacterial strain designated HYN0086\textsuperscript{T}. The 16S rRNA gene sequence similarity analysis demonstrated that the closest relative of the isolate is *Flavobacterium chungangense* (98.12%), but the new isolate formed an independent phyletic line within the genus *Flavobacterium*. Its genome is composed of a circular chromosome of 4.83 Mb with DNA G+C content of 33.9 mol%. The genome includes 4,065 protein-coding genes, and six copies of rRNA operons. Strain HYN0086\textsuperscript{T} possessed C\textsubscript{15:0}iso and C\textsubscript{16:1}\textit{ω7c} and/or C\textsubscript{16:1}\textit{ω6c} as the major cellular fatty acids. The chemotaxonomic properties and enzymatic activities of the novel isolate clearly differed from those of its closest relatives. Thus, based on the phylogenetic and phenotypic data presented in this study, strain HYN0086\textsuperscript{T} should be classified as a novel species in the genus *Flavobacterium*.

[This study was supported by the Survey of Korean Indigenous Species Program through the National Institute of Biological Resources (NIBR) funded by the Korean Ministry of Environment.]

A042

Genomic Analysis of *Nibricoccus aquaticus* Type Strain HZ-65\textsuperscript{T}, a Polysaccharide-degrading Freshwater Verrucomicrobia

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*Nibricoccus aquaticus* HZ-65\textsuperscript{T}, a Gram-strain-negative, non-motile, cocci-shaped, strictly aerobic bacterium that was isolated from hyporheic freshwater in the Republic of Korea. This study reports the complete genome sequences of strain HZ-65\textsuperscript{T} (=KACC 19333\textsuperscript{T} =NBRC 112907\textsuperscript{T}). The genome comprises 4,730,447 bp in circular chromosome with a G + C content of 62.2% with 3,769 protein-coding genes and 48 RNA genes, including 45 tRNAs and 3 rRNA operons. Among these CDSs, 304 genes encoding carbohydrate enzymes were found in the *Nibricoccus aquaticus* HZ-65\textsuperscript{T} genome. In addition, abundant putative enzymes involved in degrading polysaccharide were found. These enzymes include xylosidase, arabinanase, xylanase, galactosidase, mannosidase, glucuronidase and rhamnogalacturonase. This study showed that strain HZ-65\textsuperscript{T} may serve as a potential candidate for research of saccharometabolism and have potential biotechnological and industrial applications and play key roles in the hyporheic freshwater carbon cycle.

[This work was supported by a grant from the Nakdonggang National Institute of Biological Resources (NNIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NNIBR201902109).]
A mesophilic, straight rod-shaped, non-flagellated bacterium, designated MEBiC05444<sup>T</sup>, was isolated from a marine sponge collected from Chuuk lagoon, Federated States of Micronesia. The strain was Gram-negative, catalase- and oxidase-positive and facultative anaerobe. The isolate aerobically grew at 8–38°C (optimum range 24–32°C), pH 4.0–10.0 (optimum, pH 7.0–7.5) with an absolute requirement for Na<sup>+</sup> up to 6% (w/v) NaCl (optimum 2%). Phylogenetic analyses based on 16S rRNA gene sequences revealed that MEBiC05444<sup>T</sup> belonged to the class Gammaproteobacteria, within the family Shewanellaceae. MEBiC05444<sup>T</sup> showed close similarity to Parashewanella curva C51<sup>T</sup>, [Shewanella] irciniae UST040317-058<sup>T</sup> and Parashewanella spongiae HJ039<sup>T</sup> (98.9%, 97.2% and 95.7%, respectively). The major fatty acids were iso15:0 (19.7%), summed feature 3 (composed of 16:1ω7c and/or 16:1ω6c; 16.1%) and 17:1ω8c (10.2%). The only detected respiratory quinone was ubiquinone Q8. The genome DNA G+C content of strain MEBiC05444<sup>T</sup> was 40.8 mol%. Based on the polyphasic analysis, the strain represents a novel species of the genus Parashewanella, distinct from Parashewanella curva C51<sup>T</sup>, [Shewanella] irciniae UST040317-058<sup>T</sup> and Parashewanella spongiae HJ039<sup>T</sup> for which the name Parashewanella tropica sp. nov. is proposed (type strain MEBiC05444<sup>T</sup> = KCCM 43304<sup>T</sup>). [Supported by KIOST (PE99722) and MOF (20170431)]
A045
Isolation and Characterization of Bacillus spp. Showing Antimicrobial Activity against Methicillin-resistant Staphylococcus aureus
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There are needs for research to solve the problem of soil and water pollution caused by the exposure of antibiotics in the environmental ecosystem. In this study, we try to isolate and characterize the new and useful bacterial strains that inhibit antibiotic resistant microorganisms in the environment. We isolated seven strains of the genus Bacillus (strain JB001, JB002, NIBRBAC000003464, NIBRBAC000003491, NIBRBAC000003501, NIBRBAC000003502, and NIBRBAC000003518) which showed antimicrobial activity against Staphylococcus aureus from environmental samples. All of the isolates had antimicrobial activity against Staphylococcus aureus, but not against other pathogenic bacteria such as Vibrio parahaemolyticus, Vibrio vulnificus, Pseudomonas aeruginosa, and Listeria monocytogenes. The isolates were identified by performing homologous searches based on the results of 16S rRNA gene sequencing. Morphological characteristics were obtained by observing colony color, size and shape while culturing in solid medium and physiological characteristics were obtained by analysis using the API strips. The isolates showed maximum cell growth and antimicrobial activity when cultured in Tryptic Soy Broth (TSB) medium for 2-3 days.

A046
Identification and Characterization of a Thermostable Enzyme-producing Ruegeria sp. WJ45-6 Isolated from Seawater Sample of Jeju Island, Korea
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The strain WJ45-6 isolated from seawater in the coast of Jeju Island, Korea is a gram-negative, aerobic strain with light yellow color and no flagella. C18: 1ω7c (39.72%), 11-methyl C18: 1ω7c (14.68%) C16: O2-OH (10.71%) and C12: O3-OH (9.09%) were the major cellular fatty acid components. The G+C content in the genome of strain WJ45-6 was 63.45 mol% and contained Q-10 as a major quinone. 16S rRNA gene sequence (1,359 bp) analysis showed that strain WJ45-6 belonged to alphaproteobacter and was 99% identical to R. arenilitoris G-M8. As a result of DNA-DNA hybridization (DDH) experiment and morphological, physiological and biochemical characteristics, strain WJ45-6 was considered to be a variant of the same species of Ruegeria arenilitoris G-M8, and thus named as Ruegeria sp. WJ45-6. Although cellulolytic enzymes, such as cellulase, xylanase, and agarase, hydrolyze the cell wall components of marine plants, Ruegeria sp. WJ45-6 produced β-glucosidase and β-galactosidase which were considered to be thermostable enzymes having good activity at 50°C.
**A047**
*Siphonobacter algae* sp. nov., Isolated from Freshwater Microalga, *Chlorella* sp.
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An aerobic, gram-stain-negative, catalase-positive and oxidase-negative, designated strain HS1-24-8, was isolated from the green microalga *Chlorella* sp. Phylogenetic analysis showed that strain HS1-24-8 is affiliated with the genus *Siphonobacter* in the phylum *Bacteroidetes*. DNA sequence similarities between the 16S rRNA gene of strain HS1-24-8 and those of *Siphonobacter curvatus* HR-U*T* and *Siphonobacter aquaeclarae* DSM 21668*T* were 96.50% and 96.14%, respectively. Strain HS1-24-8 grew in the range of 10–37°C and in the presence of 0–2% (w/v) NaCl, with optimal growth occurring at 30°C, and with 0% (w/v) NaCl. On the basis of polyphasic taxonomic analysis, strain HS1-24-8 represents a novel species of the genus *Siphonobacter* in the phylum *Bacteroidetes*, for which we propose the name *Siphonobacter algae* sp. nov.

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**A048**
*Aureivirga spongiae* sp. nov., a Novel Bacterium of Isolated from Marine Sponge
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A Gram-negative, aerobic, motile by gliding, catalase and oxidase positive, rod shaped bacterial strain designated CE67*T*, was isolated from marine sponge *Callyspongia elegans* at jeju Island in South Korea. The strain CE67*T* was grew at pH 5.5-9.5 (optimum, pH 7.5), in the presence of 2-3% (w/v) NaCl and at 15-40°C (optimum, 25°C). Phylogenetic analysis based on 16S rRNA gene sequences showed that strain CE67*T* related to the genus *Aureivirga* and with highest 16S rRNA gene sequence similarities to type strains of *Aureivirga marina* VIII.04*T* (96.32%). The major fatty acids of strain CE67*T* were iso-C_{15:0} (35.3%), iso-C_{17:0} 3OH (21.8%) and iso-C_{15:0} 3OH (9.7%). The predominant menaquinone was Q-8. The polar lipids profile of strain CE67*T* contained phosphatidylethanolamine, unidentified aminolipids and unidentified lipids. On the basis of the phylogenetic distinctiveness, physiological and biochemical test, chemotaxonomic data in this study, strain CE67*T* is a representative of a new species of the genus *Aureivirga* for which we propose the *Aureivirga spongiae* sp. nov.,.
The Revision of Lichen Flora around Maxwell Bay, King George Island, Antarctic

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Maxwell Bay (62°25′S; 58°85′W) lies between King George Island and Nelson Island, Antarctica around where 8 Antarctic Scientific Stations are situated. Since the lastest floristic note was published in 2006 near King Sejong Station, Barton peninsula, meaningful research products and specimen have been accumulated steadily over 10 years. The present study aims to update the lichen flora around Maxwell bay including Barton Peninsula, Fildes Peninsula, Weaver Peninsula, and Ardley Island. About 900 lichen specimens were collected from the Antarctic expedition 2008–2016: 48 genera, 105 species were identified by their own morphology and chemistry and 33 species are endemic to the Antarctic. Molecular analysis was performed, if necessary, ITS, LSU and mtSSU loci were used. Forty-four reported species are new to Maxwell bay region and 12 among the species are also newly recorded in King George Island.

Two species are new to the Antarctic – Pertusaria aff. dactylina and Verrucaria striatula. Molecular analysis with the specimen of Pertusaria aff. dactylina is needed for avoiding the ambiguous conclusion. Ecological and geographical factors will be discussed with lichen phenotypes and habitat preference of species. Examined closely with the specimen, previously reported taxa Cladonia furcata were excluded by misidentification.

[The research was supported by the project PE19090 and project PE19180 (KOPRI).]

Myroides fluvii sp. nov., Isolated from Han River, South Korea

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A Gram-staining-negative, aerobic, short rod-shaped, pale yellow-pigmented and non-motile bacterial strain, designated CJ210T, was isolated from Han River, Republic of Korea. Strain CJ210T grew optimally at 30°C and pH 7.0 in the absence of NaCl on TSA. Flexirubin-type pigments were not produced. Phylogenetic analysis based on 16S rRNA gene sequence similarity showed that strain CJ210T belonged to the genus Myroides and was most closely related to Myroides odoratus KACC 14347T (98.1% similarity). The average nucleotide identity values between strain CJ210T and two closely related type strains M. odoratus KACC 14347T and M. injenensis KCTC 23367T were 83.7% and 73.8% respectively. The digital DNA–DNA relatedness values between strain CJ210T and the related type strains were 27.5% and 20.2% respectively. Strain CJ210T contained menaquinone-6 (MK-6) as the predominant menaquinone. The predominant polar lipids were phosphatidylethanolamine and two unidentified aminolipids. The major fatty acids of strain CJ210T were iso-C15:0, iso-C17:0 3-OH and Summed Feature 9 (comprising 10-methyl C16:0 and/or iso-C17:1 ω6c). The G+C content of the genomic DNA was 36.5 mol%. Based on polyphasic taxonomic study, strain CJ210T represents a novel species in the genus Myroides, for which name Myroides fluvii sp. nov. is proposed.

[This work was supported by a project of the National Institute of Biological Resources (NIBR) to survey Korean indigenous species]
A051

*Ferrimonas sediminicola* sp. nov., Isolated from Tidal Flat Sediment

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A Gram-stain-negative, rod-shaped, facultatively anaerobic and motile by a polar flagellum bacterium, designated strain IMCC35001<sup>T</sup>, was isolated from tidal flat sediment of the Yellow sea, South Korea. Optimal growth of strain IMCC35001<sup>T</sup> was observed at 30°C, at pH 7.0 and with 2% (w/v) NaCl. Phylogenetic analysis based on the 16S rRNA gene sequences revealed that strain IMCC35001<sup>T</sup> belonged to the genus *Ferrimonas* and shared 94.6-98.8% sequence similarities with *Ferrimonas* species. Whole genome sequencing of strain IMCC35001<sup>T</sup> revealed genome size of 3.97 Mbp and DNA G+C content of 61.0 mol%. The IMCC35001 genome shared the average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) of 70.0-84.4 and 19.6-27.8%, respectively, with other *Ferrimonas* genomes. The strain contained iso-C<sub>15:0</sub> (16.2%), C<sub>18:1</sub> ω9c (14.4%), C<sub>17:1</sub> ω8c (11.3%), and C<sub>16:0</sub> (10.7%) as the major fatty acids, and MK-7, Q-7, and Q-8 as the major respiratory quinones. The polar lipids detected in the strain were phosphatidylethanolamine, phosphatidylglycerol, and two unidentified aminolipids. On the basis of phylogenetic distinction and differential phenotypic characteristics, strain IMCC35001<sup>T</sup> is considered to represent a novel species of the genus *Ferrimonas*, for which the name *Ferrimonas sediminicola* (type strain IMCC35001<sup>T</sup> = KACC 21161<sup>T</sup> = NBRC 113699<sup>T</sup>) sp. nov. is proposed.

A052

Taxonomic Diversity and Antimicrobial Potential of *Micromonospora* spp. Isolated from Riverside Soil

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During a survey for the isolation and characterization of rare actinobacteria, 25 strains belonging to the genus *Micromonospora* were isolated from riverside soil samples using humic acid vitamin agar medium. The identification of *Micromonospora* isolates was supported by physiological characteristics, such as optimal growth conditions, carbon and nitrogen utilization profiles, and catalase and oxidase activity. Arabinose, mannose, and maltose were utilized as sole carbon sources by most strains, but little, if any, growth occurred with citrate or phenyl-acetate. All of the strains utilized alanine, citrate, and serine, but most strains did not use aspartic acid as sole nitrogen source. All of the *Micromonospora* isolates showed catalase activity. Relatively, there were fewer strains with oxidase activity. The antimicrobial tests indicated that all of the *Micromonospora* isolates exhibited activity against one or more test microbes and a high potential as the producers of antibiotics against Gram-positive pathogens than Gram-negative and fungal pathogens. As a result, two strains were selected: strain R 3-6 showing the highest antibacterial activity, and R_77 showing the highest antifungal activity. The ongoing studies include taxonomic characterization and identification of antimicrobial compounds for the two selected strains. [This work was supported by the National Institute of Biological Resources of the Ministry of Environment, Republic of Korea.]
A053

Description of Boseongicola jejuensis sp. nov., Isolated from Marine Alga Codium minus

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A marine bacterium, designated strain CCM32T, was isolated from marine alga Codium coactum collected in Jeju Island, Republic of Korea. Cells of CCM32T were aerobic, Gram-negative, rod-shaped and non-motile. The temperature range for growth of strain CCM32T was 15-37°C, with an optimum at 25°C. NaCl was required for growth at the concentration range 1-5% (w/v) NaCl (optimum at 2-3%, w/v), at pH 6.0-9.0 (optimum, pH 7.0). Phylogenetic analysis based on 16S rRNA gene sequences, showed that strain CCM32T belonged to the genus Boseongicola and was most closely related to Boseongicola aestuarii BS-W15T with a similarity of 97.2%. The polar lipid profile contained diphosphatidylglycerol, phosphatidylcholine, and phosphatidylglycerol, one unidentified aminolipid and two unidentified lipids. The G+C content of the genomic DNA was 57.9 mol%. The major respiratory quinone was Q-10. On the basis of phylogenetic analyses, strain CCM32T represents a novel species of the genus Boseongicola, for which the name Boseongicola jejuensis sp. nov. is proposed. The type strain is CCM32T (KACC 19630T =JCM 33081T).

A054

Characterization of Lactobacillus plantarum EBKLP545 Isolated from Pig Feces

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We isolated 164 Lactobacillus plantarum strains from piglet feces in June 2016 in South Korea. Among all strains, L. plantarum EBKLP545 showed the excellent antimicrobial activity. The draft genome consisted of 3,306,513 bp in 138 contigs (over 500 bp), with an N50 of 61,792, and G+C content of 44.3 %, all of which were similar to other L. plantarum genomes uploaded to the NCBI genome database. A total 3,246 genes were identified, which included 3,049 protein coding sequences (CDS), 54 non-coding RNA genes (48 tRNA and 3 rRNA), and 143 pseudo genes. After RAST annotation, we found that our draft genome has a different gene composition from those of the existing 10 other L. plantarum strains on NCBI. Although genes related programmed cell death and the toxin-antitoxin system were abundant, protein biosynthesis (tRNA) and carbohydrate utilization genes were found to be deficient compared to other strains. Only one antibiotic resistance gene (bacA) was found, which was also founded in 10 other L. plantarum strains. More piglet strains are required to be genome-sequenced to determine whether these characteristics are unique features of L. plantarum bacteria derived from piglet feces.

[This research was supported by the Collaborative Genome Program of the Korea Institute of Marine Science and Technology Promotion (KIMST) funded by the Ministry of Oceans and Fisheries (MOF) (No. 20180430)]
A055

*Arenimonas hwasunensis* sp. nov., Isolated from Orchard Soil

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A Gram-stain-negative, strictly aerobic bacterial strain, designated strain R29\(^T\), was isolated from orchard soil in Hwasun, South Korea. Cells were found to be non-motile, short rods with catalase- and oxidase-positive activities. Growth was observed to be at 15–40°C (optimum, 30 °C), at pH 7.0–10.0 (optimum, pH 8.0) and in the presence of 0–2% (w/v) NaCl (optimum, 0%). Ubiquinone-8 (Q-8) was identified as the predominant quinone. Strain R29\(^T\) contained iso-C\(_{15:0}\), iso-C\(_{16:0}\) and iso-C\(_{17:1}\) w9c as major cellular fatty acids. The G+C content of the genomic DNA calculated from its whole genome sequence was 69.7%. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain R29\(^T\) was most closely related to *Arenimonas daejeonensis* T7-07\(^T\), *Arenimonas malthae* CC-JY-1\(^T\) with sequence similarities of 98.02% and 97.1%, respectively. DNA-DNA relatedness levels between strain R29\(^T\) and the type strains of *A. malthae* and *A. donghaensis* were 26.1% and 23.1%, respectively. Based on the phenotypic, chemotaxonomic, and molecular features, strain R29\(^T\) represents a novel species of the genus *Arenimonas*, for which the name *Arenimonas hwasunensis* sp. nov. is proposed. The type strain is R29\(^T\) (=KACC 19896\(^T\) =JCM 33216\(^T\)).

A056

*Roseomonas algicola* sp. nov., Isolated from Nakdong River, South Korea

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A strictly aerobic, Gram-stain-negative, catalase-negative, oxidase-positive, and non-motile coccus bacterium, designated strain PeD5\(^T\), was isolated from algae in Nakdong river of Republic of Korea. The growth of strain PeD5\(^T\) was observed to be at 30–40°C (optimum, 35°C), at pH 5–10 (optimum, 8), and in the presence of 0–0.25% (w/v) NaCl (optimum, 0%). Phylogenetic analysis based on 16S rRNA gene sequence revealed that strain PeD5\(^T\) formed a tight phylogenetic lineage with *Roseomonas stagni* (HS-69\(^T\)) within the genus *Roseomonas*. The comparison of 16S rRNA gene sequences showed that strain PeD5\(^T\) was most closely related to *Roseomonas stagni* HS-69\(^T\) (97.66%), *Roseomonas tokyonensis* K-20\(^T\) (96.31%), and *Roseomonas riguiloci* 03SU10-P\(^T\) (95.88%). On the basis of phenotypic, chemotaxonomic and molecular analysis, strain PeD5\(^T\) clearly represents a novel species of the genus *Roseomonas*, for which the name *Roseomonas algicola* sp. nov. is proposed. The type strain is PeD5\(^T\) (=KACC 19925\(^T\)).
A057

Aliifodinibius halophila sp. nov., Moderately Halophilic Bacterium Isolated from a Gray Solar Saltern
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A Gram-stain-negative, moderately halophilic bacteria, designated strain ECH52T, was isolated from a gray solar saltern located in Shinan, Korea. Strain ECH52T was aerobic, non-motile short rod (< 1 μm in length) and grew at pH 7.0–11.0 (optimum, pH 8.0), at 28–45°C (optimum, 37°C) and at salinities of 5–25% (w/v) NaCl (optimum, 10% NaCl). Phylogenetic analyses based on 16S rRNA gene sequences indicated that strain ECH52T belonged to the genus Aliifodinibius with sequence similarity of 98.5 to 94.3 %, showing the highest sequence similarity to Aliifodinibius halophilus 2W32T (98.5%), Aliifodinibius sediminis YIM J21T (94.7%), Aliifodinibius salicampi KHM44T (94.5%) and Aliifodinibius roseus YIM D15T (94.3%) The major fatty acids were iso-C15:0 and iso-C17:1ω9c. The major polar lipids were diphosphatidylglycerol, phosphatidylcoline, and phosphatidylethanolamine. The predominant isoprenoid quinone was MK-7. The draft genome size of strain ECH52T was 4 929 456 bp with a G+C content of 48.5 mol%. Levels of DNA–DNA relatedness between strain ECH52T and the type strains of the other species of the genus ranged from 23 to 12 %. On the basis of polyphasic analysis from this study, strain ECH52T represents a novel species of the genus Aliifodinibius, for which the name Aliifodinibius halophila sp. nov. is proposed. The type strain is ECH52T.

[Supported by grants from iMAF (Project No. 918016-4)]

A058

Genomic Analysis for Identification of Mono-aromatic Compound Degradation Pathway from Novel Phenol Degradation Bacterium, Microbacterium sp. ABRD28, Which Isolated from Nakdong River
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NNIBR

The Microbacterium sp. ABRD28, capable of degrading mono-aromatic compounds such as phenol, was isolated from freshwater. The genomic DNA was obtained from the cultivated cells on R2A agar during 2 days using the Wizard Genomic DNA Purification kit (Promega, USA), following the protocol recommended by the manufacturer. The purified genomic DNA was completely sequenced by a combination of PacBio RSII and Illumina Hiseq 2500 sequencing. The whole genome, consisting of a circular single chromosome and three plasmids, was composed of total 7,613,819 bp length with 44.4 % G+C contents and 6,006 genes. The genome of strain ABRD28 contains many aromatic hydrocarbon degrading genes such as monooxygenase, ring-cleaving dioxygenase and catechol 1,2-dioxygenase. The complete genome reveals versatile biodegradation capabilities of Microbacterium sp. ABRD28.

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A059
Optimized Condition to Cultivate Sufficiently Diverse Endolichenic Fungi
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The thallus of lichen is a kind of microbiome including endolichenic fungi that live inside lichen thalli without any disease symptoms. In order to understand ecological role of endolichenic fungi in the lichen host, it is prior and essential to secure various type of cultivated endolichenic fungi. In April 2017, five fresh and healthy-looking epiphytic Parmotrema tinctorum were collected in 5 spots in Jeju island. We conducted following investigation to find out the most suitable conditions for highest isolation and diversity rate; 1) which part of lichen thallus (core, middle and tip part), 2) which size of thallus segment, 3) which kind of sterilization method of lichen thallus surface and 4) which kind of media. In total, 1148 fungi were isolated. Almost isolates are belong to Ascomycota. In Ascomycota, Xylariales is dominant order. 1) Even though middle part of lichen host showed the highest diversity, other parts are strongly recommended to use for sufficient diversity. 2) Because filamentous fungi grow rapidly, the thallus segment of 1mm² showed the highest diversity. 3) After each 1 minute treatments with 70% ethanol, 10% bleach and 70% ethanol, complete thallus surface sterilization was confirmed and showed the highest diversity. 4) When potato dextrose broth agar (PDA) was used, the highest diversity was observed. Additionally using Bold’s basal medium (BBM) could supplement a limit of only using PDB.
[Supported by Korea National Arboretum]

A060
Sulzbachromyces sinensis, an Unexpected Basidiolichen, was Newly Discovered from Korean Peninsula and Philippines, with a Phylogenetic Reconstruction of Genus Sulzbachromyces
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Most of lichens are formed by Ascomycota, less than 1% are lichenized Basidiomycota. The flora investigation of lichenized Ascomycota of South Korea has been well studied in the past three decades; however, prior to this study, none of basidiolichens was discovered. During the recent excursion, an unexpected clavarioid basidiolichen, Sulzbachromyces sinensis was collected. Morphology and ecology has been recorded in detail. DNA was extracted, and ITS, 18S, 28S nuclear rDNA were generated. In order to further confirm the systematic position of the Korean specimens, maximum likelihood and Bayesian inference analysis including all the species of the order Lepidostromatales were conducted based on the ITS. As a result, the phylogenetic tree of the order Lepidostromatales was reconstructed, which differed from the previous studies. The inferred phylogenetic tree showed that species of Sulzbachromyces in three different continents (Asia, South Africa and South America) were separated into three clades with support. In this study, the species worldwide distribution map of Lepidostromatales was illustrated, and S. sinensis had a widest distribution range (paleotropical extend to the Sino-Japanese) than other species (paleotropical or neotropical). Prior to this study, the range of distribution, southernmost and northernmost points and the fruiting time of S. sinensis were recorded, and the genus Sulzbachromyces was firstly reported from Korean peninsula and Philippines.
A061
Phenotypic and Genomic Characterization of a New Species Belonging to the SAR116 Clade in the Class Alphaproteobacteria
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Inha University

Although the SAR116 clade is one of the most predominant group in marine bacterioplankton assemblages, only two isolates, strains “Puniceispirillum marinum” IMCC1322 and HIMB100, have been isolated so far. Strains IMCC1322 and HIMB100 were isolated from the sea surface of the East Sea and Hawaii, respectively, and harbored proteorhodopsin (PR) and DMSP demethylase. In the present study, we report the isolation and genome properties of strain IMCCG8-E1T isolated from the Yellow Sea using dilution-to-extinction. Phylogenetic analysis based on 16S rRNA gene sequence revealed that strain IMCCG8-E1T belonged to the OCS28 subclade of the SAR116 clade and shared 97.0 % similarity with strain IMCC1322. The completed genome sequence of strain IMCCG8-E1T was 2.7 Mbp in size with 49.3% of G+C content. The IMCCG8-E1T genome was predicted to have 2591 protein-coding genes including PR, DMSP demethylase, urease, and sulfur oxidation. Strain IMCCG8-E1T contained summed feature 3 (C16:1 ω7c/C16:1 ω6c) and 8 (C18:1ω7c), and C16:0 as the major fatty acids and ubiquinone-10 as the major respiratory quinone. The major polar lipids detected in the strain were phosphatidylethanolamine and phosphatidylglycerol. On the basis of phylogenetic and phenotypic characteristics, it was suggested that strain IMCCG8-E1T represents a novel species of the genus “Puniceispirillum”, for which the name Puniceispirillum seosanensis sp. nov. is proposed. [Supported by a grant from the MOF (No. 20180430)]

A062
Isolation and Genomic Characterization of Bacteriophage that Infect Strain Erwinia sp. AnSW2-5T Isolate from Nakdong River
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Nakdonggang National Institute of Biological Resources

Bacteriophages (phages) are natural killers of bacteria and are an excellent tool due to their high specificity and safety for the environment. Therefore, phage therapy is the therapeutically use of bacteriophages to treat pathogenic bacterial infections. In this study, we have isolated and characterized lytic phage that infect Erwinia sp. AnSW2-5T. Erwinia is a genus of Enterobacteriaceae bacteria containing mostly plant pathogenic species. Both the host strain and two phages were isolated from surface freshwater samples collected of the Nakdong river of Korea. Bacteriophages were isolated by enrichment culture followed by plaque assay. Morphological analysis of phage particles using TEM showed that phage belong to the Podoviridae and Myoviridae. The complete genome sequence of two phages AnSW2-5PS and AnSW2-5PK are 28-43 kb long. This complete genome sequence is the report of a lytic phages that infects Erwinia, for which the name “Erwiniaphage AnSW2-5PS” and Erwiniaphage AnSW2-5PK” are proposed. Considering the rarity of phages isolates infecting this strain, the two phages and their genomes in this study would be valuable resources for freshwater virus research.
A063

Ruegeria lutea sp. nov., a Novel Strain, Isolated from Marine Sediment, the Masan Bay, South Korea
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Gram-negative, non-motile, mesophilic, coccoid-shaped, aerobic bacterium designated as 318-1T was isolated from a marine sediment collected from Masan bay, South Korea.

Strain 318-1T grew optimally at pH 6.0–7.0, at 30°C and in the presence of 2–3% (w/v) NaCl, tolerant up to 8% (w/v) NaCl. Cells accumulate PHB. The DNA G+C content was 65.75 mol%. A comparative analysis of 16S rRNA gene sequences revealed that strain 318-1T formed a distinct phyletic lineage in the genus Ruegeria (family Rhodobacteriacea, class Alphaproteobacteria) and showed the high sequence similarity to Ruegeria halocynthiae DSM 27839T (96.5%), Shimia haliotis DSM 28453T (96.3%). The sizes of the draft genomes as presented here are 4,684,909 bp. Chemotaxonomic data [predominant quinon eubiquinone Q10; polar lipid profile consisting of major compounds phosphatidylcholine (PC), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), Phosphatidylethanolamine (PE) and two unidentified phospholipid (PL); major fatty acids C18:1ω7c] supported the affiliation of strain 318-1T to the Genus Ruegeria. The results of physiological and biochemical tests allowed genotypic and phenotypic differentiation of strain 318-1T from the members of the genus Ruegeria. On the basis of the results in this study, a novel species, Ruegeria lutea sp. nov., is proposed. The type strain is 318-1T (=JCM30927T =KEMB7306-525T =KCTC 72105T).

A064

Roseomonas roseus sp. nov., Isolated from Chemical Fertilizer Treated Rice Paddy Soil
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A pink-pigmented, Gram-stain-negative, coccobacilli-shaped, motile and strictly aerobic bacterium, designated strain NPKOSM-1T, was isolated from chemical fertilizer treated rice paddy soil in south Korea. Colonies were circular with entire edges, convex and pink. Growth was observed at 15-40°C (optimum, 28°C), at pH 6.0–9.0 (optimum pH 7.0) and in the presence of 0–1.5 % NaCl (optimum 1.0 %). Phylogenetic analysis based on the 16S rRNA gene sequence indicated that strain NPKOSM-1T belonged to the genus Roseomonas and was closely related to Roseomonas sediminicola FW-3T (98.2%), Roseomonas oryzicola YC6724T (98%), Roseomonas soli 5N26T (98%), Roseomonas eburnea BUT-5T (97.8%), Roseomonas alkaliterra e YIM 78007T (97.7%), and Roseomonas lacus TH-G33T (97.6%). However, the DNA–DNA relatedness values between NPKOSM-1T and the closest phylogenetically related species were significantly below 70%. The major cellular fatty acids were summed feature 8 (C18:1ω7c and/or C18:1ω6c), C16:0 and C18:1 2-OH. The predominant respiratory quinone was identified as Q-10. The major polar lipids were PC, PE and PG. The DNA G+C content was determined to be 66.3 mol%. On the basis of phylogenetic, chemotaxonomic and phenotypic data, we conclude strain NPKOSM-1T represents a novel species of the genus Roseomonas, for which the name Roseomonas roseus sp. nov. is proposed. The type strain is NPKOSM-1T.

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A065
Isolation and Identification of a Novel Strain of Aspergillus flavus from Dead Insect
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Aspergillus flavus is known as a pathogen causing aspergillosis to plants, animals and human by producing some mycotoxin like aflatoxin. A. flavus is worldwide present and found growing in soil, dead plants and animals. Recently A. flavus is reported to be entopathogenic to some insects. This study was conducted to isolate and identify the fungi collected from the dead body of Halyomorpha halys (Stål). Isolated fungi cultured on potato dextrose agar plates and incubated at 25°C. After cultivation during several days, single spore isolation was conducted and three strains were obtained. The mycelia first appeared white or sometime gray, after green or yellow and produced numerous conidia. The structure of conidia and hyphae was observed via SEM. The conidia were 1-celled, globose and in dry basipetal chains. DNA was extracted respectively for PCR. PCR was performed using universal primers for Internal Transcribed Spacer rDNA region using ITS1/ITS4, beta-tubulin using the primer set T1/Bt2b and Calmodulin using the primer set CMD5/CMD6. The sequences of the isolate matched with 100% similarity to the A. flavus sequences in GeneBank. Furthermore, the results of the morphological characteristics and molecular data of the fungal isolates corresponded with those of A. flavus. We confirmed the effects of A. flavus that could be used as biological control agents against H. halys on apple insect.
[Supported by grants from RDA (PJ01270302)]

A066
Two New Records of Chytridiomycete Fungi Isolated from a Freshwater Sample Collected at Gwangju, Korea
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In a survey of indigenous fungal diversity in Korea, two strains of EML-HRW4-3 and EML-HRW4-5 belonging to Chytridiomycetes were isolated from freshwater samples collected at Hwangryong river located in Gwangju (GPS: 35°09'29.2"N 126°44'10.5"E), using a bait method. To identify the fungus at the species level, detailed morphological studies and rDNA sequence analyses were performed. BLASTn search indicated that the identity values of ITS rDNA sequences of EML-HRW4-3 and EML-HRW4-4 isolates represented 100% (631/631 bp), and 99.4% (163/164 bp), respectively. Based on the phylogenetic analyses, EML-HRW4-3 strain was closest to Chytriomycyces hyalinus (GenBank accession no. AY601710), and EML-HRW4-4 strain closest to Rhizophydium littoreum (GenBank accession no. JN943814). Our study showed that the EML-HRW4-3 and EML-HRW4-4 strains were identified as new undescribed species of Chytriomycyces and Rhizophydium, respectively. The finding of such rare fungi is very significantly important in diversity study of undiscovered taxa, Chytridiomycota.
A067
Rare Zygomycete Fungi, *Mucor orantesmantis* sp. nov. and *M. ardhlaengiktus* from Fecal Samples of Praying Mantis and Amphibians in Korea
Thuong T.T. Nguyen and Hyang Burm Lee
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In this study, two rare zygomycete fungi were isolated from specific niches including fecal samples of praying mantis and amphibian in Korea. Two rare fungal strains, CNUFC-MID1-1 and CNUFC-FF3-3, were isolated using direct plating method. Sequence analysis by BLASTn search indicated that the isolates, CNUFC-MID1-1 and CNUFC-FF3-3 were closest to *Mucor* sp. INBio2958 (GenBank accession no. GU827502), and *Mucor ellipsoideus* (GenBank accession no. NR_111683) (current name: *M. ardhlaengiktus*) with identity values of 94.1% (554/589 bp) and 99.5% (568/571 bp), respectively. On the basis of their morphological characteristics and phylogenetic analysis of their internal transcribed spacer regions and 28S rDNA sequences, the CNUFC-MID1-1 isolate was identified as a new *Mucor* species, named *M. orantesmantis* sp. nov. The CNUFC-FF3-3 isolate was identified as an unrecorded species, *M. ardhlaengiktus* in Korea. To our knowledge, this is the first report of *M. ardhlaengiktus* from a specific habitat of fecal sample in the world.

A068
A New Species of *Penicillium* Belonging to Section *Citrina* from Korea with Antimicrobial and Enzymatic Activity
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During an investigation of fungi of the order Eurotiales from soil collected at Dokdo Island in Korea, an isolate CNUFC-DDS11-1 was isolated. Sequence analysis of the two loci revealed that isolate belongs to the *Penicillium* section *Citrina*. The CNUFC-DDS11-1 isolate was nested between *P. terrigenum* and *P. copticola*, and differed from them morphologically and physiologically, with higher numbers of phialides per metula and metulae, and slower growth on CYA and YES at 25°C. Additionally, CNUFC-DDS11-1 produces divaricated conidiophores, which are not observed in *P. terrigenum* and *P. copticola*. Herein, a new fungal species, *Penicillium dokdoense* sp. nov., is proposed. In the present study, the CNUFC-DDS11-1 strain showed *in vitro* antimicrobial activity against *Alternaria alternata* and *Staphylococcus aureus*, and also produced proteolytic enzyme. The results of the study suggest that *P. dokdoense* CNUFC-DDS11-1 might be useful as biocontrol agent and as a potential source for new enzyme.
Three New Records of Sordariomycete Fungi from Freshwater and Cypress Plant Samples in Korea
Monmi Pangging, Naila Khan Bangash, Sehyun Kim and Hyang Burm Lee*
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During an investigation of fungal species belonging to Sordariomycetes, three new records were isolated from freshwater samples collected from Yeosu, Jeonnan Province and Sangju, Gyeongbuk Province, and cypress plant sample from Chonnam National University Arboretum in Gwangju, Korea. Based on the results of phylogenetic analysis and morphological characteristics, the isolated strains CNUFC-YJS7-1, CNUFC-SCL1-1 and CNUFC-PL4, were identified as *Mariannaea fusiformis*, *Sarocladium zeae* and *Seridium cupressi*, respectively. Species within these genus are readily identified based on the sequence analyses of ITS (internal transcribed spacer) of primer sets (ITS1/ITS4), LSU (large ribosomal subunit) regions of primer sets (LROR/LR5F) and beta-tubulin (Bt2a/Bt2b) gene regions. These species have not been previously reported in Korea.

Two New Records of Ascomycete Fungi Isolated from Soil Samples in Korea
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During a survey of fungal diversity of Ascomycota in Korea, two strains EML-HPTS2-29 and EML-HPTS2-29-1 were isolated from soil samples collected at Geumgol Mt. located in Jindo, and one strain EML-HRS5-3 was isolated from reddish soil sample collected at Hwangyong river located in Gwangu, Korea. Sequence analysis by BLASTn search indicated that the isolates EML-HPTS2-29 and EML-HRS5-3 were closest to *Metapochonia goniodes* (GenBank accession no. DQ522458) and *Lectera nordwiniana* (GenBank accession no. MK047462) with identity values of 99.68% (949/952 bp) and 99.05% (520/525 bp), respectively. Based on the morphological characteristics and sequence analysis of the RNA polymerase II (RPB2) gene and internal transcribed spacer (ITS) regions, the isolates HPTS2-29 and EML-HPTS2-29-1, and EML-HRS5-3 were confirmed as *Metapochonia goniodes* and *Lectera nordwiniana*, respectively. To our knowledge, this is the first report of *M. goniodes* and *L. nordwiniana* species in Korea.
**B001**

**The Characteristics of Microbiota Cultivated Kimchi Cabbage (Brassica campestris ssp. pekinensis) with Increased Productivity on Crop Rotation System**

Gyeryeong Bak, Taeyoung Kim, Gyejun Lee, and Samnyu Ji*

*Rural Development Administration*

Kimchi cabbage (*Brassica campestris* ssp. *Pekinensis*) is one of the most important crops in Korea. Because Kimchi cabbage is a cool-season crop, kimchi cabbage can only be cultivated on highland area in summer season. When the kimchi cabbage was cultivated continuously, soil borne diseases were increased and productivity was decreased. To avoid these problems, farmers transported new soil almost every 2 years, nevertheless soil erosion was more severe. To solve this problems, we try to apply crop rotation systems with soybean (*Glycine max* L.) and potato (*Solanum tuberosum* L.), and identifying as an aspect of microbiota to kimchi cabbage cropping in pot experiment.

The productivity and plant nutrients showed significant differences between rotation and replanting cropping systems. Total-Nitrogen, Calcium, Magnesium and Natrium were higher in rotation system while only phosphate was higher in replanting system. Because plant nutrient absorption is highly related to soil fungal community, rhizosphere soil fungal microbiota was analyzed through ITS1 region targeted next generation sequencing (NGS).

Diversity index showed higher community richness in rotation system, while evenness index showed no differences. PCoA analysis was revealed that clear classification between two cropping systems. In comparison with two cropping systems, 271 distinct OTUs were detected through Kruskal-Wallis H test in the level of 5% significances.

[Supported by grants from RDA]

**B002**

**Trends in Taxonomic and Functional Structures of Microbial Communities along the Chronosequences of a High Arctic Glacier Foreland**

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*Korea Polar Research Institute*

Microorganisms are the initial colonizers of newly exposed soils after glacial retreat, however, little is known about their taxonomic and functional structures along the successional chronosequences of glacier foreland. We studied the trends in taxonomic and functional structures of soil microbial communities along the chronosequences of Midtre Lovénbreen Glacier using shotgun metagenomic sequencing. The taxonomic and functional structures of microbial communities were strongly influenced by soil age. The relative abundance of some of the dominant bacterial phyla (*Acidobacteria* and *Chloroflexi*) increased while others (*Betaproteobacteria* and *Gammaproteobacteria*) decreased over succession. The relative abundance of genes associated with carbohydrate metabolism was increased, whereas the relative abundance of nitrogen metabolism related genes decreased over succession. Furthermore, the relative abundance of *nifH* gene (involved in nitrogen fixation) showed a hump-backed curve along the successional age gradient, and relative abundance of *amoA* gene (involved in nitrification) showed a positive correlation with soil age, but genes involved in denitrification (*nirK, nirB* and *nosZ*) displayed negative correlation with soil age. Overall, our results demonstrate that soil age play important role in structuring taxonomic and functional compositions of microbial communities along the chronosequences of Midtre Lovénbreen Glacier foreland.

[Supported by grants from KOPRI and KRF]
B003
Temporal Succession in Bacterial Biofilm Communities on a Biofilter Installed in a Swine House for Removal of Odorous Gases
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Biofilters utilize microbial biofilms to degrade odorous compounds present in exhaust air of livestock buildings, however, little is known about the temporal succession in bacterial biofilm communities immobilized on packing materials of biofilters. Here, we investigated the temporal shifts in community composition of bacterial biofilm communities on a biofilter system installed in a swine house to reduce the emissions of odorous compounds using Illumina MiSeq sequencing. We found that odor removal efficiency of biofilter system was linearly increased with time. The composition of bacterial biofilm communities was strongly influenced by time and followed a successional trajectory, and to a lesser extent, the bacterial biofilm communities were also influenced by filtration stage and interaction between time and filtration stage. The bacterial biofilm communities were dominated by numerous bacteria taxa which are known for degrading odorous compounds. The temporal succession in bacterial biofilm communities detected on the biofilter in this study is a key first step towards understanding the dynamics of bacterial biofilm communities on biofiltration systems.
[Supported by a grant from MAFRA]

B004
Fumonisin B₁ Biodegradation and Antifungal Activity against Toxigenic Fusarium spp. by Streptomyces spp.
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In this study fumonisin B₁ biodegradation and antifungal activity against toxigenic fungi by isolated strains, Streptomyces sporoverrucosus JS383 and S. lavendulae JS669 were examined. Fumonisin B₁ is toxic secondary metabolites produced by Fusarium spp. Strains JS383 and JS669 degraded fumonisin B₁ (0.1 mg/L) by 94.1 and 99.0%, respectively in nutrient broth (12 h, 30°C). JS383 and JS669 showed good thermostability in fumonisin B₁ degradation (up to 75°C). They also rapidly removed fumonisin B₁ by 91.1 and 97.9%, respectively during initial 30 seconds. Their antifungal activity was evaluated by co-culture with 4 strains of fumonisin B₁ producing Fusarium spp. (F. fujikuroi KACC46888 and 48352, F. verticillioides KACC48354 and F. proliferatum KACC48356). JS383 and JS669 produced inhibition zones of 9.0 to 18.3 mm dia. against 4 strains of toxigenic Fusarium spp. They effectively inhibited mycelial growth (74.9 to 85.9%), and suppressed sporulation of toxin producing fungal strains up to 94.7 and 97.2%, respectively. They also showed capability of spore degradation and inhibition of spore germination. JS383 and JS669 produced siderophore up to 113 and 110 µM, respectively, as antifungal substance, and also showed chitinase activity. Ethyl acetate extract of bacterial cultures showed minimum inhibitory concentrations of 1.25–2.50 mg/ml for target fungi. Conclusionally, JS383 and JS669 can be used for fumonisin B₁ removal and control of toxigenic fungi in food and feed industry.
B005
Characterization of Growth and Enzymatic Activities of a Marine-derived Yeast, *Rhodotorula mucilaginosa* GSU-CS3
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National Marine Biodiversity Institute of Korea

This study on the characteristics of mycelium in *Naematoloma sublateritium*. It was excellent, and SADY medium, MMA medium was investigated, but suitable optimum culture medium appeared to mycelium growing of *Naematoloma sublateritium* in the first, existing other study to PDA medium it was investigated. Suitable temperature and provisional results regarding ph of *Naematoloma sublateritium*, proper temperature appeared with 25 degrees, and proper ph was investigated to 6.5–7.0. This study showed to excellent hypha growing at Glucose in circular the carbon which was suitable for the third, hypha growing of *Naematoloma sublateritium* provisional results carbon circle regarding a nitrogen circle, and cultures of *Naematoloma sublateritium* looked at malt extract in case of organic nitrogen circles. However, a kind circular carbon nitrogen used to test is restrictive, and provisional shall consist of various elements by a foundation. This study looked in phosphoric acid circle to affect the fourth, mycelium of *Naematoloma sublateritium* to growth and development. Also, if this study added it was investigated p-aminobenzoic acid in vitamin circle so that hypha growing was comparatively good.

[This paper consisted by assistances of a technology development assignment scientific forest]

B006
Identification and Characterization of a Chitinase-producing Fungus, *Acremonium* sp. YS2-2 Isolated from Seawater
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National Marine Biodiversity Institute of Korea (MABIK)

Chitin is one of the main components of crustacean shells and the most abundant biopolymer in marine environments. To facilitate chitin utilization, our laboratory isolated fungi from marine environments and screened them for chitinolytic activity. One chitinase-producing strain, designated YS2-2, was identified as *Acremonium* species based on morphological and phylogenetic analyses. *Acremonium* species are ubiquitous in both terrestrial and marine environments, but their chitinolytic activity remains to be studied. YS2-2 readily grew at 15–28°C, but did not grow at 37°C. In response to NaCl, YS2-2 development was inhibited at NaCl concentrations higher than 7.5% (w/v). The optimum chitinase activity of YS2-2 was observed at pH 6.0–7.6, 23–45°C, and 1.5% NaCl. A putative chitinase gene in YS2-2, designated *chiA* was identified via degenerate PCR. The expression of *chiA* was drastically induced in response to colloidal chitin compared to levels under starvation, crude chitin powder, and glucose conditions. In addition, the *chiA* transcript levels were positively correlated with chitinase activities under various colloidal chitin concentrations, suggesting that ChiA is associated with chitinolytic activity in YS2-2. Our results provide a basis for additional studies of marine-derived fungi aimed at discovering valuable natural compounds including enzymes.

[Supported by a grant from MABIK (2019M00700)]
B007
Culture-independent and Dependent Analyses of Bacterial Community in the Phycosphere of Cyanobloom-forming Microcystis aeruginosa
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Roles of epiphytic bacteria on harmful cyanobacterium Microcystis aeruginosa are largely unknown. Confocal and scanning electron microscopic observation confirmed strong bacterial association on the surface of M. aeruginosa cells. DNA-based analysis of 3-μm pore filtered bacterial community (BC) was conducted using two laboratory-grown M. aeruginosa strains and eight newly collected cyanobloom samples. M. aeruginosa was the most dominant species (66-100%) within the phylum Cyanobacteria. At the genus level, Rhizobium, Hydrogenophaga and Brevundimonas species were commonly found and Flavobacterium species is only present in all environmental samples (ES). Total 396 colonies from various samples were screened to reveal that most culturable bacteria belong to Alpha-proteobacteria (19%) including Rhizobium, Brevundimonas, and Porphyrobacter species. The most prevalent genus recovered from cultivable members were Rhizobium, Brevundimonas and Pseudomonas species. Rhizobium sp. MK23 isolated from one EC appeared to promote the growth of axenic M. aeruginosa NIES-298 under co-culture condition. Our data suggested that epiphytic bacteria such as Rhizobium species could be beneficial to the growth of M. aeruginosa probably due to bacterial stress protection and nutrient supply. [Supported by a grant from the National Institute of Biological Resources.]

B008
Species Composition and Chemotype of Mycotoxigenic Fusarium Species from Cereals
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Microbial Safety Team, National Institute of Agricultural Sciences, Rural Development Administration

Fusarium is one of the important fungal pathogens of cereals and cause contamination with mycotoxins that have adverse effects on the health of humans and animals. In this study, we isolated Fusarium strains from oat, sorghum, millet and adlay samples from fields in 2017 to identify mycotoxigenic fungal flora. Fungal colonies were isolated based on morphological characteristics and identified using the DNA sequence of the translation elongation factor 1-α (TEF-1α) gene and internal transcribed spacer (ITS) region. A total of 2250 Fusarium isolates were identified and comprised of F. graminearum species complex (FGSC), F. fujikuroi species complex (FFSC), F. incarnatum-equiseti species complex (FIESC) and F. avenaceum/F. arthrosporoides/F. tricinctum species complex (FTSC). The oat samples were dominated by F. asiaticum (85.6%) and FIESC (5.8%), whereas sorghum samples were dominated by F. graminearum (28.8%), F. thapsinum (25.8%), and F. proliferatum (18.6%). Millet and adlay samples were dominated by FIESC (60.6% and 47.5% for each plant) and F. fujikuroi (16.7% and 28.0%). The potential to produce fumonisin and trichothecene chemotype were evaluated using FUM1 and TRI13/TRI12 genes. This is the first report of occurrence of the mycotoxigenic Fusarium species on oat, sorghum and millet in Korea.
B009

Nasal Microbiome is Linked with Elevated Total IgE Levels in Allergy Patients
Dong-Wook Hyun and Jin-Woo Bae*

Kyung Hee University

We sought to characterize the microbiota of the site of allergic rhinitis, the inferior turbinate, in subjects with allergic rhinitis (n = 20) and healthy controls (n = 12) and to examine the relationship of mucosal microbiota with disease occurrence, sensitized allergen number, and allergen-specific and total IgE levels. Microbial dysbiosis correlated significantly with total IgE levels representing combined allergic responses but not with disease occurrence, the number of sensitized allergens, or house dust mite allergen-specific IgE levels. Compared to the populations in individuals with low total IgE levels (group IgE\textsuperscript{low}), low microbial biodiversity with a high relative abundance of Firmicutes phylum (Staphylococcus aureus) and a low relative abundance of Actinobacteria phylum (Propionibacterium acnes) was observed in individuals with high total serum IgE levels (group IgE\textsuperscript{high}). Phylogeny-based microbial functional potential predicted by the 16S rRNA gene indicated an increase in signal transduction-related genes and a decrease in energy metabolism-related genes in group IgE\textsuperscript{high} as shown in the microbial features with atopic and/or inflammatory diseases.

B010

Host Habitat Shapes the Gut Microbiome of Fish to a Greater Extent Than Host Taxonomy
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There are approximately 28,000 species of fish, representing greater species diversity than any other group of vertebrates. In the last decades, numerous studies explored the animal gut microbiota; however, most studies focused on the gut microbiota of mammals. To better understand the evolutionary basis of symbiotic relationship between animal host and indigenous microbes, it is necessary to investigate gut microbiota of non-mammalian vertebrate species. We comprehensively characterized gut bacterial communities of fish. We analyzed 227 individual fish representing 14 orders, 42 families, 79 genera, and 85 species. The fish gut microbiota was dominated by Proteobacteria and Firmicutes (>50%). The gut microbial community of fish was strongly shaped by host habitat compared to host taxonomy and trophic level. An analysis involving a machine learning approach trained on microbial community composition or predicted functional profiles demonstrated that the host habitat exhibited the highest classification accuracy. PCoA revealed that the gut bacterial community of fish significantly differs from those of other vertebrates (reptiles, birds, and mammals). Our data provide a reference for future studies on the gut microbiome of aquatic animals, and insights into the relationship between fish and their gut bacterial community.

[This work was supported by the Collaborative Genome Program for Fostering New Post-Genome industry (2015M3C9A2054299) from NRF, Korea.]
Nematodes are the most ubiquitous and abundant invertebrates, and the second most diverse phylum in the animal kingdom. Aiming to profiling the soil nematodes in mountain regions in South Korea, as well as to understand how the diversity and community composition of soil nematode vary along elevational gradients, we investigated the soil nematode communities along a ~1,400 elevational range on Mt. Seoraksan, South Korea, by sequencing their 18S rRNA gene. We found that the nematode community on Seoraksan Mountain as a whole was dominated by the family Prismatolaimidae, followed by an Enoplean family (unclassified), Nygolaimidae, Qudianematidae, Chromadoridae, Mononchidae and other 32 nematode families. Although the diversity of the nematode community of each elevational isocline band were not significantly different, nematode community structure indicated some differentiation according to the different elevational isochline bands, for example, the nematodes on low elevation are significantly different from other higher isocline bands. Our study confirmed the effectivity and reliability for using DNA barcoding methods to investigate nematode communities, as well as to study how nematode ecology differs along gradients. [Supported by grants from NRF.]

The aim of this research was to develop an effective bacterial consortium and evaluate their ability to overcome nitrogen requirement for the enhanced degradation of diesel oil. For this, different bacterial consortia were developed using oil-degrading and nitrogen-fixing bacteria. The diesel degradation efficiency of developed consortia was determined by delivering the bacterial consortia to the diesel-contaminated soils. The bacterial consortium K-6 + Y2-2 + nutrients showed the highest degradation (85.3%) of diesel from the contaminated soil. Soil treated with the consortium K-6 +Y2-2 +KCTC 2426 degraded 83.1% of the diesel after 40-days. The assessment of total nitrogen content found higher amounts of nitrogen in soil treated with the diazotrophic bacteria compared to soil supplemented with exogenous inorganic nitrogen. These findings revealed that the consortium containing diazotrophic and oil-degrading bacteria degraded adequate amounts of diesel which is similar to the amounts degraded by the consortium containing oil-degrading bacteria and exogenous inorganic nitrogen. This suggests that the constructed consortium K-6 +Y2-2 + KCTC 2426 compensated for the nitrogen limitation and eliminated the need for exogenous nitrogen in bioremediation of diesel-contaminated soils.
**B013**

**Molecular Analysis of Soil Bacterial Community Structures for Environmental Risk Assessment with Genetically Modified Soybean**

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With the advance of gene technology, genetically modified (GM) crops have increased in recent years. GM crops offer us various benefits. But there are potential risks of GM crops on the environment. In this study, the impacts of transgenic plants on soil microbial community structures were assessed by using both cultivation and molecular methods. We using the total viable count and OTU-based community profiling with Illumina MiSeq platform for measure the changes of microbial density over time between GM and non-GM plants. The results showed that the microbial dynamics of GM subplots were quite similar compared to non-GM subplots. Only the density of Rhizobium associated with legume plants increased in soybean soils. This study showed that the bacterial communities of the experimental field soils were not significantly affected by cultivation of GM soybean. There were not meaningful differences between GM and non-GM lines based on culture-dependent and molecular approaches.

[This work was supported by the National Research Foundation of Korea Grant (NRF-2018R1D1A1B07047456)]

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**B014**

**Research on Characteristic Analysis of Growth Environment of Clavicorona pyxidata**

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The study was accomplished for the gene academy excavation and the cultivation of the forest mushroom using the conifer material. The characteristic analysis of the growth environment is always necessary in the generated mushroom for artificial cultivation of a *Clavicorona pyxidata*. It was clarified that the relative temperature was 60.6%, the relative humidity was 2.9%, the humidity of the soil was 1.2%, and upper layer crown degree of closure was 2.4%. Such a result of the survey was increased and 8% increase also increased the mushroom generation by about 5.7% compared with June as a result of measuring the amount of the mushroom generation and in foundation in August. Therefore, it was analyzed that the specific gravity with considerably important illuminance and humidity was occupied to the mushroom generation and growth.

[Supported by National Forest Science Institute]
**B015**

**Enrichment of Uncultured Ammonium Oxidizing and Denitrifying Bacteria from Antarctic Soil**

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Bacteria are critical contributors to the nitrogen cycle of ecosystems, especially in limited habitats such as Antarctica. For the cultivation of bacteria involved in the nitrogen cycle of the Antarctica, three soils from King George Island were enriched for nitrogen fixation (NF), ammonium oxidation (AO) and denitrification (DN). Changes in N₂O gas, ammonium, nitrite and nitrate concentrations were measured every 14 days. Ammonium oxidation and denitrification were confirmed by measuring changes in nitrogen concentration, and 16S rRNA gene was amplified and analyzed for bacterial communities. Functional gene *amoA*, which is an ammonium oxidizing gene, and *nirK*, *nirS* and *nosZ*, denitrifying genes, were confirmed. As a result of the bacterial community analysis, it was found that the culture of ammonium oxidizing bacteria were cultivated with *Micavibrio*, *Oxalobacteraceae* and *Pseudomonadaceae*. *Oxalobacteraceae*, *Pseudomonadaceae* and *Propionibacteriaceae* were cultivated in denitrifying bacteria enriched culture. The denitrification pathway and the dissimilatory nitrite reductase pathway were found in the DN_1B and DN_3A denitrifying bacterium cultured in the SEED profile. The ammonia assimilation pathway was more abundant in AO_2C cultured with ammonium oxidizing bacteria. And environmental genetic analysis of the cultures obtained by enrichment will help to understand the ecological function and role of bacteria in the ecosystem.

[Supported by the Korea polar Research Institute (Grant PE19090)]

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**B016**

**A Novel Bacterial Strain from the Tomato Rhizosphere Resistant to Bacterial Wilt Has an Antagonistic Activity against *Ralstonia solanacearum***

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Soil ecosystem is composed of diverse microorganisms including bacteria and fungi. Especially in the rhizosphere, narrow regions of soil immediately adjacent to plant roots, plenty of microorganisms inhabit and some may be involved in plant defense against plant pathogens. In our previous study, we performed a whole metagenomic analysis of the rhizosphere communities of two tomato cultivars, Hawaii 7996 and Moneymaker, which are either resistant or susceptible to bacterial wilt, respectively. Through the taxonomic analysis of the whole metagenome data and phylogenetic binning, we reconstructed the genome of a novel uncultured *Flavobacteriaceae* bacterium, designated TRM1, from the metagenomic sequences that exist only in the Hawaii 7996. Based on the genome information, the bacterium from the rhizosphere, which contributes to the wilt disease resistance, was successfully isolated. The isolated bacterium was proposed to represent *Flavoflexilis rhizosphaerae* gen. nov., sp. nov. by polyphasic characterization. Physiological features of the isolate were identified through experiments including bacterial growth, antibiotics resistance, and carbon source utilization. To identify how TRM1-10 can reduce the bacterial wilt disease, we performed an in vitro co-cultivation experiment of TRM1-10 and *Ralstonia solanacearum* SL341 and TRM1-10 inhibited the growth of SL341 but the growth of TRM1-10 itself was not affected.
Currently decomposition of methane hydrates is occurring across continental shelves of the Arctic Sea. In the shallow sediment overlying methane hydrate deposits, active methane oxidation associated with sulfate-reducing consortia is commonly found. We therefore hypothesized that sulfate-reducing bacteria (SRB) may actively methylate Hg(II) in these sediments, as SRB are one of the major mediators of Hg(II) methylation in marine sites.

We quantified total Hg and MeHg concentrations from the seven cores, and dissimilatory sulfite reductase, dsrB, that catalyzes sulfite reduction to sulfide, and methyl coenzyme M reductase, mcrA, that catalyzes methanogenesis from the two cores. The non-hydrate coastal sediment (St 28) showed the highest fraction of MeHg over total Hg (0.78%) and the highest copy number of dsrB at 0-2 cm sediment depth. The mcrA copy number was relatively low at the overall depth (0-20 cm) of the same core, as was typically found in temperate coastal zones. On the contrary, the methane hydrates core (St 04) showed the highest MeHg fraction over total Hg (0.1%), and the highest copy number of dsrB at the depth of 6-8 cm, while mcrA copy number was higher at the surface. Based on this and microbial community data, we expect to better understand how MeHg production is related to sulfate reduction and methane production in the Arctic sediments.

[This work was supported by the Polar Academic Program (PE18900) of the Korea Polar Research Institute.]

Endophytic bacteria, with a rich source of bioactive secondary metabolites, are ideal candidates as an environmentally benign agent. In this study, 366 endophytic bacteria associated with Pinus spp. were screened for their nematicidal activities. One strain, named as AE170020, was selected for the purification of nematicidal substances based on its high nematicidal activity. Bioactivity-guided fractionation of the fermented mycelium of strain AE170020 was used to isolate and determine the bioactive constituents responsible for the nematicidal activity. Two compounds responsible for the activity were identified, and their chemical structures were determined using spectroscopic analysis. In in vivo experiments, these two compounds effectively suppressed the development of pine wilt disease at the tested concentrations in five-year-old plants of Pinus densiflora. The potency of endophytic strains and its secondary metabolites suggests applications in controlling Bursaphelenchus xylophilus and opens an avenue for further research on exploring the bioactive substances against the pine wood nematode.

[This work was supported by a grant from the National Institute of Forest Science (Project No. FE0702-2016-02 "Development of environment-friendly control agents against pine wilt disease based on BT"). This research was supported by a grant (NRF-2013M3A9A5076601) from the Ministry of Science, ICT and Future Planning of the Korea Government]
B019
Rapid Determination of *Salmonella enterica* Serotypes Using Pan-genome Based on Real-Time PCR Method
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*Salmonella* is one of the most important food-borne pathogens causing salmonellosis and consist of more than 2,600 serotypes. Therefore, their serological identification is very important in epidemiological studies. Because the conventional serological method is expensive, laborious, and time-consuming, it is necessary to develop a new simple method to identify the serotype of *S. enterica*. In this study, complete genome sequences of 16 different serotypes of total 62 *S. enterica* strains were compared to determine the serotype-specific DNA sequence regions using pan-genome analysis. Interestingly, two specific genes were found to be specific for *S. Typhimurium* (*hxiA*) and *S. Enteritidis* (*hokC*), suggesting that they may be target genes for their rapid serotyping from other serotypes of *S. enterica* by real-time (RT) PCR. New primer-probe sets targeting these genes were designed and their RT-PCR conditions were optimized. To validate this, 18 strains from seven different serotypes of *S. enterica* were selected and used. Subsequent RT-PCR results showed that this PCR works for rapid serotyping of *S. Typhimurium* and *S. Enteritidis* from other serotypes. This rapid detection and identification method may contribute to food safety from food-borne outbreaks via ingestion of various *Salmonella*-contaminated foods.

[This research was supported by grants (14162MFDS972, 19162MFDS037) from Ministry of Food Drug Safety in 2019]

B020
Nematocide Active Substances for *Bursaphelenchus xylophilus* Isolated from Actinomycetes
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Pine wilt disease (PWD) is caused by the pine wood nematode (PWN) *Bursaphelenchus xylophilus*. This causes the PWN to be transferred by the insect, and when the weather is warm, the PWN grows rapidly. Currently, avermectin and derivatives are used as pesticides to suppress PWD. However, there are disadvantages due to high cost and low water solubility. Therefore, a new insecticidal active substance was sought to solve the problem. Actinomycetes are known to produce a large amount of physiologically active substances, and avermectin is also a substance isolated from actinomycetes. In this study, the nematocide active substances was isolated from actinomycetes. About 8,000 actinomycetes were screened for nematocide active compounds. The structures of the compounds, using the MS / MS and NMR analysis were used to interpretation the structure of the compounds. Compounds isolated in this study are the first reports of nematocide activity against PWN. This study then provides the basic data for the formulation of compounds and the further research to be carried out.

[This work was supported by a grant from the National Institute of Forest Science (Project No. FE0702-2016-02) and the grant (NRF-2013M3A9A5076601) from the Ministry of Science, ICT and Future Planning of the Korea Government.]
B021
Comparison of Enkephalin and Gramicidin-S as Internal Standard in Measuring Microcystins from Cyanobacterial Biomass
Ji-Min Hwang, Bo-Ri Kim, Ji-Soo Shin, Jae-Hun Lee, Hye-Ryoung Kim, Kyoung-Hee Oh, and Young-Cheol Cho*
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Microcystins (MCs) are hepatotoxins produced by harmful cyanobacteria such as Microcystis, Anabaena, and Oscillatoria, found in every summer in Korean freshwaters dominantly. To quantify these toxins in cyanobacterial biomass or soluble forms in recreational and tap water sources using HPLC precisely, the appropriate internal standard (IS) is needed. Gramicidin-S is recommended as IS in the Korean Standard Method to measure the concentrations of MCs in tap water. In this study we proposed a new IS, enkephalin, and evaluated the suitability in measurement of MCs. Enkephalin showed similar recovery rates to MCs. The relative standard deviations under repeatability and reproducibility conditions of enkephalin were lower than those of gramicidin-S. Separation condition with enkephalin in HPLC analysis was also less complicated and took shorter time than with gramicidin-S. These results indicated that enkephalin can be used as a suitable IS in quantification of MCs using HPLC in the cyanobacterial biomass and soluble form.
[Supported by Human Resource Development Project for Waste to Energy of Korea Ministry of Environment]

B022
Distribution of Antibiotic Resistance Genes within Viral Metagenomes of Urban Wastewater Treatment Plants
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Bacteriophages (phages), viruses that infect bacteria, are found in diverse environments including soil, river, wastewater, and guts. As phages infect their hosts, they may randomly acquire a piece of their host genomes, leading to spread of the gene to another host or to its progeny. One of the well-known bacterial genes that are carried by phages is antibiotic resistance genes (ARGs). Gut microbiomes, which are often exposed to diverse antibiotics and have developed ARGs, are commonly released to environment through wastewater treatment plant (WWTP) effluents, along with their phages. This study focuses on the analyses of viral metagenomes (viromes) generated from 4 WWTPs in Seoul and Gwangju of South Korea to observe the distribution of ARGs within phage genomes. For all 4 WWTP viromes, viral fractions of the raw sewage contained the highest ratio of ARGs, which comprised up to 0.48% of virome reads while less than 0.05% of the virome reads of neighboring surface waters were predicted to be ARGs. The most commonly found ARG within the viromes were β-lactamases and multidrug efflux pumps. Interestingly, types of β-lactamases found in two cities differed that in Seoul, class C β-lactamases were dominant while those of class A and B showed dominance in Gwangju. Collectively, the phages must be considered as significant vehicles of ARGs, especially of β-lactamases.
[Supported by the Korean Ministry of Environment as “the Environmental Health Action Program” (201600135004)]
B023

Development and Optimization of Methods to Quantify Microcystins in Fish Tissues and Cyanobacterial Biomass

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Microcystins (MCs) are cyclic heptapeptide hepatotoxins produced by harmful cyanobacteria, which can be concentrated in fish tissues. Consumption of fishes lived in algal blooming areas is one of the major routes to human exposure to MCs. In this study, the extraction and purification steps were developed and optimized for quantification of MCs in fish tissues. To extract MCs from fish tissues the heat extraction method was developed and compared with the conventional ones. The extraction efficiencies to MC-LR, -RR, and -YR, which are main congeners found in Korean freshwaters, were higher than those of ultrasonic extraction or solvent extraction methods. Lipid, which is major contaminant in the extracts from fish tissues, could be removed efficiently through solvent separation method using chloroform. The extraction and purification steps proposed in this study were estimated the superior ones in terms of time and cost, thereby it can be used as a Standard Method to monitor MCs concentration in fish tissues and cyanobacterial biomass taken from algal blooms.

[Supported by Human Resource Development Project for Waste to Energy of Korea Ministry of Environment]

B024

Transcriptomic Response of Bacillus mesoane H20-5 to Salt Induced Osmotic Stress

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Excess salt concentration in the soil and water resources turns fertile fields to barren lands. Microorganisms inhabiting the province of plants significantly contribute to plant growth promotion and salinity tolerance. We had previously observed that Bacillus mesoane H20-5, is a beneficial bacterium which alleviates abiotic stress of plant. In the present study, to induce osmotic stress, salt solution was prepared by combination of different salts and RNA-Seq-based transcriptome analysis was utilised to examine adaptations of B. mesoane H20-5 to salt induced osmotic stress. The transcriptome of the cells was sequenced using Illumina Miseq sequencing platform. Through the NGS technique, a total of 99,331,404 and 68,069,730 sequence reads were obtained from non-stressed (control) and stressed samples respectively. After QC drop, 4.8 million (49.1%) and 2.8 million (42.2%) of total reads were mapped against the genome of Bacillus mesoane H20-5. In which 2.7 million (28.1%) and 1.7 million (25.8%) mRNA reads from total RNA. The eggNOG (evolutionary genealogy of genes: Non-supervised Orthologous Groups) and KEGG (Kyoto Encyclopaedia of Genes and Genomes) databases were used to elucidate the overall effects of osmotic stress on the organism.

[Supported by grants from RDA]
B025

Relationship between Cyanobacterial Numbers and Cyanobacterial Biomass Determined by Phycocyanin Concentration

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Cyanobacterial blooms produce toxins and odorous substances that adversely affect the health of aquatic organisms and even humans. In Korea the direct counting method under microscope is used as the standard method to count cyanobacteria, which is considered as a labor intensive, inaccurate, and non-reproducible one. It has known that the concentrations of chlorophyll a are not correlated with the cyanobacterial numbers especially when the algae other than cyanobacteria are dominant. In this study, we propose a method to rapidly and accurately measure the number of cyanobacteria using phycocyanin which is a pigment exclusively found in cyanobacteria and is a indicator of cyanobacterial biomass. Phycocyanin concentration was estimated using fluorometer or absorption spectrometer. Phycocyanin concentrations showed strong correlation with the number of cyanobacterial cells (n=118, r=0.95, p<0.05) than that of chlorophyll a. It was also found that the fluorometry method was appropriate than absorption spectrometric method because the former showed strong correlation with the number of cyanobacterial cells and it did not need pretreatment allowing real-time measurement. This method can be used to preliminarily quantify and monitor cyanobacterial cells in situ real-time in Korean freshwaters.

[Supported by Human Resource Development Project for Waste to Energy of Korea Ministry of Environment]

B026

Optimization of Nested PCR Method for Monitoring Naegleria fowleri and Acanthamoeba spp. in Sewage Treatment Plants

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Naegleria fowleri and Acanthamoeba spp. are opportunistic pathogenic free living amoebas (FLAs), and the former is popularly known as brain-eating amoebas. According to the previous studies, FLAs are distributed in the aquatic environments in Korea. Usually effluents from sewage treatment plants (STPs) are considered as one of the major sources of the pathogenic microorganisms. To confirm whether the effluents are one of the sources of FLAs, the monitoring of these organisms in the reactors of STPs is required. It is difficult to use conventional PCR method for the detection of FLAs in the reactors because of false-negative if the prokaryotic DNA concentration in the sample is high or the FLAs concentration is too low. To solve these problems, we optimized the detection method of FLAs using nested PCR with the newly designed primers from 18S rRNA gene of these organisms. The applicability of primers was verified with isolated and cultured FLAs. The presence of FLAs in the samples collected from several STPs was determined, and the results will be shown. The method proposed in this study is expected to be useful to sensitively detect FLAs in the biomass-rich samples such as from reactors in STPs and from lakes and rivers with algal blooms. [Supported by Human Resource Development Project for Waste to Energy of Korea Ministry of Environment]
B027
Isolation of Methane Oxidizing Bacteria with Their Related Heterotrophic Bacteria and Characteristics of Mixed Culture
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To isolate methane oxidizing bacteria (MOB) from various types of soils (paddy field, wetland, garbage landfill, etc.), enrichment culture was performed for 2 weeks at 30°C using nitrate mineral salt (NMS) medium with methane as sole carbon and energy source. Twenty four MOBs were isolated from the enrichment NMS culture medium. The 16S rRNA gene sequences of eight strains that grow fast among the isolated MOBs were analyzed. They belonged to Methylophilus sp., Methylosinus sp., and Methylocystis sp.. In addition, the specific growth rates (μ) in NMS medium contained in the 70 ml gas tightly sealed vial supplemented with methane/air gas mixture (50/50, v/v) were 0.031-0.178. On the other hand, more than 40 heterotrophic bacteria, which were co-cultured with MOBs on NMS agar medium in the first subculture, were isolated from LB agar medium in the second subculture. Several mixed culture broths showed high OD600 values of 10 within 5 day cultivation. It was found that some of mixed cultures showed higher OD600 values than pure cultures of corresponding MOBs, but the other presented lower OD600 values. This result suggests that a certain MOB and its related heterotrophic bacterium[a] are symbiotic with each other by exchanging carbon sources or growth promoting substances, but are competitive with each other by inhibiting cell growth.

[This work was supported by a research grant of Ministry of Science and ICT (NRF-2018R1A2B2001006).]

B028
Inferred Metabolic Capabilities of Novel Marine Bacterial Clades of the Family Halieaceae
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The family Halieaceae (OM60/NOR5 clade) represents one of the most abundant bacterioplankton groups in the ocean surface. However, understanding of this lineage has been limited by insufficient cultured representatives and genomes. In this study, using the whole genomes of six strains belonging to family Halieaceae, which have been sporadically isolated from the Yellow Sea and the East Sea by dilution-to-extinction culturing or standard dilution plating, we conducted a comparative genomic analysis and metabolic reconstructions to investigate their evolution and ecology. The phylogenies indicated that these strains each represent a novel species assigned to five novel genera and genus Halioglobus. Three of the isolates were found to be the first cultured representatives of the uncultivated NOR5 subclades. Genome analysis revealed that all of them have heterotrophic lifestyles; five strains were featured by phototrophs with harboring puf operons for aerobic anoxygenic phototrophy or green-absorbing proteorhodopsin genes, coinciding with their adaptation to euphotic ocean surface. Carbohydrate utilization capability inferred from CAZyme analyses suggested that the strains might be closely associated with phytoplankton blooms. The cultures together with their genomes will provide a rich foundation for further study of the Halieaceae lineage using diverse approaches such as metatranscriptomics.

[Supported by grant from the KIMST funded by the MOF, Korea (No. 20180430)]
B029
Understanding Complete Ammonia Removal Mechanism Based on Taxonomic Dynamics in Flat-panel Air-cathode Microbial Fuel Cells Treating Domestic Wastewater
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The flat-panel air-cathode microbial fuel cell (FA-MFC) system consisted of five units successfully removed organics and ammonia in domestic wastewater within a short hydraulic retention time of 1.5 h. The removal of organics commonly occurs in MFC but the removal of ammonia to satisfy discharge limits is exceptional phenomena. To elucidate the mechanism of simultaneous removal of organics and ammonia, microbial communities on the surface of anode, separator, and cathode of each unit were analyzed by Illumina MiSeq. Based on the taxonomic dynamics, potential mechanisms have been identified as (1) nitritation, (2) nitratation, (3) heterotrophic and autotrophic denitrification, (4) anammox, (5) nitric oxide and nitrous oxide reduction and (6) nitrate reduction by iron-related bacteria for nitrogen cycle, (7) fermentation and (8) aerobic removal of organics by denitrifying bacteria for carbon cycle, and (9) electricity generation. Mechanisms (1), (2) and (8) occurred nearby air-cathodes and (3), (4), (5), (6), (7) and (9) occurred nearby anodes. The FA-MFC system could induce simultaneous nitrification, anammox and denitrification similar to granules in the full-scale partial-nitritation anammox system. The potential for microbial communities to affect simultaneous nitrification, anammox and denitrification was expressed by FA-MFC design, which suitably diffused oxygen from the air into the reactor.

[Supported by grants from NRF-2018R1A2A3075622]

B030
Targeted Isolation of DNRA Bacteria from Denitrification-dominant Agricultural Soils Using a Novel High-throughput Screening Method
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Recently, scientific interest in the soil DNRA has been reinvigorated, motivated by its potential in limiting nitrogen loss and greenhouse gas emissions from agricultural soils. The traditional strategy that had been used for isolation of DNRA organisms require extensive menial labor for screening out a few DNRA isolates from overwhelming number of denitrifiers when applied to denitrification-dominant agricultural soils. Here, we have developed a novel high-throughput screening method for targeted isolation of bacteria capable of actively transforming nitrate to ammonium via the DNRA pathway, utilizing the well-established salicylate method for ammonium detection and quantification. Reductive transformation of nitrate was examined for four DNRA organisms isolated from rice paddy soils using this rapid inexpensive screening method affiliated to Bacillus (belonging to Firmicutes phylum), Shewanella, Citrobacter, and Aeromonas (belonging to Proteobacteria phylum) genera. This novel screening method is anticipated to enable expansion of current library of soil DNRA organisms, which will lead to new opportunities for biotechnological applications of these lesser explored group of bacteria.

[Supported by Global Top Environment R&D Program Ministry of Environment, Republic of Korea]
B031
Dilution-to-Extinction Culturing Combined with Catalase Supplementation Yielded Diverse Previously-uncultured Oligotrophic Bacteria from Lake Soyang
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High-Throughput-Culturing method (HTC) based on dilution-to-extinction has been improved in various ways for the efficient isolation of unstably growing or uncultured bacterial groups. In a recent study, catalase supplementation into a culture medium as a hydrogen peroxide scavenger showed a great enhancement of cellular growth of previously uncultivated freshwater bacterioplankton, the acl clade. In this study, the catalase-amended HTC was applied to surface lake water collected from Lake Soyang every three months from November 2016 to August 2017. Cells in the water samples were diluted with sterilized lake water with a final density of 2 cells/ml and aliquoted into each well in multiwell plates with 10 U/ml of catalase. The multiwell plates were incubated at 20°C for 4 weeks and microbial growth was measured using a flow cytometer. Phylogenetic analysis of 16S rRNA gene showed that catalase-amended HTC yielded many oligotrophic bacterial isolates belonging to diverse freshwater bacterioplankton clade, such as acl, aclV, and LD28. Particularly, bacterial strains belonging to the acl and aclV clades accounted for approximately 25% of growth-positive strains. This result showed that acl and aclV clades of Actinobacteria, known to be abundant in freshwater environment but difficult to be isolated, can be isolated more efficiently by the simple catalase-amended dilution-to-extinction culturing method.

[Supported by a grant of the Mid-Career Research Program through the NRF]

B032
Importance of Functional Diversity in Assessing the Restoration of the Microbial Community after the Hebei Spirit Oil Spill in Korea
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Over 10 years after the Hebei Spirit oil spill, the concentrations of pollutants, such as TPH and PAHs, in spilled crude oil have recovered to background levels, but in some areas, the environment has not fully recovered. In particular, PAHs were more resistant to degradation, and their persistence could have deleterious impacts on the sediment ecosystem. The objective of present study is to evaluate the microbial recovery of coastal sediments from the HSOS by analyzing the structure and diversity of the microbial community and its functional contribution to PAHs degradation. There was a significant difference in taxonomic abundance between the 2007 sediment and the sediments collected over seven years old. In contrast, there was little difference between sediments after 2014. Although the overall microbial abundance in 2014 and 2016 was similar, several taxa associated with PAHs degradation showed higher abundance in 2014 than in 2016. That is, even if the pollutants are completely degraded, the microbial community has not yet completely recovered from the contamination. The evaluation of microbial ecosystems in contaminated environments should consider both the fate of pollutants and the dynamics of microbial species that make functional contributions to the degradation of pollutants.
**B033**

**Metagenome and Metatranscriptome Analysis Reveal the Key Microbes and Metabolic Features during Fermentation of Ganjang, Korean Traditional Soy Sauce**

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Ganjang samples were collected periodically during the entire fermentation periods and the metagenomes analysis of ganjang samples were conducted to investigate the key microbes and their metabolic features during ganjang fermentation using Illumina MiSeq approaches. The community analysis using amplicon-based and raw metagenome sequencing data revealed that *Tetragenococcus, Chromohalobacter, Marinobacter, Halomonas, Idiomarina, Bacillus, Staphylococcus* and *Corynebacterium* showed predominant bacteria and *Aspergillus, Wickerhamomuces, and Debaryomyces* showed predominant fungi during ganjang fermentation. To reconstruct the genomes of key microbes during ganjang fermentation, the assembly and binning process were conducted using ganjang metagenome data. The total 16 genomes were reconstructed through assembly and binning process. Most of binned genomes showed high genome quality (> 90% identity, < 5% contamination rate) and the binned genomes covered most of metagenome reads in ganjang samples, suggesting that most of microbial genomes in ganjang samples were well reconstructed. The metabolic features against binned genomes during ganjang fermentation were investigated by KEGG and CAZyme analysis and fermentative metabolic features during ganjang fermentation were investigated through transcriptional analyses. These results reveals the fermentative metabolic features of microbes in Korea traditional ganjang, contributing to understand the fermentation properties of ganjang.

**B034**

**Metagenome-based Analysis of Antibiotic Resistome and Mobilome in Urban Sewerage System**

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Urban wastewater is considered as a significant source of antibiotic resistance genes (ARGs) that spread into the environment. However, the role of sewerage system in shaping wastewater resistome remains poorly characterized. In this study, we analyzed the metagenomes from various sites in a municipal sewerage system, including untreated and treated wastewater of university hospitals, intercepting sewer contents, and the influent, effluent and sludge of wastewater treatment plants (WWTPs), tracing variations in bacterial community, resistome and mobilome throughout the system. The ARG diversity peaked in the sewers contents rather than in the samples from hospitals and WWTP. The density of ARGs, however, was highest in untreated hospital wastewaters. Wastewater treatment processes resulted in dramatic reduction in ARG density, but less in ARG diversity. The ARGs frequently associated with class 1 integron, such as *sul*1, *aadA, aac(6)*, *blaOXA*, and *blaGES*, constituted the core ARGs of the sewerage system. Notably, clinically relevant ARGs such as *blaKPC-1, blaKPC-2, blaNDM, blaCTX-M*, *mcr* were detected in untreated hospital wastewater and sewer contents, but not in the treated wastewaters. Our results suggest that the urban sewerage systems convey highly diverse resistome including clinically relevant ARGs. [This work was supported by a grant from the Korea Ministry of Environment as the Environmental Health Action Program.]
B035

Changes in Bacterial Community Structure during Shrimp Production in a Biofloc-based Aquaculture System

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Shrimp (Litopenaeus vannamei) aquaculture is one of the most important aquaculture industries in Asia. The Biofloc technology that is based upon zero or minimal water exchange has been recently employed in L. vannamei aquaculture and led to dramatic increase in shrimp production. Bioflocs consist of a variety of bacteria, fungi, microalgae, and other suspended organisms and play a key role in the growth of shrimp via removal of toxic nitrogen species and serving as nutritional feed. However, bacterial community structure of biofloc-based aquaculture system and variation of the community during shrimp rearing have been rarely identified. In this study, we investigated the bacterial community structure of rearing water and bioflocs in the shrimp aquaculture using 16S rRNA gene amplicon sequencing. The 16S rRNA gene sequence analysis revealed that members of the Rhodobacterales, Flavobacteriales, and Chitinophagales were dominant in the bioflocs, while members of the Flavobacteriales, Chitinophagales, and Balneolales were predominantly present in the rearing water throughout the entire aquaculture period. Albeit present in minor, bacterial groups of ammonia oxidizing bacteria and nitrite oxidizing bacteria were detected and their relative abundances in the bioflocs were 200 times higher than those in the rearing water.

[This study was supported by a grant from the Collaborative Genome Program of the KIMST funded by the MOF (No. 20180430), Republic of Korea]

B036

Application of Beneficial Bacteria Changes the Rhizosphere Bacterial Community of Soybean

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The rhizosphere is the part of the soil ecosystem where plant roots, soil and the soil biota interact with each other. Rhizosphere bacterial community composition is likely to be determined by many different selection factors that influence the growth and size of different bacterial populations. In the present study, the MiSeq Illumina sequencing platform was used to analyze the soybean rhizosphere bacterial community composition. The rhizosphere bacterial community compositions and diversity were altered by application of beneficial bacterial strains (Pseudomonas montelli : SHK11, Novosphingobium sedimenticola : SHK7, Pseudomonas saponiphila : GHR1-1). In the soils, the predominant phylum was Proteobacteria (41%) and followed by Acidobacteria (15%), Actinobacteria (11%), Bacteroidetes (4%), and Chloroflexi (3%). The soils treated with beneficial bacteria had higher abundance of phyla such as Bacteroidetes, Candidate division WPS-1 and Firmicutes than the control soil. The abundance of the phylum Acidobacteria and Actinobacteria was reduced in beneficial bacteria treated soils.

[Supported by grants from RDA]
**B037**
**The Ecological Role of Marine Algicolous Fungi *Arthrinium* spp. in Defending Algal Pathogens**
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Marine *Arthrinium* spp. has been reported as an internal symbiotic fungi of seaweed, especially brown algae. However, until now there has been no specific proposal to explain their ecological role in symbiosis. In this study, 28 strains of marine *Arthrinium* spp. isolated from seaweeds, intertidal sediments, and sandfish eggs were cultured and extracted with MeOH and EtOAc, and antimicrobial activities were investigated to evaluate biological control ability. As a result, 13 strains showed antifungal activity against algal pathogenic fungi, *Asteromyces cruciatus* SFC20161110-M19 or *Lindra thalassiae* NBRC106646. In particular, 12 strains inhibited the growth of *L. thalassiae*, a pathogen of brown algae causing raisin disease. In our previous study, most of the marine *Arthrinium* strains showed high antioxidant activity, and some also exhibited quorum sensing inhibitory activity. Our results therefore demonstrate that marine algicolous *Arthrinium* spp. can support regulate reactive oxygen species and protect against pathogens in symbiotic algae. In other words, they form a symbiotic relationship in a way that increases the viability and environmental competitiveness of symbiotic algae in exchange for nutrients such as laminarin and mannitol, the photosynthetic products of brown algae.

**B038**
**The Lichenized Fungal Species *Psoroma hypnorum* in Antarctica Diverged from the Arctic**
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The lichenized fungi *Psoroma hypnorum*, the type species of that genus, is prevalent both in near-polar regions. In order to have insights into evolutionary and phylogeographic histories of the bipolar-population species, we extensively sampled *P. hypnorum* specimens from Alaska and Norway in the Northern Hemisphere and from southern Chile, Falkland Islands and King George Island in Southern Hemisphere. We subsequently generated DNA sequence dataset, which consists of four loci; 5.8S-ITS2 rDNA, nuLSU, MCM7, and mtSSU. Phylogenetic analyses using the multi-locus molecular sequences resulted in two distinctly separated monophyletic groups, each of which was composed of the Southern Hemisphere and Northern Hemisphere isolates, respectively. *P. hypnorum* isolates from the Northern Hemisphere were more heterogeneous than those from the Southern Hemisphere. In addition, our phylogenies shows that the most recent common ancestor of the Northern Hemisphere isolates predates that of the Southern isolates. Along with the result that *P. hypnorum* was colonized earlier in near-Arctic regions, this result indicates that the species in the Southern Hemisphere, especially from the Antarctica, were migrated later from the Northern Hemisphere. We here shows the geological times of the colonization in near-Arctic and migration to the Antarctica that were secondarily calibrated by fossil records of the *P. hypnorum* neighbors. [Supported by the Korea Polar Research Institute (Grant PE19090)]
**B039**

**Comparison of the Fecal Microbiota in Arctic Migratory Birds during Breeding Season**

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The gut microbiota of vertebrates play an important role in affecting host health. Despite the large amount of data available on the mammals gut microbiota, relatively no information available on the avian gut microbiota. Migratory birds in arctic have a unique behaviors that enables them to breed successfully during the mating seasons. In this study, we collected faecal samples to characterize the prevalence of gut bacteria of three migratory arctic birds (Snow bunting, Sanderling and Pink footed goose) by using Illumina Miseq platform to sequence bacterial 16S rRNA gene. Next generation sequencing has been widely used to characterize the prevalence of fecal bacteria. Our finding indicated that three arctic birds were dominated by three bacterial phyla (Proteobacteria, Firmicutes and Bacterioidetes) and that each species has its own species-specific gut microbiota. There were significant differences in the bacterial communities of omnivorous and herbivorous arctic birds. The results from this study suggest that the bacterial composition among those birds possibly altered by its diet during the breeding season.

[This study was supported by Korea Polar Research Institute, "Basic research for behavioral ecology in Sirius Passet, North Greenland" (PM19370).]

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**B040**

**Comparative Diversity of Marine Arthrinium by Substrates: Egg Masses of Sailfin Fish and Seaweed**

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The genus *Arthrinium* are well known as producer of various bioactive compounds. Most of *Arthrinium* are plant-associated fungi and isolated from territorial substrates. Recent study, *Arthrinium* species were reported from seaweed and eggs of sailfin fish. According to the general fact, the sailfin fish spawn on seaweed. For this reason, seaweed and the eggs are assumed to have physical correlation and same *Arthrinium* diversity. To verify the assume, we collected marine sources such as unidentified seaweed, *Sargassum fulvellum*, *Agarum cribrosum*, and eggs of sailfin fish from 8 regions in South Korea and isolate the *Arthrinium*. Total 25 *Arthrinium* strains were isolated and identified by molecular analysis using internal transcribed spacer (ITS), beta-tubulin (TUB), and translation elongation factor-1α (TEF) region. For the phylogenetic analysis, Bayesian analysis was conducted by MrBayes v3.2.1. Eleven *Arthrinium* species were identified as novel candidates and four as recorded species. As far as I know, there have not been many *Arthrinium* reported from marine. On the other hand, unlike expectation, *Arthrinium* from seaweed or eggs of sailfin fish were few overlapped each other. As *Arthrinium* are potential producer of high added value bioactive compounds, it is important to find out the correlation and origin of *Arthrinium* species with symbiotes. [Supported by National Research Foundation of Korea (NRF) funded by the Korean government (MSIT) grant number 2017R1A2B4002071]
B041
Antibacterial and Antitumor Activity of Culturable Micromonospora sp. Isolated from Monochoria korsakowii Plant in Freshwater, Korea
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The genus Micromonospora belonging to the family Micromonosporaceae are widely distributed in various environments: soils, sea sands, near-shore sediment, marine sponge, plants and well known for producing bioactive substances. Nevertheless previous reports for bioactive substances produced by endophytic Micromonospora sp are a few. In this study, to obtain bioactive substances, we have collected lake side plant and then isolated bacterial strains. Total 74 bacterial strains in the 25 genera, were isolated from Monochoria korsakowii and 42 strains of them, are actinomycetes. Interestingly, 33 of 49 strains were isolated from the root-hair, were included to the genus Micromonospora while none of shoot and root part. Also they made distinct 8 clade within the genus clade based on 16S rRNA gene sequence. Isolated 42 actinomycetes strains were cultivated 2 weeks using R2A broth and then individual culture broth was tested for antibacterial activity against 10 bacterial strains by drop test. Finally, we have obtained M. wenchangensis M 2 and M. matsumotoense M 14 and M16 strains that showed antibacterial activity against specific Gram positive bacteria (Staphylococcus and Bacillus). Especially, Crude cultured broth of M 2 showed 30% anticancer activity to BF16-F10, MCF7. This results was similar to previous reports of enediyne antitumor antibiotics, Paulomycins and Tetrocarcin etc. At present, isolation of bioactive compound and elucidation of structure are remaining.

B042
The Bacterial Community Structures at Deep Sedimentary Biosphere of South Pacific Gyre
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The IODP (Integrated Ocean Drilling Program) Expedition 329 had been progressed to study the subseafloor life of the SPG (South Pacific Gyre). SPG is the largest ultra-oligotrophic environment on the Earth and the amount of organic compounds by primary production supplied to abyssal sediment is low. Among the drilled 7 sites (U1365~1371), 6 sites (U1365~1370) tended to penetrate oxygen more than 50mbsf. However, U1371 showed a significant difference that TOC concentration is relatively higher than other sites in overall depth and oxygen penetration is detected only within 1mbsf. Therefore, we wanted to know the microbial community structure forming the deep biosphere at each site by selecting several depths exhibiting distinct features at each 3 sites (U1365, U1370, U1371). The 16S rRNA amplicon analysis was performed to compare the microbial community pattern difference between the three core sites. As a result, Chloroflexi (Dehalococcoidia) was highly dominant at majority of depths in the three sites. The distinctive feature of U1371 is figured out that the bacteria such as SAR406, SAR202 and Desulfobacteriales which are able to use nitrate and sulfate instead of oxygen can be detected correspondingly to characteristics of each depths. Furthermore, the result of correlation analysis between bacterial composition and environmental factors reveals Dehalococcoidia indicate negative correlation with oxygen and positive correlation with chloride.
[Supported by KIOST(PE99622)]
**B043**

**Blooming of Human-related Antibiotic Resistance Genes in Anthropogenically Influenced River**

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Anthropogenic activities have been considered to have significant impacts on environmental resistome. Ecological and evolutionary processes including the introduction and dissemination of human-related antibiotic resistance genes (ARGs) into the environment, however, remain to be fully understood. In this study, we analyzed ARGs in Han River metagenomes from the sites under various human impacts. Anthropogenically impacted river samples harbored more ARGs common to human gut resistome, compared to relatively less polluted samples. Comparison of the β-lactamase repertoires in the river, gut, and pathogens demonstrated that the river resistome carried the most diverse ARGs, covering more than 50% of β-lactamases in pathogens. Furthermore, some ARG sequences (>99% identity) were shared between the river metagenomes and the pathogen genomes, whereas the sequences of phylogenomic marker genes were less shared, suggesting horizontal gene transfer (HGT) of ARGs, presumably caused by anthropogenic impacts on the river. These ARG sequences dominated the river resistome and were frequently associated with mobile generic elements, also supporting the importance of HGT in the spread of ARGs in the environment. Our study suggests that mobile ARGs commonly present in human gut and pathogens are the major component of river resistome driven by anthropogenic impacts.

[This work was supported by the Korea Ministry of Environment as ‘the Environmental Health Action Program (2016001350004)’.]

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**B044**

**Effects of Feed Additives on Growth Performance and Microbial/Viral Composition in Broilers**

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Following the ban on antibiotics, various feed additives such as probiotics, prebiotics, and bacteriophages were found to replace antibiotics to improve the performance of broilers. However, there is still a lack of researches on the effects of these substitutes on chicken intestinal and environmental microorganisms. Here, we evaluated the effects of feed additives (bacteriophage, probiotics, and antibiotics) on the growth performance and microbial/viral compositions in the broiler house. Among the additives, bacteriophage showed higher growth performance than other groups. Both gut and environment microbial compositions showed a similar pattern. Overall, Firmicutes was significantly increased during the experiment period. Without the bacteriophage and antibiotic-treated group, the proportion of Proteobacteria was significantly decreased during the experiment period. Contrariwise, Actinobacteria was significantly increased without an antibiotic group. In viral classification, Streptococcus related bacteriophage was highly counted. High pathogenic avian influenza (HPAI) virus was not detected. Our results provide the effects of feed additives on broilers gut microbiome and the results will be used as a basis to choose adequate feed additives in the poultry industry. [This study was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2016R1C1B2016246) and Brain Korea 21 plus program.]
B045
Variation of Methanotrophic Communities by Different Methane Flux Regimes in the Mud Volcano of the Canadian Beaufort Sea
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To obtain knowledge on the spatial variations of methanotrophic guilds along the methane flux regimes, we performed geochemical and microbiological analyses within a mud volcano (MV420) of the Canadian Beaufort Sea. Sediments were collected from visually discriminative chemosynthetic fields, bare of organisms (BO) with the naked eye, covered with bacterial mats (BM), or siboglinid tubeworms (ST) of MV420 and reference site. The methane flux decreased in the order of the BO, BM and ST sites. With the down core stratification of biogeochemical and microbial profiles within each site of MV420, lipid biomarker and 16S rRNA analyses revealed the spatial difference of aerobic methane oxidation (MOx)- and anaerobic methane oxidation (AOM)-related groups along the sites of MV420, which were distinctly different with the reference site. MOx-related bacteria, Methylococcales dominated the surface layer of BO site whilst AOM-related archaea, mostly ANME-3 and sulfate reducing bacteria of Desulfobacteraceae and Desulfobulbaceae were predominant in the sediments of BO and ST sites. Accordingly, our results suggest that a niche diversification within this MV system has shaped distinct methanotrophic communities due to the availability of electron acceptors in association with varying degree of methane fluxes and bioirrigation activity.
[Supported by the KOPRI, KIMST, and the David and Lucile Packard Foundation]

B046
Characterization of High Density DBP(dibutyl phthalate) Degrading Bacterium, Newly Isolated Novosphingobium sp. ABRDHK-2
Hye Kyeong Kang, Byung-Gon Ryu, Ji Young Jung, Sang-Soo Han, and Hyun Mi Jin*
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Dibutyl phthalate is (DBP) the top priority toxicant responsible for carcinogenicity, teratogenicity and endocrine disruption. This study demonstrates the DBP degradation capability of the newly isolated bacteria from nakdong-river samples. The isolated bacterium was designated as Novosphingobium sp. ABRDHK-2 after transmission electron microscopy, Gram-staining, 16S-rRNA gene identification and phylogenetic studies. Growth of ABRDHK2 occurred at 15-40°C, pH 5.0-8.0, with 1% (w/v) NaCl. 16S rRNA gene sequence analysis of strain ABRDHK2 showed highest sequence similarity to Novosphingobium aromaticivorans DSM 12444T (97.93 %). The DNA G+C content was 66.07 mol%. It was able to grow on dimethyl phthalate(DMP), Diethyl phthalate(DEP), Bis(2-ethylhexyl) phthalate(DEHP). It degraded 70% of the initial DBP in minimal salt medium for 6 days and can degrade from 10 ppm to 4000 ppm.
B047
Influence of Inoculated Microorganisms on Plant Rhizosphere
Ju Hee An, Songhwa Kim, Shailesh Sawant, Mee Kyung Sang, Hang-Yeon Weon, and Jaekyeong Song*
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The rhizosphere of a plant becomes a habitat of various microorganisms. Diverse microorganisms affecting plants have been discovered and studied, but the effect of plant-beneficial microorganisms on rhizosphere community is unclear. The present study was conducted to investigate the impact of three microbial inoculants, Trichoderma, Rhodobacter, and Streptomyces on the rhizosphere bacterial community of pepper, cucumber, and ginseng respectively. The MiSeq Illumina sequencing platform based on 16S rRNA gene was used for microbial community analysis. Rhizosphere bacterial diversity decreased in all three crops as compared to the control. At the Phylum level, in cucumber Actinobacteria increased significantly in the treated pot and at the class level Alphaproteobacteria increased in all crops than the control. The results from this study show that inoculation of microorganism changes the rhizosphere microbial community structure.

[Supported by grants from RDA]

B048
Metagenomic Insights into Potential Impacts of Tetracycline on the Human Intestinal Microbiota Composition and the Emergence of Antibiotic Resistance in a Chemostat Model
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Microbial Research Department, Nakdonggang National Institute of Biological Resources (NNIBR)

The stable human intestinal microbiota could be altered by ingestion of antibiotic residues in animal-derived foods. In this study, we determined by metagenomic approaches if tetracycline residue can impact the microbial community composition and antibiotic resistome in human fecal samples. The effects of 0.015-150 µg/ml tetracycline in 3% (w/v) human fecal suspensions were investigated using chemostat model. The evaluation of intestinal bacterial community changes showed that tetracycline could lead to differences in the intestinal microbiota composition. In particular, metagenome-based taxonomic profiling showed that Bacteroides (B.) species are major resistant microbes increased by tetracycline treatment. B. ovatus and B. strain 2_1_22 increased at tetracycline concentrations of 1.5 and 15 µg/ml from 2 days after tetracycline treatment and B. caccae increased at 150 µg/ml. 13 SEED subsystems was shifted at 1.5 µg/ml or above, and it appeared to be correlated to the increase of Bacteroides. The total number of TRGs was slightly increased at 1.5 and 15 µg/ml and highly increased at 150 µg/ml. In addition, there were also the increase of different type of antibiotic resistance genes. Our investigation showed that tetracycline exposure in a dose-dependent manner can impact the intestinal microbiota with Bacteroides sp. as a key tetracycline-resistant microbial group. In addition, certain type of antibiotics could also influence the profile of antibiotic resistance genes.
B049
Ameliorative Effect of Isolate Leclercia adecarboxylata MO1 on Cucumber Plant under Zinc Stress
Sang-Mo Kang, Muhammad Aaqil Khan, Yu-Na Kim, Chang-Wook Park, Hee-Soon Park, and In-Jung Lee*
School of Applied Biosciences, Kyungpook National University

Due to global industrialization, hazardous pollutants such as Zinc are released and accumulated in soil because of industrial operation like smelting and mining. The increase in zinc concentration in the soil hinders the growth and metabolic process of the plant which result decrease in crop yield and its production. Plant growth promoting rhizospheric bacteria (PGPR) have been reported that ameliorate the adverse effect of heavy metals (Zn) and regulate plants growth. This study plant growth promoting rhizospheric Leclercia adecarboxylata MO1 was used that produce siderophore, indole acetic acid and have the capability to solubilize insoluble zinc. Zinc stress were applied to cucumber plants along with the combine inoculation of isolate MO1 that ameliorate and reduce the toxic effect of zinc stress to cucumber plants and enhance growth attribute, biomass and chlorophyll contents compared to control plants (zinc only). Furthermore, inoculation of isolate MO1 significantly decreased endogenous salicylic acid content and enhanced mitigation of Zn stress in cucumber plants. In conclusion, based on the ameliorative qualities and plant growth-promoting activity of the strain MO1, we show that it can make an important contribution to mitigating zinc stress relief, increase plant growth and also be utilized as an eco-friendly bio-fertilizer.

B050
Diversity, Properties of Benzo(α)pyrene Degrading Bacteria Isolated from Polluted Soil
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Chungnam National University

The purpose of this study is to obtain benzo(α)pyrene-degrading bacteria from soil and to analyze the enzymatic activity of the isolated strains to degrade benzo(α)pyrene. The soil samples were collected at the two garbage burning sites where exhaust gas exposure of vehicle was severe. A total of 158 strains were isolated from the first site and 123 strains from the second site, securing a total of 281 strains. Bacteria grown from Bushnell Haas agar (BHA) containing 10 ppm of benzo(α)pyrene were picked up by random selection with various morphologies. The isolates were identified based on the 16S rRNA sequence. As a result, Streptomyces spp. were most abundant, comprising 48% of the total isolates. The 281 strains were tested for chromogenic assays to determine the potential of enzyme activity. To investigate the enzymatic activity of peroxidase, laccase and dehydrogenase, three dyes Poly R 478, ABTs and INT were used. Chromogenic activities were positive for 84 strains with Poly R 478, 92 strains with ABTs (2,2′-azino-bis(3-ethylbenzothiazoline-6-sulphonic acid), and 142 strains with INT (Iodonitrotetrazolium chloride). The chromogenic activity was compared with phylogenetic trees based on 16r RNA sequence. Each clusters had specific activity and each isolate showed two chromogenic activities. Many of the isolated bacterial strains had benzo(α)pyrene degrading potential, which could be further developed for efficient use in biodegradation of benzo(α)pyrene.
B051
Characterization of Novel Mono-aromatic Compounds Degrading Bacterium, *Rhodococcus* sp. Strain ABRD24, Using Genomic and Metabolic Analysis
Hyun Mi Jin, Hye Kyeong Kang, Sang-Soo Han, Ji Young Jung, Byung-Gon Ryu, and Eu Jin Chung*  

NNIBR

An enrichment culture was established using freshwater containing BTEX compounds to isolate a BTEX degrading bacterium from contaminated freshwater. The genomics and metabolomics analysis were established for the BTEX-degrading bacterium which was isolated from slurry type enrichment system with BTEX as a sole carbon and energy source. Strain ABRD24 which have degradation abilities for monoaromatic compounds were isolated from enrichment system. The monoaromatic compounds degradation pathway was estimated from genomics and GC/MS based metabolomics analysis. BTEX-degrading bacterium, *Rhodococcus* sp. ABRD24, were isolated from contaminated river sediment with aromatic compounds. Degradation tests revealed that isolated strains had a great degradation ability for BTEX compounds in freshwater sediment. In addition to physiological analysis, complete genome sequence and detected metabolites showed that strains harbors genes encoding many oxygenase such as toluene mono-oxygenase and hydroxylation enzymes responsible for degradation of various aromatic hydrocarbons. Although annotated genome information does not contain xylene monooxygenase, genomic and metabolic analysis results support that three type of xylene compounds can degrade by toluene monooxygenase. Further studies may be characterize the new gene cluster of the new pathway and discuss their functions in BTEX biodegradation of these strains.

B052
Dissolved Organic Carbon Dynamics and Its Relation to Microbial Community Succession during Ecosystem Development Following Deglaciation
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Korea Polar Research Institute (KOPRI)

Understanding of soil organic carbon (SOC) dynamics is important to ecological succession, because the change in the quality and quantity of soil carbon is closely related to the microbial species turnover. Many studies have been conducted separately on SOC dynamics and microbial community thus, we investigated the linkage between SOC dynamics, particularly DOC more readily available to microbes, and microbial community composition together during succession on glacier foreland in high Arctic. In this study, we applied high-resolution Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR MS) to investigate the molecular characteristics of dissolved organic carbon (DOC) and their dynamics along the deglaciation. Soil samples were collected in the foreland of the Midtre Lovénbreen glacier (78.8˚N, 12.0˚E) in Ny-Ålesund, Svalbard, Norway. As a results so far, the diversity of DOC molecules shows unique pattern, especially in Proteins-, Lipids- and Lignins-, following deglaciation. Changes in DOC chemical composition is related more strongly with RNA-based community dynamics of bacteria and protist than fungi and archaea. It will be discussed which factor, such as microbial taxa and abiotic factor, drives the unique pattern of DOC molecules with further analysis.

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**B053**

**Investigation of Biocontrol Activity of Bacteriophage against Bacterial Wilt and Effect on Microbial Community**

Seung Yeup Lee, Hyo Jeong Kim, Roniya Thapa Magar, Kihyuck Choi, and Seon-Woo Lee*

*Department of Applied Bioscience, Dong-A University*

*Ralstonia solanacearum* is a devastating plant pathogenic bacterium causing lethal wilt in members of solanaceous plants and is difficult to control the wilt disease. As the environmental problem have become more prominent, bacteriophage, environmentally friendly control method, was selected to investigate their potential to manage bacterial wilt. We isolated bacteriophages from field soils cultivating various crops using 5 different strains of *R. solanacearum*. As a result, 72 phages were isolated and they were divided into ten distinct groups based on their host range and plaque size. Representative phages of the groups were further characterized for their morphology and physiology via transmission electron microscopy, genomic characteristics, phage stability at various temperature and pH. Three phages from each group were typical members of podoviridae with double strand DNA genome, and one phage was typical member of inoviridae containing single strand DNA genome. Most of the phages were stable in wide range of temperature and pH. Phage application into soils with tomato plants exhibited bacterial wilt prevention. Rhizosphere microbiome community of tomato plants treated with a phage RpY1 was analyzed and phage application at a density of $10^8$ pfu/g of soil did not significantly alter microbial community structure.

[Supported by grants from IPET]

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**B054**

**Biocontrol Potential of Lytic Bacteriophage Cocktail against Bacterial Wilt by *Ralstonia solanacearum***

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Bacteriophages infecting diverse bacteria are good candidates for the environmentally friendly biocontrol of many plant bacterial diseases. In this study, we isolated bacteriophages infecting *Ralstonia solanacearum* causing bacterial wilt in Solanaceous plants from soil samples of various crop-cultivating fields of Korea. Some of the selected phages were characterized and tested to check if they have biocontrol potential against *R. solanacearum*. Morphological characterization of phage T1 and Y2 using transmission electron microscopy (TEM) revealed that both phages shared similar characteristics with other members of the Podoviridae family. Complete genome analysis demonstrated that the phages contain 40 kb genome size with similar features to Podoviridae family. Phage T1 was found to be most stable at lower temperature compared to higher temperature. Similarly, phage T1 was more stable at basic or neutral pH. Treatment of phages T1 and Y2 at $10^8$ pfu/g of soil either as individual or by cocktail in the rhizosphere of tomato cultivar Zuiken, a susceptible cultivar, revealed biocontrol activity against bacterial wilt. Similarly, 10-fold dilution of both phages from previous experimental setup were also able to suppress the plant disease. In addition, both T1 and Y2 phages were stable in upland and nursery soil compared to forest soil over 2 weeks. We are currently investigating the biocontrol potential of these phages cocktail by mixing with adjuvant and emulsifier.
B055
Influence of Soil Microbiome on Bacterial Wilt Disease of Tomato Plant
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Department of Applied Biology, Dong-A University

Microbiota associated with the plants plays an important role of plant growth and health. In this study, we hypothesized that the treatment of soil microbiome contributes to form tomato-specific rhizosphere microbiome and may influence plant traits such as disease resistance. To test this hypothesis, we first developed an analysis system for plant-microbiome interaction (ASPMI). The effects of four different natural soil microbiomes were tested on bacterial wilt occurrence in a susceptible and resistant cultivar of tomato plant using ASPMI. Among four different soil microbiomes, upland and forest microbiome were selected for further research according to the disease response. For the selection of core microbiome contributing to disease progress, we deeply analyzed rhizosphere microbiome of both cultivars inoculated by upland and forest microbiome under ASPMI in the different time points. In the analysis of beta-diversity, the bacterial community was clustered by the treatment of microbiome regardless of cultivars and time points. Interestingly, several OTUs were only observed in the treatment of upland microbiome, showing less disease occurrence in the resistant cultivar of tomato. Especially, the relative abundance of OTU33 belongs to OD1 phylum negatively correlated with OTU7 belongs to R. solanacearum. Taken together, rhizosphere microbiome affects positively or negatively disease resistance of tomato.

[Supported by grants from Woo Jang-Choon program of RDA]

B056
Isolation and Characterization of Anaerobic Bacteria from Tidal Sediment in Korea
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National Marine Biodiversity Institute of Korea

Tidal sediments are characterized by nutrient inputs from the open sea and the hinterland resulting in a high microbial turnover and mineralization of organic matter. Especially, the western coastal area of the Korean Peninsula consists of muddy-tidal flats. The microbial diversity of tidal flats has been lots of studied, however there are few studies about the isolation of anaerobic bacteria. Recently, we isolated and characterized anaerobic bacteria from tidal sediments in Korea. From our enrichment performed under anaerobic condition (30-37°C), 30 strains were isolated and identified by the 16S rRNA gene sequence analysis. All tested strains were affiliated with phylum Clostridia and Bacteroidia. The end products of glucose fermentation were identified as ethanol and acetate, whereas gaseous product was mainly CO₂ and H₂. Three strains belonging to the Bacteroidia were found to be able to iron (Fe³⁺) corrosion. This study showed that anaerobic microorganisms in the tidal sediments may serve as a potential candidate for research and biotechnological applications.
B057
Temperature Dependent Microbial Community Dynamics Modulates Methane Cycle in Permafrost-affected Soils
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Thawing permafrost promotes microbial degradation of carbon sink leading to the biogenic production of greenhouse gases such as carbon dioxide and methane. This study aims to understand how methane cycle is modulated by microbial community changes driven by different temperatures and incubation times under anaerobic condition in permafrost-affected soils. Alaska Council soil cores were incubated at 5°C, 15°C and 25°C with 13C-labelled substrates for 11 months under anaerobic condition. Soil DNA was extracted and then 16S rRNA gene targeting bacteria and archaea was sequenced. There are distinct patterns in bacterial and archaeal community composition between active layer and permafrost. In permafrost three methanogenic genera responded distinctively to different temperature and incubation time settings. There is a clear shift in major methanogen lineage from low to higher temperatures. ‘Ca Methanoflorens’ was replaced by Methanosarcina at 15°C and 25°C, suggesting the modulation in methane production at different temperatures occurs by turnover among major methanogen lineages differing in their temperature specificity. These results help to understand the effect of different temperatures and incubation times on metabolic interactions between anaerobic microbes in a moist acidic Arctic tundra.

[This research was supported by a National Research Foundation of Korea Grant from the Korean Government (NRF-2016M1A5A1901769).]

B058
Dissemination of Antibiotic Resistant Genes in Freshwater from the Wastewater of Livestock and Aquaculture Farm
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Antibiotics used in livestock are released into the environment and affect the accumulation of antibiotic resistance genes (ARGs) and antibiotic resistant bacteria (ARB). In particular, wastewater from livestock farm and aquaculture is one of the major contributors to antibiotic contamination in the environment. This study identified the changes in bacterial community and ARGs in 6 rivers in Korea. Samples were obtained from 14 livestock and 4 fisheries. And a total of 57 samples were used for the metagenome analysis. The dominant genus in all samples was Flavobacterium, Limnohabitans, Fluviicola, and Sediminibacterium. A total of 193 subtypes within 15 ARG types were detected in all samples, and the most common types in the environment were Sulfonamide, Aminoglycoside, and Tetracycline. Total relative abundance of ARGs increased about 4 times in the effluent and decreased in the downstream water, but relatively higher than upstream water. Arcobacter, Novosphingobium, and Acinetobacter were increased in the effluent samples, and the pattern of abundance change was similar to that of ARGs. Therefore, this study suggests that the intensive use of antibiotics would lead a continuous influx of ARB and ARGs from wastewater into the environment, which would have a significant impact on aquatic environmental contamination and further on human health.
**B059**

**Effect of Intestinal Microbiota Change on the Control of Obesity by the Use of Dapagliflozin and Butyrate Combination in db/db Mice**

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A variety of drugs are used to improve obesity, a major risk factor for diabetes. Dapagliflozin (Dapa), a kind of sodium-glucose cotransporter-2 (SGLT-2) inhibitor, has recently studied to induce calorie loss and force glycosuria. However, SGLT-2 inhibitors alone do not result in significant weight reduction, and consequently, additional intervention are required to modulate adiposity. In diabetes-related microbiome studies, the abundance of butyrate-producing bacteria increased in normal human gut. Butyrate is a short chain fatty acid produced by gut microbiota fermentation, suggesting that it can control appetite by enhancing intestinal gluconeogenesis. To evaluate combination effects of Dapa and butyrate-induced gut microbiota changes in appetite regulation and body weight, we assigned six-week-old male db/db mice into four groups: vehicle with normal chow diet (NCD), Dapa with NCD, vehicle with 5% sodium butyrate-supplemented CD (NaB) and Dapa with 5% NaB. Dapa (1 mg/kg) was administered via oral gavage for six weeks. In two groups, vehicle with NaB and Dapa with NaB, showed decreased food intake and body weight. The gut microbiota of the Dapa and NaB combination group was characterized by the increase of Bacteroidetes to Firmicutes ratio. In genus level, the decrease of Adlercreutzia, Alistipes, Anaerotruncus, and Mucispirillum as well as an increase of Streptococcus in combination group. Especially, Streptococcus showed opposite correlation with total fat gain.

**B060**

**Bacteroides spp. Isolate from Human Gut Attenuates Chronic Metabolic Syndrome in a Mouse Model of Obesity**

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Gut microbiome is an important factor modulating immune and metabolic dysfunctions in development of obesity. As two dominant phyla in the human gut microbiome, the Firmicutes to Bacteroidetes ratio (F/B ratio) has been known as a microbial biomarker representing the obese status of host. Although the significant correlation between abundances of Bacteroides spp. and host obesity has been reported in many clinical and animal studies, the causal effect and related mechanisms of Bacteroides spp. on regulating obesity is not clear. In this study, we isolated Bacteroides spp. from healthy human fecal specimens and investigated the effect on weight gain and glucose intolerance in a diet-induced obesity mouse model. Bacterial strain was daily administered by oral gavage for 17 weeks (1X10⁹ CFU/mouse/day). The Bacteroides strain significantly reduced weight gain, glucose intolerance, adipose tissue weight, and metabolic inflammation. Immune cell profile also revealed that increased M2 polarization in white adipose tissue. Furthermore, Bacteroides colonization increased the inner mucus thickness and the expression levels of related genes (muc2, muc4, muc13, klf4, zo-1, and occludin) in colon tissues. Taken together, Bacteroides spp. isolate successfully alleviated obesity and metabolic disorder and can be applied to a microbiome-based therapy for obesity.

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B061

The Structure of Skin Microbiome is Dependent on Skin Sensitivity

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Sensitive skin is a syndrome occurring from unpleasant sensations such as burning, pain, pruritus, and tingling in response to irritation which normally should have not provoked such sensations. Sensitive skin has been explained by cutaneous, environmental, lifestyle, and endogenous factor. But until now, there has not been much research on skin sensitivity from the perspective of a skin microbiome. We focused on the relationship between skin sensitivity and skin microbiome. Bacterial and fungal community were analyzed by 16S rRNA gene and ITS1 region amplicon sequencing. Principal coordinate analysis (PCoA) identified a significant difference between non-sensitive and sensitive skin microbiome. In fungus, sensitive skin group was significantly diverse than non-sensitive skin group. *Mucor racemosus* and *Phanerochaete* were significantly increased in sensitive skin. The co-occurrence skin microbiome network more collapsed in sensitive skin group compared to non-sensitive skin group. A multivariate analysis suggested self-assessment sensitivity of individuals was related to the skin microbiome. The factors such as allergic experience, unpleasant feeling, and the extent of pimple also correlated with the bacterial and fungal community of sensitive skin. These observations show that skin microbial community shifts are related to skin sensitivity. This will provide the basis of the microbiome-based remedy on sensitive skin.

B062

A Snapshot of the Gut Microbiome of the Dead Sea Turtles

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The objective of this study was to characterize and compare the gut bacterial communities between Green turtle (GT), Longgerhead turtle (LT) and Olive Redley (OR) using high-throughput sequencing analysis targeting V1-V3 regions of the bacterial 16S rRNA gene. A total of fourteen intestine samples were collected from dead-frozen sea turtle. As the result of analyzing the microbial community in the intestines, 15 phyla were assigned. In most of the samples, Firmicutes, Bacteroidetes were dominant followed by Fusobacteria, Proteobacteria, Plancomycetes. The Firmicutes/Bacteroidetes ratio in GT was low, but significantly high in LT and OR. Although accurate information cannot be obtained in this study, quite important differences in the microbiota could be detected, which may be related to the influence of feeding.

[This work was supported by a grant from MABIK in-house program (2019M00300)]

Ethical Statement: The intestine samples were collected from dead sea turtles. All sea turtles were kept Authorized Organization, MABIK (as defined by the Korean Ocean and fishery regulation).
Metagenomic Analysis Exploring Taxonomic and Functional Diversity in Dermatologic Surgical Instruments

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Surgical suction device for laser treatment is diverse collection of human skin microflora as well as human cutaneous cells. Here, we investigated microbial diversity and functional implications through a high throughput metagenomic sequencing of DNA from laser instrument (suction tube and suction funnel) in dermatology. We obtained 47,630,203 and 48,890,010 high quality reads from suction tube and suction funnel, respectively. In taxonomic classification, the most abundant bacterial genera were Micrococcus luteus and Brevibacterium casei in suction tube, and Dermacoccus and Janibacter hoylei in suction funnel. Micrococcus luteus and Dermacoccus are found as a part of the normal flora of the mammalian skin. Janibacter hoylei was reported as a potential pathogen causing bacteremia in young children and Brevibacterium casei is the most frequently reported opportunistic pathogens from clinical specimens. Additionally, Alphapapillomavirus 8 (Human Papillomavirus 7, 40, 43, and 91), which is responsible low-risk mucosal and cutaneous lesions was found with small portion from suction funnel. We found 60,477 and 56,389 CDS from 15,462 (suction tube), and 16,702 (suction funnel) assembled contigs using prokka. The potential of medical device-mediated pathogen transmission among patients and doctors remain to be further studied. In summary, this study provide insight into microbial community including infectious microorganisms and their functions in laser surgical instruments.

Prevalence of Foodborne Pathogens from Livestock and Broiler Farm Environments in South Korea

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Foodborne pathogens from the food supply systems remains an ongoing concern. This study was conducted to investigate the prevalence of 10 foodborne pathogens in broiler and livestock farm environments of 5 farms (2 bovine, 2 swine, and 1 chicken farm) in South Korea. The prevalence of Bacillus cereus, Clostridium perfringens, Clostridium botulinum, Campylobacter, E. coli, Listeria monocytogenes, Salmonella enterica, Shigella, Staphylococcus aureus, and Yersinia enterocolitica were investigated. A total of 300 isolates in a range of environments common to most livestock farms such as soil, feed, and water sources as well as animal feces were cultured using selective agar media. The 16S rRNA gene sequencing and basic local alignment search tool (BLAST) were used to confirm the identity of the bacterial species. Pathogens tested were identified in all the samples regardless of the farms. Moreover, fecal samples showed the highest diversity of pathogens, containing 10 of the 10 pathogens tested. The highest occurrence of E. coli, Salmonella enterica, and Clostridium perfringens was confirmed in the samples tested. Monitoring contamination levels of food borne pathogens may help control the spread of bacterial species through the farm environment which is a natural source of these microorganisms.
[Supported by grants from Ministry of Food and Drug Safety].
B065
Microbial Communities Associated with Mercury Methylation in Vegetated Ganghwa Intertidal Sediments, Yellow Sea

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Methylmercury (MeHg) that acts as a neurotoxin is susceptible to biomagnification, which ultimately affect human health. MeHg is mainly produced by anaerobic microorganisms methylating Hg(II) to MeHg in environments. Some of sulfate- and iron-reducing bacteria (SRB & FeRB) have been well known as major Hg-methylators. Currently, the studies on hgcAB gene required for Hg-methylation have reported various Hg-methylating communities, including syntrophs, methanogens, and Firmicutes in freshwater environments. However, it is little known in coastal salt marsh with a large influx of organic and heavy metal contaminants. We investigated vertical distribution of total mercury (THg) and MeHg concentrations and microbial communities related to Hg-methylation in vegetated mudflat (VMF) and unvegetated mudflat (UMF) in Ganghwa salt marsh (GSM) where active metabolism of SRB and FeRB was detected. The concentrations of THg and MeHg were higher in surface sediments of the VMF site (42.5 and 0.3 ng g⁻¹ in dry weight, respectively) than in the UMF site (33.2 and 0.08 ng g⁻¹, respectively), which indicate that the presence of vegetation influences on distribution of THg and MeHg. The amplification of hgcA gene from all sediment samples indicated the presence of Hg methylation potential in the sediments of GSM. Further, we discuss the effect of vegetation on the distribution of microbial communities related to Hg-methylation.

[Supported by grants from NRF, MOF, and MOE]

B066
Prevalence and Diversity of Carbapenem-hydrolyzing β-Lactamases in Environmental Bacteria

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Carbapenems, known as “the last-resort antibiotics”, are effective against severe infections caused by multidrug-resistance bacteria. The emergence of carbapenem resistance mediated by carbapenemases is one of the major concerns in public health. In this study, the prevalence and diversity of carbapenem-resistant bacteria and carbapenem-hydrolyzing β-lactamases were explored in Han River. Carbapenem-resistant bacteria isolated from 15 river samples were examined by phenotypic and genotypic analyses. Among 220 meropenem-resistant isolates, a total of 78 strains were shown to have carbapenem-hydrolyzing activities. *Chryseobacterium* was the most abundant genus, followed by *Stenotrophomonas* and *Aeromonas*. Genes encoding carbapenemases were determined by PCR using 46 carbapenemase-specific primers. The most common carbapenemases were the CGB/IND type of subclass B1. In addition, blaIND, blaCGB, and blaPDC type sequences showed significant variations compared to the known sequences. Two genes belonging to clinical OXA-211 family β-lactamases were discovered in Han River. These results indicated that carbapenem-hydrolyzing β-lactamases were prevalent in the river environment. The presence of microbes carrying clinically related carbapenemases in river suggests the importance of antibiotic resistance surveillance in the aquatic environment.

[This work was supported by the Korea Ministry of Environment as the Environmental Health Action Program.]
B067
Effects of Invasive Spartina anglica on Microbial Communities in Intertidal Sediments of Ganghwa Island, Yellow Sea
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To elucidate the impacts of invasive Spartina anglica on microbial communities, we performed high-throughput sequencing of 16S rDNA in combination with biogeochemical analyses in the sediments inhabited by S. anglica (SA site) and unvegetated mudflat (UMF site). The rates of sulfate reduction and iron reduction were similar between the two sites. However, the reduced metabolites (NH₄⁺ and PO₄³⁻) in pore water were more accumulated at UMF than at SA, which indicates that SA sediment appeared to be relatively more oxidized than UMF because dense roots and well-developed rhizome of S. anglica supply oxygen to deeper layer. As the analysis of 16S rDNA, microbial diversity and richness analysis conducted at three layers (0-2, 4-6, and 8-10 cm) were higher in SA site than in UMF site. In SA site, microbial community structure appeared to be similar within all depths. The most abundant groups were Chromatiales and Desulfobacterales (17% and 13% on average, respectively). Meanwhile, microbial community were different for each layer in UMF. The Alteromonadales and Flavobacteriales (26% and 14% in total reads) were most dominant groups at 0-2 cm depth. But, these bacterial groups decreased with increasing depth, while Desulfobacterales and Chromatiales were increased (14% and 13% on average, respectively). Our results suggest that the extension of S. anglica leads to change the benthic microbial community governing biogeochemical cycling.
[Supported by grants from NRF, MOF, and MOE]

B068
The Time-series Metagenome Reveals Dynamic Shifts of Microbial Community from the East Sea, Korea
Taeyune Kim, Hoon Je Seong, and Woo Jun Sul*
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The epipelagic zone is the photic zone that microorganisms play an important role in the carbon cycle. The microbial community shifts depending on sunlight and oceanic current are important to the microbial community and function such as the carbon cycle. Here, we collected seven time-series epipelagic ocean samples (Sampling seven times every six hours) from the ocean in front of the Uljin, Korea. To find out how microbial community change, we analyzed metagenome data based on the amount of sunlight and East Korea warm current. For profiling the assembly based microbial community, we reconstructed 1482 metagenome-assembled genomes (MAGs) from ocean metagenome data using CONCOCT. After pruning of the MAGs, a total of 224 pruned novel MAGs obtained. Also, we profiled the function of the epipelagic zone of marine habitat using assembled protein coding sequences. This study reveals our understanding of dynamic shift of microbial community from the East Sea, Korea
Cloning and Identification of Lipolytic Enzyme from Marine Metagenomic Library and Characterization of a Novel Lipase Gene

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Lipolytic enzyme can be classified into lipase (EC.3.1.1.3) and carboxylesterase (EC.3.1.1.1). Lipase hydrolyzes triglycerides to fatty acids and glycerin and carboxylesterase hydrolyzes carboxylester to alcohol and carboxylate. These two enzymes have low substrate specificity and they can be found in various microbial environment such as digestive tract, marine, and soil. In this study, we found 11 lipolytic enzyme from marine metagenomic library using Uniprot database (sequence similarity > 50%). We selected 4 lipolytic enzymes, which have broad spectrum in ocean metagenome and synthesized double-stranded gene fragments based on sequencing results. For enzyme activity assay, we cloned into E. coli and tested their lipolytic activity using agar plate and colorimetric assay. As a result, 1 lipase gene showed lipase activity in colorimetric method. This suggest that a possibility to represent the criteria that indicates the similarity and function of the metagenome data.

Relationship between Microenvironmental Features and Distribution of Lichen Cladonia in Antarctica

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The Barton Peninsula of King George Island, Antarctica, is a small area but their topographical features including a variety of slopes, aspect, and elevation result in a various microclimate and diverse vegetation such as lichens, mosses, liverworts, and vascular plants. Among terrestrial vegetation, lichens are sensitively affected nearby environmental condition because the whole body of a lichen is directly exposed to external environments. However, the environmental factors that largely determine the distribution of lichen in Antarctica have been poorly understood across the Barton peninsula. To investigate the distribution pattern of lichens Cladonia squamosa and C. gracilis complex that are widely distributed in Barton Peninsula and the factor that influences their distribution, a total of 177 Cladonia samples were collected in 11 different sites and frequency of distribution of vegetation, microclimatic and topographic data were obtained at each site. There were several sites, which were observed to inhabit only one species of Cladonia. Correlation analyses between the distribution of Cladonia species and environmental data revealed that distribution of moss Chorisodintium aciphyllum, aspect, temperature, and moisture were closely related to a distribution of Cladonia species. These results imply that various geographical features and microclimate conditions can affect the distribution of lichen and environmental shift may cause a change in a distribution of vegetation.
**B071**
**Identification of OXA Gene Activity by Metagenome Expression Cloning from Marine Microorganisms**
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The OXA gene is encodes an antibiotic enzyme that hydrolyzes the antibiotic structure to the microbe resistant to antibiotics which have the beta lactam ring like penicillin, cephalosporin, and carbapenem. Recently, it has been reported that quite many species appear which are not killed by antibiotics because of the spread of these antibiotic resistance genes. In this study, we performed a functional analysis to identify antibiotic resistance genes, OXA genes, and to suggest similarity criteria for gene annotation by metagenome analysis of a marine environment called a reservoir of many microorganisms. Metagenome data obtained by sampling in Taro Ocean, Uljin, Sokcho, Jindo, Wando and Tongyeong were searched for CARD with E-value <1e-10, Similarity> 70% and Coverage> 70%. This ORF was cloned into *E. coli* and confirm activity by paper disc assay with 10 antibiotics (amoxicillin, cephalothin, cefotaxime, ceftazidime, cefepime, aztreonam, doripenem, ertapenem, imipenem, and meropenem).

**B072**
**Identification of Staphylococcus Originated from Human Skin by Using Raman Microspectroscopy**
Jubin Kim, Jin Ju Kim, Hye-Jin Kim, and Woo Jun Sul*

Department of Systems Biotechnology, Chung-Ang University

*Staphylococcus* plays a major role with *Cutibacterium acnes* in skin microbiome. It takes an important part in atopic dermatitis, psoriasis and other skin diseases. Skin microbiome vary widely by sex, age, race and so on, so the samples obtained from human skin are very valuable. To get *Staphylococcus* from human skin, we rubbed the person’s right cheek and forehead with a cotton swab for 2 minutes and culture them in 5 ml of Tryptic Soy Broth for 48 hours with shaking. Then culture them on Tryptic Soy agar, Mannitol Salt agar, Blood agar with 5% sheep blood and Baird-parker agar. We obtained about three-hundreds of microorganisms. Through Baird-parker agar, we predict about 170 samples are *Staphylococcus*. But since we can’t know the exact species of the microorganisms by looking the shapes and features on the agar plates, Raman microspectroscopy is a way to identify the characteristics of the microorganisms by sorting the single cell. We analyze eleven samples in total with four samples of *S. aureus* controls, three samples of *Staphylococcus* candidates and four samples of *S. aureus* candidates. As a result, we were able to isolate *Staphylococcus aureus* and *Staphylococcus epidermis* from many strains. The study supports the probability of Staphylococcus distinction from other microorganism by using raman microspectroscopy.
**B073**

**Differently Developed Infancy Gut Microbiome According to Severity of Atopic Dermatitis**

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The early of life are important for immune system development and can affect health in adulthood. Perturbations of the gut microbiota in early life can be disrupt the development of immune system and directly associated with the risk of allergic diseases. The alteration of infant gut microbiome with atopic dermatitis has been reported: however, the differences according to severity is not fully understood. We analyzed the composition and functional gene profiles of infant gut microbiome according to AD severity. Gut microbiome was analyzed from 206 children between 6 and 72 months of age. The bacterial composition were analyzed by Illumina MiSeq system. The functional profile of gut microbiome was analyzed by whole metagenome sequences. The amount of total bacteria in feces were quantified by real-time PCR. We compared the observed microbiota composition at different gut progression phases according to AD severity. Firmicutes/Actinobacteria dominated microbiota and Firmicutes/Bacteroidetes dominated microbiota were found in each gut progression phases. Adult-type gut bacteria are more abundant in the severe group than mild and control groups. These results can help to understand the potential role of gut microbiome in the pathogenesis of AD according to severity.

[This research was supported by the Bio & Medical Technology Development Program of the National Research Foundation (NRF) funded by the Korean government (MSIT) (2017M3A9F3043826).]

**B074**

**Fungal Communities Associated with Deciduous Broadleaf Forests Soil (Fraxinus rhynchophylla and Carpinus cordata) in Mt. Jeombong**

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Fungal community performs important role in forest ecosystem. According to their modes of nutrition, fungal community can be distinguished to several guilds like symbiotrophs and saprotrophs. Though their ecological roles are important, the influence of abiotic and biotic factors to fungal community is unclear. In this study, forest soil fungal communities of two broadleaf tree species, *Fraxinus rhynchophylla* and *Carpinus cordata*, were compared with Illumina MiSeq platform. Both tree species are known as climax tree species in Korean forests. We compared the reactions of fungal communities in two forests against environmental factors (tree species, seasons, and soil properties). In our analysis, the fungal communities in forest soil were largely influenced by environmental factors. Tree species were one of the significant factors, even located in close sites. The reaction of fungal communities to other factors like soil properties or seasons showed significant difference between two forests. In fungal guilds, both symbiotrophs and saprotrophs showed different patterns against tree species and seasons.

[This study was supported by the research projects for exploring fungal diversity in forest soil from Korea National Arboretum.]
B075

**Spindle-shaped Viruses Infect a Marine Ammonia-oxidizing Thaumarchaeon**

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Ammonia-oxidizing archaea (AOA) from the phylum *Thaumarchaeota* are ubiquitous in marine ecosystems and play an important role in the carbon and nitrogen cycling. Although viruses are known to have a key impact on the functioning and mortality of their hosts, thereby regulating the global biogeochemical cycles, not a single virus infecting thaumarchaea has been isolated thus far. Here we report on the isolation and characterization of the *Nitrosopumilus* spindle-shaped viruses (NSV) which infect a marine AOA and are distinct from other known marine viruses. The genomes of NSVs consist of linear dsDNA molecules of ~28 kb in length containing 176 bp-long terminal inverted repeats. NSVs do not display appreciable sequence similarity to other known archaeal or bacterial viruses. During the infection life cycle, viral DNA replication occurred concurrently with the AOA growth and was accompanied by ammonia oxidation. In resource poor oceans with low host cell densities, these properties might represent an optimal strategy for predation of NSV on chemolithoautotrophic AOA host. Widespread distribution of NSV in marine environments esp. in particulate matter-rich bays, corals, and sediments with high AOA abundance implies that NSV predation regulates the diversity and dynamics in the AOA community.

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B076

**Catalase-containing Amonia-oxidizing Archaea are Key Players in Rhizosphere Nitrification**

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To investigate structure and function of the plant rhizosphere microbiome, pepper (*Capsicum annuum*), ginseng (*Panax ginseng*) and tomato (*Solanum lycopersicum*) plants were used in this study. Since ginseng is a perennial plant, rhizospheres of 2~6 years-old plants were used. First, microbial community structures were evaluated using universal 16S rRNA gene amplicons analysis. Microbial communities between rhizosphere and bulk soils of each plant were different, and there was no consistency between rhizospheres of the plants. PCA analysis showed that rhizosphere soils host distinct microbial communities depending on the age of ginseng. Interestingly, archaeal communities between plant rhizospheres were similar each other but distinct from bulk soils. Ammonia-oxidizing archaea (AOA) abundance was higher than ammonia-oxidizing bacteria (AOB) and *Nitrospira* in both bulk and rhizosphere soils. Since *Nitrosososmicus oleophilus* MY3-like AOA were commonly dominant in all rhizosphere soils, we assumed that *N. oleophilus* MY3-like AOA as the key players in rhizosphere nitrification. Real-time quantitative PCR supported that archaeal *amoA* was dominant in both rhizosphere and bulk soils compare to bacterial *amoA*. Among AOA, one of the unique traits of *N. oleophilus* is presence of catalase gene in its genome. This study suggest that catalase-containing *N. oleophilus*-like AOA might be associated with nitrification in rhizospheres of various plants.

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B077
Copper Complexation by Organic Matter Constrains Archaeal Ammonia Oxidation in Municipal Wastewater Treatment Plants

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Nitrification is a crucial process used to reduce nitrogen in municipal wastewater. In this study, we identified ammonia-oxidizing archaea (AOA) were less abundant than ammonia-oxidizing bacteria (AOB) in activated sludge of aeration basins from municipal wastewater treatment plants (WWTPs). And also, growth of AOA strain inoculated into cell-free wastewaters of the aeration basins was significantly inhibited, whereas AOB strain actively grew. To investigate the possible mechanisms, organic matter was supplemented to the cultures of four AOA and an AOB strains to create similar environment to wastewater. Complex and single organic compounds tests were highly inhibitory to AOA strains rather than AOB. Further single organic compound test showed strong inhibitory effect of amino acids with high metal complexation potential implying the inhibitory mechanism of organic carbon as reduced bioavailability of essential metal. In fact, the inhibitory effect of yeast extract and histidine on AOA was found to disappear by augmentation of copper to organic compound-inhibited cultures. Likewise, UV-degradation of organic matter in the cell-free wastewaters and augmentation of copper to mixed liquors of WWTPs successfully stimulated the growth of AOA strains. Our results could provide a basis for developing approaches for modulating the composition of nitrifying communities in terrestrial, aquatic, and engineered environments on a global scale.

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B078
Physiological and Genomic Characterization of a Thiotrophic Methanotroph from Isolated from Acidic Peat Bog

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Facultative methanotrophic bacteria have been demonstrated in several members of the genera Methylocystis, Methylocapsa, Methylocella and “Methylacidiphilum”, that is, capable of growing on the methane and other alternate substrates as short-chain carbon compounds or H₂ + CO₂. In this study, we isolated and characterized a facultative methanotroph strain, Methylovirgula strain HY1, from an acidic peat bog and its genome sequence was compared to those of closest relatives. Genomic analysis confirmed that this strain encoded a cytosolic methane monooxygenase (sMMO) while a membrane-bound methane monooxygenase (pMMO) was absent. Genes for methanotrophic growth were present. Strain HY1 shares highest 16S rRNA gene sequences (98.63%) with Methylovirgula ligni BW863³. Comparative genomic analysis between strains HY1 and BW863 demonstrated that strain HY1 harbors many distinct genes for niche specialization in addition to methanotrophy: sulfur oxidation, microaerophilicity, and hydrogen utilization, which might be important for adaptation to methane and oxygen limitation. Strain HY1 shows higher versatility in substrate utilization, being able to use short-chain carbon compounds, which is comparable to Methylocella spp. Our finding provides information on ecological niches of facultative methanotrophs and provide evidence of its environmental importance in carbon and sulfur cycles in acidic wetlands.

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**B079**

*Nocardioides* sp. JGR 007 with Algal Polysaccharide Degradation Potential

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Strain JGR007 isolated from Jeju coastal areas was found to have the capability to degrade major seaweed polysaccharides. In particular, several kinds of polysaccharide such as agar, carrageenan, chitin, cellulose, starch, etc. were tested to evaluate the industrial application of their intermediates, showing that strain JGR007 had the ability to degrade agar, carrageenan, and chitin, with additional abilities to degrade several Tween groups (Tween 20, Tween 40, Tween 60 and Tween 80). Light and electron microscopic analysis showed that cells of strain JGR007 were Gram-positive, smooth surface, rod-shaped, 2.44 μm–2.83 μm in length, 0.39 μm–0.41 μm in width. Strain JGR007 had a range of growth temperature from 10°C to 30°C, pH 6 to pH 8 and 0% to 7% salinity through physiological test. 16S rRNA sequence of strain JGR007 shared 98.6% similarity with that of Nocardioides cavernæ YIM A1136. It had multi-drug resistance to antibiotics such as polymixin B, novobiocin, lincomycin, nalidixic acid, penicillin G, rifampicin, ampicillin, gentamycin, streptomycin and tetracycline.

**B080**

*Tropicibacter* sp. nov. Isolated from a Sea Cucumber Aquaculture Farm Sediment

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This study revealed that strain SD-34, isolated from a sea cucumber aquaculture farm sediment of Taean, Chungnam, was found novel species. It was aerobic, Gram-negative, immotile, and rod-shaped with yellow colony color. Scanning electron microscopy showed that SD-34 was 0.79 μm in length and 1.28 μm in width. GC content was 59.9 mol%, and the quinone type was Q-10. It was positive for esterase (C4) and esterase lipase (C8). It was resistant to antibiotics such as polymyxin B, licomycin, nalidixic acid, penicillin G, ampicillin, carbenicillin, gentamycin, streptomycin, chloramphenicol, and tetracycline, while it was sensitive to novobiocin, oleandomycin, kanamycin, rifampicin, erythromycin, and neomycin. The optimal growth range was pH 7.0-8.0, 25-37°C, 3.0-8.0% (w/v, Sea Salt). SD-34 was closest to *Tropicibacter multivorans* MD5\(^T\) with 96.6% based on comparative analysis of 16S rRNA sequence.
B081
Analysis of Novel Genes and the Predicted Proteins Responsible for Chemotaxis in *Pseudomonas taeanensis* MS-3 Capable of Petroleum Oil Degradation
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*Pseudomonas taeanensis* MS-3 already has been known as a marine bacterium capable of degrading a broad range of petroleum oils (Lee *et al*., 2012; Kim *et al*., 2017, 2018), and its total genome sequence was reported as well (Lee *et al*., 2014). It has been one of very attractive works for our environmental microbiologist group to understand how *P. taeanensis* MS-3 moves to its attractant petroleum oils to get their carbon and energy sources. This study focuses on analysis of novel genes and the predicted proteins responsible for chemotaxis which might play a key role in the mechanism to move to MS-3’s attractant, petroleum oils. At least 15 genes for chemotaxis in *P. taeanensis* MS-3 were found to be organized into a cluster which is composed of response regulator (RR), CheA, CheW, chemotaxis protein 1 (Che1), CheR, CheD, chemotaxis protein 2 (Che2), DEAD/DEAH box helicase, Ycel protein domain-like hypothetical protein, cytomochrome B561, adenosylmethionine-8-amino-7-oxononanoate aminotransferase, chemotaxis protein 3 (Che3), protein PilI, CheY, PilG, glutathione synthetase, and energy transducer TonB. The movement mechanism for chemotaxis of *P. taeanensis* MS-3 in response to petroleum oils will be proposed.

B082
Effects of Temperature on Bacterial Communities, Metabolites, and Flavoring Compounds during Kimchi Fermentation
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To investigate the effects of temperature on kimchi fermentation, two sets of kimchi samples were fermented at 4°C and 10°C and their pH values, 16S rRNA gene copy numbers, bacterial communities, metabolites, and flavoring compounds were analyzed for 30 days. The pH values at 4°C decreased gradually to pH approximately 4.7 during the entire fermentation period, whereas at 10°C they decreased very quickly to approximately 4.0 within 10 days. qPCR showed that bacterial abundance increased slowly over the entire fermentation period, while they increased very quickly to $5.0 \times 10^{11}$ within 10 days. The community analysis showed that *Weissella*, *Lactobacillus*, and *Leuconostoc* were dominant at both temperatures. Among the three genera, *Weissella* was most abundant at both temperatures, but *Lactobacillus* and *Leuconostoc* were different depending on temperatures. At 4°C, *Lactobacillus* was more abundant than *Leuconostoc*, while at 10°C, *Leuconostoc* was more abundant than *Lactobacillus*. Metabolite analysis showed that the decrease of fructose, glucose, and sucrose and the increase of lactate, acetate, and ethanol were occurred more rapidly at 10°C than 4°C, but their proportions were also different depending on temperatures. Fructose decreased more rapidly than other carbohydrates at 10°C, of which decrease was in accordance with mannitol increase. The proportion of lactate at 10°C was higher than 4°C and volatile compounds were different depending temperatures.
B083
Optimization of In Vitro Culture Conditions to Study Complex Microbiome in the Airway
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Microbiome in the human airway plays important roles in prognosis of airway diseases. Various studies reported that diverse microbes coexist in the human airway and they are always interacted with each other and host. However, most of in vitro culture studies have focused specific pathogens for airway diseases. Therefore, we tested various culture conditions for airway microbes and have improved the conditions for various microbes in co-culture system. Airway swab samples were inoculated in three different media, which are widely used media for airway microbes. Furthermore, we modified these media with unknown chemicals in swab samples by using autoclaved swab sample media solutions. Samples were cultured during 48 hours in microaerophilic and anaerobic conditions at 37°C. Metagenomic DNAs were extracted from each culture medium, and the cultured microbes were analyzed. The cultured bacterial amounts were quantified by real-time PCR. The cultured microbes were different between culture conditions, and the highest bacterial amounts were detected in ASM medium with 2.5% swab sample solutions. The improved culture conditions will be used to analyze the metabolic capacity of airway microbiome related to airway disease, and this improvement can be applied to develop mimicking systems for airway microbiome.
[This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2017R1D1A1B03029282)]

B084
Developing New Molecular Markers for Phylogeographic Study of Lichen Genus Usnea
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The lichen genus Usnea is one of the dominant flora in the terrestrial Antarctic environments. They are distributed from Southern South America to the Antarctic continent. Despite phenotypic plasticity along geographical distribution, their genetic distribution of population is not well known. Traditional phylogenetic markers, such as ITS, LSU, mitochondrial rRNA genes, did not provide enough information to resolve the relationships among those populations. So, new molecular markers with high resolving power are required to studying biogeography. In this study we developed new molecular markers using genome information of several lichens that constitutes terrestrial Antarctic environment. We compared information contents of new markers with traditional molecular markers. It is expected that they will provide better information to understand biogeography of genus Usnea around Antarctic environment.
[Supported by grants from KOPRI]
**B085**  
Establishment of Hazardous Microbial Management System in Response to Climate Change  
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In this research, we will review the management of harmful microorganisms in the environment that have been operated due to frequent weather changes due to climate change and prepare a system to counter the possibility of exposure of new harmful microorganisms that cannot be controlled by current water quality standards. Six strains of pathogen bacteria, including *Escherichia coli* O157:H7, were selected first as harmful microorganisms related to climate change, and the distribution status of the domestic water system was investigated. Based on the forecast scenario of climate change as the target area, water sources and streams of five locations were selected based on subtropical climate, subtropical forecast area, and exception area. Based on the detection of some microbes in each region, continuous analysis and monitoring of harmful microbe is deemed necessary. For example, *E. coli* O157:H7 was not detected in April and June in Soyang River in the past nine years, and it was detected twice in August (2012, 2013), twice in October (2013; 2015), and seven times in February (2014, 2018). In addition, for Nakdonggang River, a total of seven detections were detected in the last survey in April 2010 and December 2013, February 2014 and February 2016 and February 2018. By utilizing such diverse data, it is possible to identify the status of harmful microorganisms and establish a management system.  
[This research was supported by KEMB.]

**B086**  
Diversity and Distribution Patterns of Endolichenic Fungi in Jeju Island, Republic of Korea  
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Lichens are symbiotic organisms consisting of mycobiont (lichen-forming fungi) and photobiont (algae and/or cyanobacteria) which have mutualistic relationship. Recent researches have shown that diverse microorganisms live together within lichen thalli and they can influence on the physiology of host lichen. Endolichenic fungi are one of other symbionts within lichens, and have potential ecologically and industrially because they can produce various secondary metabolites. In Korea, however, there is no study for diversity and ecology of endolichenic fungi. In this study, we investigated the diversity and distributional patterns of endolichenic fungi isolated from various lichens. A total of 80 lichen specimens were collected from 29 sites in Jeju Island. Among 620 fungal isolates, most endolichenic fungi were belonging to Xylariales (Sordariomycetes, Ascomycota). In genus level, *Nigrospora* was dominant, followed by *Daldinia*. Community structure of endolichenic fungi was significantly different depend on the identity of host lichens, and some endolichenic fungi showed host specificity.  
[This study was supported by a research grant from the Korea National Arboretum.]
B087

Analysis of Intestinal Microbiota of Sea Cucumber Apostichopus japonicus
Sang-Eon Kim, Young-Sam Kim, and Kyoung-Ho Kim*
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The species of sea cucumber, Apostichopus japonicus, belonging to class Holothuroidea, phylum Echinodermata, an economically important marine invertebrate in China, Japan, and Korea. Understanding of its microbiome could help enhance its economic values. The diversity of intestinal bacteria was investigated in anterior and posterior regions of the intestines of A. japonicus on the different sizes and sampling times. Intestinal microorganisms were analyzed by 16S rRNA gene amplicon sequencing using the Illumina Miseq platform. The results showed that major phyla are Proteobacteria, Bacteroidetes, Verrucomicrobia, and Planctomycetes. The richness of the bacteria was higher in the anterior intestine than in the posterior intestine. The taxonomical classification profiles and the Unifrac PCoA chart showed the effect of sizes and sampling times on the bacterial communities in the different intestinal regions.

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B088

Comparative Biodiversity of Tidal Flat and Saltern from Yeongjong-do, Republic of Korea
Yeonjae Yoo, Dong wan Lee, Hanbyul Lee, and Jae-jin Kim*
Korea University

Coastal ecosystem include diverse types of habitat where interaction of the sea and land process occur. This specific environment supports a diversity of animal, plant, insect and micro-organism. While tidal flat and saltern, the habitat components of coastal ecosystem, share same water current, the aspect of microbial community and plants differ in significantly both environments. In this study, we performed an environmental metagenome analysis and characterized microbial diversity based on 16S rRNA from the sediment collected in both tidal flat and saltern at Yeongjong-do (37°26′N, 126°23′E), Republic of Korea, to compare biodiversity between the two different regions. As a result, the metagenome analysis showed notable difference in microbial community between the two regions. Fifty-seven strains and ten strains of culturable bacteria were obtained from the tidal flat and the saltern, respectively. Afterwards, they were grown on medium containing 10%, 15%, 20% (v/v) sea-salt to compare the predominant feature of halotolerant bacteria from both saline environments. Halophiles were classified based on their salinity for growth into mild (1-6%), moderate (7-15%), and extreme halophiles (15-30%) based on their halotolerance. The result showed that the ocurrence of halotolerant bacteria from these two habitats were different.
Kimchi is a traditional fermented food in Korea. Kimchi is made from kimchi cabbage, which is a main ingredient, and various ingredients. Fermentation takes place by microorganisms in well-mixed ingredients, and the process is mainly carried out by lactic acid bacteria (LAB). The taste and flavor of kimchi is determined mainly by the result of fermentation metabolism of LAB. During fermentation, the microbial community of kimchi changes due to various causes such as temperature, ingredients, and salinity. The amount and type of fermentation metabolites also change accordingly. Carbon dioxide (CO$_2$) is one of the final products of heterolactic fermentation of LAB in kimchi. Here, we studied the effect of CO$_2$ on the fermentation process of kimchi. The microbial communities and metabolites of kimchi with and without CO$_2$ treatment were analyzed. Metatranscriptomic analysis was also performed at each stage of fermentation. Bacterial community analysis showed that the _Weissella koreensis_ (heterofermentative LAB) was dominant in CO$_2$ treated kimchi, while _Lactobacillus sakei_ (homofermentative LAB) was the dominant species in kimchi without CO$_2$ treatment. The concentrations of lactate and ethanol were also different, and the results of metatranscriptomic analysis using RNA sequencing also supported bacterial community analysis results. Collectively, our results highlight that the pre-treatment of CO$_2$ in kimchi production is capable of affecting the microbial and metabolic profiles during the fermentation.
**B091**

**The Role of Alpha- and Gamma-proteobacterial Methanotrophs as the Modulator of Nitrous Oxide Emissions from Soil Denitrifying Microorganisms**

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In our recent study, we have observed that methanobactin (Mb) secreted from *Methylosinus trichosporium* OB3b inhibits N\textsubscript{2}O reduction in axenic denitrifier cultures, leading to N\textsubscript{2}O emissions. To investigate whether this interplay between methanotrophs and denitrifiers is relevant to soil environments with established complex microbiomes, denitrification and N\textsubscript{2}O production in methanotroph-enriched soil and sediment suspensions were monitored in laboratory settings. 0.1 g of rice paddy soils and varying amounts of *M. trichosporium* OB3b culture (cell number: 1/25, 1/5, 1, 5, 25 of 250,000) was added to 50 ml minimal medium. Initial enrichment with 20% of CH\textsubscript{4} was followed with addition of 5 mmoles NO\textsubscript{3} and N\textsubscript{2}O production was monitored. In another set of cultures originating from rice paddy soil, indigenous methanotrophic population was enriched with CH\textsubscript{4} and denitrification progression was monitored after addition of acetate and NO\textsubscript{3}.

0.157–0.238 \(\mu\) moles N\textsubscript{2}O-N production was observed when soil suspension was incubated with more than 250,000 (1, 5, 25 of 250,000) of strain OB3b, while transient accumulation of 2.46–4.44 \(\mu\) moles N\textsubscript{2}O-N was observed when lower than 250,000 of strain OB3b (1/25, 1/5 of 250,000) were examined. Furthermore, >1000-fold increase N\textsubscript{2}O emission was observed in the indigenous methanotrophic population enriched with CH\textsubscript{4} where *Methylomonas* was the vast majority and Alphaproteobacterial methanotrophs were unseen minority. These findings suggest that methanobactin-mediated N\textsubscript{2}O emission enhancement may be an environmentally-relevant phenomenon in copper-depleted soils and also that Gammaproteobacterial methanotrophs may also utilize a yet unidentified copper-sequestering mechanism.

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**B092**

**Genome Characteristics of Kordia antarctica IMCC3317\textsuperscript{7}, a Potential Nitrous Oxide Reducer Belonging to the Family Flavobacteriaceae**

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*Kordia* is a bacterial genus belonging to the phylum *Bacteroidetes*, found in various marine environments and forms a phylogenetically distinct lineage comprising eight species with validly published names. Currently four draft genome sequences of *Kordia* species are publicly available but very limited genome analyses have been performed.

In the present study, we obtained the complete genome sequence of strain IMCC3317, the type strain of *K. antarctica* and analyzed genetic characteristics of IMCC3317 together with other *Kordia* genomes. The genome of IMCC3317 was 5,500,985 bp in size which was the largest genome among *Kordia* species, with DNA G+C content of 33.2%. A total of 4,761 genes were predicted in the genome with 9 rRNA genes and 49 tRNA genes. The major COG categories were translation, ribosomal structure and biogenesis (7.7%), coenzyme transport and metabolism (6.0%), and inorganic ion transport and metabolism (5.3%). Based on the comparative genomic analysis, strain IMCC3317 shared common metabolic pathways with other strains of the genus *Kordia* but had a unique nitrous oxide reductase (nosZ) gene. This suggests that strain IMCC3317 is one of a few marine *Bacteroidetes* that have a physiological potential for non-denitrifying nitrous oxide reducer.

[This study was supported by a grant from the Marine Biotechnology Program (PJT200620), funded by the Ministry of Oceans and Fisheries, Korea.]
C001
Effects of High Density Microbes on the Performance, Odor Reduction and Antibody Titer in Broiler Chickens
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A broiler experiment was conducted to investigate the effect of high density bacteria (feeding, Leuconostoc pseudomesenteroides JLRI 01; Spray, mixture of Bacillus thuringiensis JLRI 02, Pseudomonas caeni JLRI 03 and Rhodobacter sphaeroides JLRI 04) on the growth performance, odor reduction and antibody titer in broiler chicken. The feeding rate and spray volume were 0.5% during whole feeding periods (35 days) and 0.2 L/m² twice a week, respectively. Three thousand hat hatched broiler (Ross) were assigned to 3 treatments; control (no microbes), T1 (normal density bacteria, $1 \times 10^6$) and T2 (high density bacteria, $1 \times 10^8$). There were no significant differences in growth, feed intake, feed efficiency and mortality among the treatments. But T2 showed marked removal activity of ammonia gas (66%) and amines gas (80%) ($P < 0.05$). The Newcastle disease (ND), infectious bronchitis virus (IBV) and infectious bursal disease virus (IBDV) vaccines induced good seroconversion which was confirmed by agar gel precipitation (AGP) test in all treatments and especially antibody titer of IBV tended to be higher in T2 than those control and T1 ($P < 0.05$). In conclusion, the application of microorganism with high concentration showed numerical advantages in productivity, improvement of livestock environment and disease resistance compared to the control and T1.

[Supported by a research grant from Jeollanamdo Province]

C002
Assessment of Bacteriophage-insensitivity in Antibiotic-resistant Klebsiella pneumoniae
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This study was designed to evaluate the physiological properties of bacteriophage-insensitive Klebsiella pneumoniae (BIKP) mutants. Klebsiella pneumoniae ATCC 23357 (KPWT), ciprofloxacin-induced antibiotic-resistant K. pneumoniae ATCC 23357 (KPCLP), and clinically isolated antibiotic-resistant K. pneumoniae 10263 (KPCIP) were used to isolate BIKP mutants against KBP1, PBKP02, PBKP21, PBKP29, PBKP33, and PBKP35. PBKP35-induced mutants, including BIKPW, BIKPCIP, and BIKPCLI. BIKPWD, BIKPCIP, and BIKPCLI were resistant to KBP1, PBKP02, PBKP21, PBKP29, and PBKP33. The antibiotic cross-resistance was developed in of BIKPWT against cefotaxime, cephalothin, chloramphenicol, ciprofloxacin, erythromycin, kanamycin, levofloxacin, and nalidixic acid. The relative expression levels of vagC was increased by more than 8-folds in BIKPW, corresponding to the increased β-lactamase activity. The aac(6′)-Ib-cr was overexpressed in BIKP mutants, responsible for aminoglycoside and quinolone resistance. The results provide valuable insights for the BIKP mutants, which must take into consideration for the therapeutic use of bacteriophages.

[This research was supported by a grant of the Korea Health Technology R&D Project through the Korea Health Industry Development Institute (KHIDI), funded by the Ministry of Health & Welfare, Republic of Korea (Grant number : HI15C-1798-000016).]
We evaluated the immunometabolic functions of novel *Lactobacillus* strains (KBL374 and KBL375) isolated from feces of healthy Koreans. The levels of inflammatory cytokines, such as interleukin (IL)-2, interferon-γ, IL-4, IL-13, and IL-17A, were decreased, and that of the anti-inflammatory cytokine IL-10 was increased, in human peripheral blood mononuclear cells (PBMCs) treated with the KBL374 or KBL375 strain. When these strains were orally administered to mice with dextran sulfate sodium (DSS)-induced colitis, both KBL374 and KBL375 showed beneficial effects on body weight, disease activity index score, colon length, cecal weight, and histological scores. Furthermore, both KBL374 and KBL375 modulated the innate immune response by improving gut barrier function and reducing leukocyte infiltration. Consistent with the PBMC data, both KBL374 and KBL375-treated DSS mice demonstrated decreased Th1-, Th2-, and Th17-related cytokine levels and increased IL-10 in the colon compared with the DSS control mice. Administration of KBL374 or KBL375 to mice increased the CD4+CD25+Foxp3+ Treg cell population in mesenteric lymph nodes. Additionally, KBL375 increased the abundance of beneficial microorganisms, such as *Lactobacillus* spp. and *Akkermansia* spp. Both KBL374 and KBL375 may alleviate inflammatory diseases, such as inflammatory bowel disease, in the gut by regulating immune responses and altering the composition of gut microbiota.

The aim of this study was to investigate the optimal conditions for increasing the growth yield of *Bacillus subtilis* SRCM102046, a strain possessing potential biopreservative properties. *B. subtilis* SRCM102046 showed remarkable antibacterial activity against a wide range of bacterial foodborne pathogens that cause serious food spoilage, as well as high antioxidant capacity. Response-surface methodology (RSM) was used to optimize medium composition to enhance *B. subtilis* SRCM102046 biomass. The effects of 14 different components on biomass production were investigated and three significant positive factors, molasses, sucrose, and peptone, were selected as the main factors for improving biomass based on a Plackett-Burman design (PBD). Next, we optimized the concentrations of these three factors using a central composite design. The predicted optimized concentrations were 7 g/L molasses, 7 g/L sucrose, and 2 g/L peptone. The coefficient of determination (R2, 0.9755) for the model and probability value showed that our model was highly significant. Finally, an overall approximate 9-fold increase in dry cell weight yield (22.03 g/L) was achieved using the optimized medium compared with the non-optimized medium (2.47 g/L). Furthermore, we confirmed that the antibacterial activity and antioxidant activity also increased by 140% and 100.41%, respectively.
**C005**

Newly Discovered Bacteriophage Bϕ-R1869 Improves Survival in a *Galleria mellonella* Infection Model and Decreases Bacterial Load of Mouse Infected with the Colistin-resistant *Acinetobacter baumannii*

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The recent dissemination of multi-drug-resistant (MDR) *Acinetobacter baumannii* has caused significant global healthcare problems. As a promising alternative, bacteriophages (phages) have been reviewed as an alternative strategy for controlling these MDR pathogens. Bϕ-R1869, a novel phage of the family *Myoviridae*, can lyse colistin-resistant *A. baumannii* clinical isolates. The genome of the phage has 42,555 bp linear ds DNA. In the evaluation of its therapeutic potential against colistin-resistant clinical isolates, Bϕ-R1869 increased the survival rates of *G. mellonella* larvae (from 0% to 75% with MOI=10 at 72 h) in post-infection and bacteria loads of the phage-treated group in the mouse lungs were reduced from 8.1 log<sub>10</sub> to 5.2 log<sub>10</sub> CFU (*p=0.0137) compared with the bacterial-infected group at day 1, and most of the bacteria were eliminated from the lungs at day 5. Also, histological results corresponded with the above findings. This study strongly suggests that Bϕ-R1869, could be an alternative antibacterial agent to control colistin-resistant *A. baumannii* infections. This study is the first report to show *in vivo* evaluations of the therapeutic efficacy of a phage by using two *in vivo* models against colistin-resistant *A. baumannii* infections. [This work was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2017R1D1A1B03034730).]

**C006**

Germicidin A and B, Antioxidant Activities of a *Streptomyces* sp. SC552S Isolated from Marine Sediment

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Antioxidant compounds, Germicidin A and B, have been isolated from the fermentation broth of the marine-derived bacterium *Streptomyces* sp. SC552S. The planar structure of Germicidin A and B was elucidated by 1D, 2D NMR, and MS spectroscopic data analyzes. These two compounds are known to inhibit spore germination, and the polyketide type III pathway related protein, Gcs, is also known. The antibacterial activity against Gram-positive bacteria is known as a physiological activity effect, and there is no anticancer effect on breast cancer cell and lung cancer cells. Germicidin A and B were found to have antioxidant activities using ABTS and DPPH radical scavenging assays. We have isolated pure antioxidant substances from *Actinomycetes* derived from marine sediments. By providing a natural antioxidant substance that is safe and low in price from natural sources and cultivable sources, it can contribute to the expansion of food, cosmetics and other related industries and contribute to the public health. [This work was supported by a grant from the National Marine Biodiversity Institute of Korea (2019M00700).]
C007
Calcium Carbonate Precipitation and Spore Formation by Alkaliphilic Bacillus sp. AK13 for Self-healing Concrete
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The use of bacteria resistant to high temperature and alkaline environments is essential for the biological repair of damaged concrete. Alkaliphilic and halotolerant Bacillus sp. AK13 was isolated from the rhizosphere of Miscanthus sacchariflorus. Increased pH in urea-minus condition during the growth of the AK13 strain promoted calcium carbonate (CaCO₃) formation. Irregular vaterite-like CaCO₃ minerals tightly attached to cells were observed using field emission scanning electron microscopy. Energy dispersive X-ray spectrometry profile and X-ray diffraction analysis confirmed the presence of CaCO₃ around the cell or on the surface. CaCO₃ minerals derived from calcium acetate-added condition had small spherical shapes and formed compact aggregates with cells and spores. However, the amounts of CaCO₃ crystals and spores under calcium lactate are less and CaCO₃ shapes are rough aragonite-like aggregates with smaller sizes although growth patterns of the AK13 strain in both conditions are similar. The amounts of spore grown in spore-inducing Difco™ sporulation media (DSM) were similar to those in LB media. Only 0.1% sporulation rates were observed after reaching the early stationary phase (24 h) in both DSM and LB media, suggesting that further environmental modification is needed to optimize efficient spore production. Alkaliphilic, halotolerant, and spore-forming Bacillus sp. AK13 is a promising candidate for self-healing concrete.

C008
Extract of Streptomyces sp. R301 as a Highly Potent Tyrosinase Inhibitor
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Tyrosinase inhibitors have prominent influence in the whitening of skin in cosmetic world. In this study, the mushroom tyrosinase inhibitory effect of Streptomyces sp. R301 was investigated in vitro. Bioassay-guided purification stipulated that the ethyl acetate extract of Streptomyces sp. R301 demonstrated the highest mushroom inhibitory activity (IC₅₀ = 36.83 ± 4.42 µg/ml) when compared to commercial standard, arbutin (IC₅₀ = 50.54 ± 6.61 µg/ml). The ethyl acetate extract of Streptomyces sp. R301 was non-toxic to human melanoma cell lines (B16F1 and B16F10). This study anticipated that the ethyl acetate extract of Streptomyces sp. R301 has significant potential for application in cosmeceuticals industry.
C009
Characterization of Bacteriophage-binding Receptors in Antibiotic-resistant Salmonella Typhimurium
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This study was designed to assess the bacteriophage resistance mechanism of antibiotic-resistant Salmonella Typhimurium and also to profile the bacteriophage-binding receptors on the mutants. Salmonella Typhimurium ATCC 19585 (STWT), ciprofloxacin-induced antibiotic-resistant S. Typhimurium ATCC 19585 (STCIP), S. Typhimurium KCCM 40253 (STLAB), and clinically isolated antibiotic-resistant S. Typhimurium CCARM 8009 (STCLI) were used to induce bacteriophage-insensitive S. Typhimurium (BIST) mutants against P22, P22-B1, PBST10, PBST13, PBST32, and PBST35. P22-resistant mutants were assigned as BISTWT, BISTLAB, and BISTCLI, which were sensitive to PBST10, PBST13, PBST32, and PBST35. The antibiotic susceptibilities of BIST mutants against ampicillin and cephalothin compared to STWT, STLAB, and STCLI, respectively. Correspondingly, no significant changes in β-lactamase activity were observed for all strains. The relative expression levels of rafL, btuB, fliC, fhuA, ompC, and tolC were decreased in BIST mutants, suggesting their low adsorption rates. These results might provide useful information for designing an effective bacteriophage therapy.

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C010
Biocontrol Activity of Pantoea dispersa against Black Rot Disease of Sweetpotato Caused by Ceratocystis fimbriata
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Endophyte has a great potential of biotechnological applications in diverse areas, and it has already produced commercial formulations as microbial pesticides. The aim of this work was to evaluate the possibility of exploiting bacteria in order to control black rot disease of sweet potato caused by phytopathogenic fungi Ceratocystis fimbriata. Genus Pantoea is one of a major portion of the microbes which isolated from bulk soil, tuberous roots of field-grown sweet potato plants. To define a role of genus Pantoea in sweet potato plants, eleven Pantoea isolates were evaluated the antifungal activity against C. fimbriata. results show that four Pantoea dispersa (P. dispersa) strains RO-18, RO-20, RO-21 and SO-13, displayed strong inhibition of mycelium growth of C. fimbriata (63-72% reduction), while P. ananatis strains SH-1, SH-3, SH-5, SH-9, SH-13, RO-1 and RO-22 were observed weak by 19-34%. Moreover, the cell-free supernatants (CFS) from P. dispersa strains could inhibit the spore germination and alter the morphology of fungal hyphae. Finally, P. dispersa strains significantly suppress the C. fimbriata growth on leaves and tuberous roots of sweet potato (cv. Yulmi). Our finding suggests that P. dispersa strains, an associating with sweet potato tissue, could strongly inhibit C. fimbriata growth and hyphal formation. P. dispersa is highly worthwhile for biocontrol agent of sweet potato.

[This work was supported by grants from KRIBB Research Initiative Program]
C011
Genomic Insight into the Salt Tolerance of Enterococcus faecium, Enterococcus faecalis and Tetragnococcus halophilus
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To shed light on the genetic background behind the salt tolerance of Enterococcus faecium, Enterococcus faecalis and Tetragnococcus halophilus, we performed comparative genome analysis of twenty-four strains; E. faecalis (10 strains), E. faecium (11 strains) and T. halophilus (3 strains). Three species genomes possessed the carbohydrates, protein metabolism, and amino acids and derivatives abundantly. Examination of the pan-genome of three species showed that the conserved core genome retained the genes for general physiological processes and survival of the species. In this comparative genomic analysis, the factors for salt tolerance that distinguish the species from each other were identified. Among the three species, T. halophilus was more possessed the potassium transporter and the osmoprotectant synthesized genes than other two species. Especially, only T. halophilus might be synthesized glycine betaine from choline and glutamate from citrate. These two molecules are well-known osmoprotectants, so we suggested that these gene conferred the salt-tolerance into T. halophilus.

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C012
Bioconversion of Potential Efficacy Compound in Medicinal Plants through Lactic Acid Bacteria Isolated from Kimchi
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The purpose of this study was to develop functional foods for anti-metabolic disease that work simultaneously on various targets through microbial conversion of compounds in medicinal plants. For the screening of strains with bioconversion activity, about 200 strains of lactic acid bacteria (35 species in 5 genera including 2 novel species) were isolated from a traditional Korean fermented vegetable, kimchi. Among them, bioconversion was confirmed in the Leuconostoc sp. and Lactobacillus spp. and through the submerged fermentation with medicinal plants. Representatively, Leuconostoc sp. demonstrated that initially abundant paeoniflorin in the paeonia lactiflora are converted into its corresponding metabolite after the fermentation at 37°C for 48 h without additional nutrient supplementation. The bio-converted metabolite and anti-diabetic effect will be discussed in detail in this text.

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C013
Activity Improvement through Whole Cell Bio-conversion of Gardenia jasminoides Ellis with Probiotics
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Gardenia jasminoides Ellis (Rubiaceae), one of well known traditional herbal medicines, which is used as functional food in our modern life owe to its multi-functions: anti-obesity, diabetic, oxidant, inflammatory and insomnia. Genipin and geniposide are both bioactive components of Gardenia jasminoides. Genipin is aglycon part of geniposide structurally, and has much better activity comparing with geniposide. Though, the only problem is that Gardenia jasminoides contains genipin in a micro-scale.
In this study, our purpose is to evaluate Gardenia jasminoides by bio-conversion of geniposide to genipin through fermentation with GRAS level lactic acid bacteria (LAB). More than 200 LABs were isolated from Korean traditional food (Kimchi) and screened with Gardenia jasminoides through fermentation. Lactobacillus brevis sp. 1 and Lactobacillus brevis sp. 2, two LABs strains had the strongest conversion activity. Bio-conversion have Gardenia jasminoides showed much higher glucose uptake activity and anti-inflammatory. This study may provide a new insight into bio-conversion of compounds from traditional herbal medicines for potentially improving functions to make people have more healthy life.
[This research was supported by a grant (NRF-2013M3A9A5076601) from a study on the strategies of improving the value of microbial resources funded by Ministry of Science and ICT of the Korea Government and a grant from KRIIB Research Initiative Program]

C014
Genotypic and Phenotypic Characteristics of Staphylococcus aureus Exposed to Tetracycline
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The emergence of antibiotic-resistant pathogens has received a great attention in terms of treatment and detection of their infections. Therefore, this study was designed to assess genotypic and phenotypic properties of Staphylococcus aureus exposed to different levels of tetracycline. Strain of S. aureus was exposed to a half MIC, 1×MIC, and 2×MIC for 10 min or 1 h. Antibiotic susceptibility, β-lactamase activity, efflux pump activity, and gene expression were measured to evaluate phenotypic and genotypic properties of S. aureus. All the genes tested in S. aureus were overexpressed when exposed to tetracycline. The highest expression levels of leus, mgrA, pta, recA, rpoB, rpsE, thrS, and tsf were observed for S. aureus exposed to a half MIC for 1 h, while dnaK, mepA, and thrS showed the highest expression level at a half MIC for 10 min. The β-lactamase and efflux pump activities were well corresponded with the specific gene expressions. The results provide unique information to develop a method to detect antibiotic-resistant S. aureus.
[This research was supported by a grant of the Korea Health Technology R&D Project through the Korea Health Industry Development Institute (KHIDI), funded by the Ministry of Health & Welfare, Republic of Korea (Grant number : HI15C-1798-000016).]
C015
Analysis of Aerotolerant Campylobacter for Management System of High Risk-human Infection
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Campylobacter jejuni is the leading bacterial cause of human gastroenteritis worldwide. Due to the increasing rates of human Campylobacteriosis, C. jejuni is considered as a serious public health concern. C. jejuni is a microaerophilic, fastidious bacterium. To develop human infection, C. jejuni must survive in oxygen-rich conditions during foodborne transmission to humans. C. jejuni forms biofilms and viable-but-non-culturable (VBNC) cells under aerobic conditions to sustain its viability. In contrast to our common knowledge about the oxygen sensitivity of C. jejuni, we found Aerotolerant and hyper-aerotolerant C. jejuni strains are highly prevalent (over 90%) in patient specimen in Korea. Interestingly, the hyper-aerotolerant strains were classified predominantly to the MLST sequence types (ST21 MLST type) that are frequently implicated in human infection. Oh et al. reported that the ratio of aerotolerant, aero-tolerance, and hyper aero-tolerance strains of C. jejuni isolated from Canadian poultry did not differ. Our results demonstrate that high oxygen resistance strains of C. jejuni derived from animals are likely to survive and become infected to humans. In order to control the infection of C. jejuni, it is important to control oxygen resistant strains that are at high risk of infection among poultry contaminated pathogens.

[This study was supported by a grant from the Korea Centers for diseases Control and Prevention (grant no. 2017-NI41003)]

C016
Pullulan Nanoparticles as New Prebiotics Formula Enhanced the Antimicrobial Ability of Lactobacillus plantarum
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Probiotics have been used as alternatives to antibiotics due to their ability to inhibit the colonization on the gut barrier or to directly kill the pathogens through their secreted bacteriocins. Among the probiotics, Lactobacillus plantarum (LP) has shown strong antimicrobial activity against Escherichia coli K99, a major livestock pathogen. In this study, we aimed to investigate the antimicrobial activity of phthalyl pullulan nanoparticle (PPN)-treated LP. Interestingly, when PPNs were added to LP, the PPNs were internalized into the LP through an energy-dependent galactose transporter-dependent mechanism. Additionally, more plantaricin, a natural antibacterial peptide, was secreted from PPN-treated LP than from untreated or pullulan-treated LP. Furthermore, antimicrobial activity against Gram-negative Escherichia coli K99 and Gram-positive Listeria monocytogenes by PPN-treated LP was higher than those of untreated or pullulan-treated LP. It is thought that the enhanced antimicrobial properties of the PPN-treated LP are due to intracellular stimulation. Overall, this research provides a new method of producing plantaricin in LP through intracellular stimulation by internalized PPNs.

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C017

In Vitro Characterization and Evaluation of Fermented Microorganisms Isolated from Korean Traditional Fermented Foods for Industrial Applications

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From eight Korean traditional fermented foods, total 1,589 bacteria were previously isolated. Among them, 16 probiotic strains (nine Lactococcus lactis, five Lactobacillus plantarum, and two Lb. breve) were selected. They were evaluated in two characteristic categories of food processing (oxygen tolerance, heat tolerance, and gastric/bile acids tolerance) and probiotic functions (mucin adhesion, cholesterol lowering, and immunomodulation). Oxygen tolerance test showed that they were grown up to OD₅₉₅ 1.0 in 36 h under the shaking aeration (180 rpm). In addition, gastric/bile acid tolerance tests showed that they are tolerant to the acids. In particular, Lactobacillus (>89.2% survival) were more resistant to the acids than Lactococcus (<75.3% survival), suggesting that they may have fair tolerance activities under food processing conditions. Furthermore, mucin adhesion activities were evaluated, showing that they have >73.3% adhesion abilities and especially Lactobacillus showed the highest adhesion abilities (>86.6%). The cholesterol lowering test revealed that cholesterol removing activities were ranged from 35.6% to 89.5%. In addition, their immunomodulation activities were measured using Raw 264.7 cells with LPS control and Lactobacillus showed high amount of IL-10, suggesting that Lactobacillus may have good immunomodulation activities. These results suggest that these selected probiotics may have required characteristics and functions for food industrial applications.

C018

Synbiotic Effect of Selective Lactobacillus spp. with Gastrodia elata, and Their Potential as Neuroprotective Functional Food

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Traditional medicinal herbs, Gastrodia elata include 4-HBA, which is known to treating brain diseases including dementia. When Gastrodia elata fermented with a specific Lactobacillus isolated from kimchi, it was completely converted to 4-HBA from gastrodin. In other word, gastrodin was converted to 4-HBA in the intestines by specific Lactobacillus that exerts neuroprotective efficacy. As a result of analysis of the basic characteristics of this Lactobacillus, it was confirmed that the acid resistance, bile acidity and intestinal adherenc are excellent. Whole genome sequencing analysis of this strain show Lactobacillus plantarum spp.. And Gastrodia elata was known to having many polysaccharides including oligosaccharides. In our study, some pathogens can not grow using this, but this Lactobacillus grow well using polysaccharide of Gastrodia elata and extra materials. Therefore, intaking Gastrodia elata fermented by this GRAS Lactobacillus is possible as synbiotics having neuroprotective function.

[This research was supported by a grant (NRF-2013M3A9A5076601) from a study on the strategies of improving the value of microbial resources funded by Ministry of Science and ICT of the Korea Government and a grant from KRIIB Research Initiative Program.]
C019
Cometabolic Degradation of Chlorinated Ethenes by Acidophilic Methanotroph Isolated from Acidic Peat Bogs
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All Methanotrophs have long been studied for bioremediation of soils and groundwater contaminated with chlorinated solvents. Reductive dechlorination using Dehalococcoides is the standard protocol in the industry; however, application of reductive dechlorination to acidic soils is not feasible, as vinyl chloride (VC) reduction cannot be carried out in environments with pH<6.0.

Here, we propose cometabolic degradation using methanotrophs for removal of chlorinated ethenes from acidic environments. Two acidotolerant methanotrophs were isolated from peat samples collected from two different peat bogs in Korea. Enrichment of the peat sample with CH₄ adjusted to pH 5.0 and subsequent isolation procedure using the dilution-to-extinction method resulted in isolation of Gamma- and Alphaproteobacterial methanotrophs. The chlorinated ethene-degrading capability of the isolated strains was examined by incubating the isolated methanotroph with 20% CH₄ in the headspace and VC at initial dissolved concentration of 45 μM. CH₄ and VC concentrations were monitored until the reactions were complete. Except for pMMO expressing Methylomonas sp. MJC1, the injected VC was entirely degraded within 3 days. To verify application for practical environment, peat enrichment was examined with similar method of above VC degradation test. The injected VC was entirely degraded within 7 days. From these results, we concluded that methanotrophs in acidic environment are capable to degrade VC.

C020
The Potential of Glehnia littoralis Fermented by LAB
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The objective of this study was to determine the processing method of Glehnia littoralis (Gl) fermentation by Lactic Acid Bacteria (LAB) and the antibacterial, antioxidant, and anti-melanization efficacy of fermented Gl containing the GABA(γ-Aminobutyric acid) produced by the LAB. Gl were extracted for 4-6 hours in 85°C water, inoculated into each extract with LAB, Lactobacillus plantarum (Lp) and Pediococcus acidilactici (Pa) used in the experiment. The extracts of Glehnia littoralis (HeGl) was sterilized before fermentation by LAB, filtered, and then used for experiments. To enhance GABA concentration in the fermented Gl (HeGl-LpPa) culture conditions including nutrient factors and temperature are optimized. The GABA production and viable LAB growth were observed in the HeGl at 30°C. These results showed that GABA concentration and antioxidant activity were higher in the HeGl-Lp and HeGl-Pa than in the HeGl, and antibacterial effect was no significant difference both Propionibacterium acne and Malassezia furfur. Additionally, this fermented HeGl by LAB with GABA had high antioxidant, innoxious and antibiosis effect. This suggests that the fermented HeGl have potential for application in various scalp care, cosmetic, and food products for which a natural GABA additive is desired.

[This work was supported by the Technological Innovation R&D Program of Small and Medium Business Administration (S2600449).]
C021
Application of LAB for Improving Storage of Protaetia brevitarsis as Food
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Protaetia brevitarsis (Pb) has been temporarily registered as a food material by the Ministry of Food and Drug Safety of Korea (MFDS) but not ensured of safety for storage and distribution. In order to initiate and provide controlled and predictable Pb as food, the production of fermented foods is based on the use of lactic acid bacteria (LAB) as starter cultures. This study investigated change and characterization in physiochemical properties of LAB cultures (HePb-LAB) in hot water extract from Pb (HePb). Fermentation test of HePb conducted with 2% dextrose and some carbon source for cultivating LAB, lyophilized, and then counted the viable LAB (10^9-10^11 cfu/mg). Our results showed that antioxidant, antibacterial and potential enzyme activity were higher in HePb-LAB than in HePb, but not in the non-fermented Pb. These results provide basic or first data for the development of fermented food with edible insect.

[This work was supported by IPET through Agri-Bio industry Technology Development Project, funded by MAFRA (118034-2).]

C022
Tomato Plant Growth Promoting Flavobacterium Species and Effect on Rhizosphere Microbial Community
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The rhizosphere microorganisms play a crucial role for plant functions such as plant growth. In the previous research, a novel species of Flavobacterium isolated from tomato rhizosphere was selected for further research. To test plant growth promotion (PGP) effect, we treated the culture of the strain to germinate d tomato seedlings and after one week, these inoculated seedlings were planted into both non-sterilized and sterilized upland soil. Tomato plants grown for five weeks in the non-sterilized soils showed the significantly increased fresh weight and dry weight. Moreover, the tomato plants inoculated by the strain showed the remarkably earlier flowering and produced more fruits compared to the non-treated control. To investigate the alteration of rhizosphere microbiome by the treatment of the strain, we analyzed 16s rRNA amplicon sequencing data generated by MiSeq using QIIME pipeline. The analysis of rhizosphere microbiome treated by the strain showed no significant difference (p=0.367) with the non-treated control, however, the relative abundance of certain group of family was significantly different between the treatment of the strain and non-treatment control.
C023

Effect of ybeD Expression on Thermotolerance in Escherichia coli

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Heat-resistance of microbial hosts are necessary for mitigation of heat-stress occurring in high cell density cultivations at large scale culture processes. We provide a new evidence of the YbeD protein that allows the microorganism to maintain cell growth at high temperatures. The ybeD homologs were identified in all of the 88 completed genomes of E. coli strains. ybeD gene expression was increased at high temperature. The growth of ybeD deleted in E. coli is inhibited at high temperature. However, overexpression of ybeD increases the cell growth rate at higher temperature than that of wild type strain. Also, the ybeD overexpression leads to enhancement of growth in other E. coli strains of MG1655, W3110, DH10B, and BW25113 at high temperature. In conclusion, YbeD protein causes microorganism to grow efficiently at high temperature as it has a substantial role in heat shock protein.

C024

Unveiling of Complex Signaling Networks that are Involved in the Developmental Process of Cryptococcus neoformans

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The fungal pathogen Cryptococcus neoformans causes cryptococcosis by the inhalation of infectious spores generated by unisexual or bisexual reproduction. To understand complex signaling networks modulating the developmental process, a complete understanding of genome-scale transcription factors (TFs) and kinases is needed. Previously we reported that 37 TFs and 42 kinase mutants constructed in C. neoformans MATα H99 strain background exhibited altered mating efficiency. To further elucidate the mating regulatory mechanism, we constructed knockout mutants of the mating-regulating TFs and kinases in YL99 strain—MATa isogenic strain of H99 strain—to monitor unilateral and bilateral mating, and to perform an analysis of their function in the developmental process. We constructed 22 gene-deletion strains representing eleven TFs and are currently constructing gene-deletion strains for the remaining mating-regulating TFs and kinases. For confirmed mutant strains, we are examining mating phenotypes during bilateral mating: mating pheromone production, cell fusion efficiency, filamentous growth, formation of basidia and basidiospores. Furthermore, we are examining transcript profiles of mating-regulating TFs and kinases at different developmental stages of sexual reproduction. Ultimately, this study will focus on mapping and discovering the functions of the mating-regulating TFs and kinases, and elucidating complex signaling networks in the developmental process of C. neoformans.
C025
The Role of Three Galactolipids Synthase Gene in Microalgal Lipid Turn-over from Membrane Lipid to Neutral Lipid
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Recently, research on lipid turnover within cells has investigated elucidation of the relationship between membranes and neutral lipids. In microalgae, lipid turnover could be usefully facilitated to convert an abundance of membrane lipids to rare neutral lipids, which can be used as feedstock for a biodiesel. In this study, we tried to down-regulated gene expression associated with membrane lipid metabolism to verify the role in lipid turnover between membrane lipids and neutral lipids. Three gene, MGD1 (Cre13.g585301.t1.1), DGD1 (Cre13.g583600.t1.2), SQD1 (Cre16.g656400.t1.2) MGD1, were generated to down-regulated mutants using amiRNA method in Chlamydomonas reinhardtii strain CC-124. Transgenic lines mgd-1, dgd3 and sqd13 were 67%, 53% and 49% downregulated in each gene expression levels. While the galactolipid transformants had half the amount of MG DG, DGDG, and SQDG, neutral lipid was increased approximately 3 – 6 fold in each transformatns lines. We assumed that significant reduction of galactolipids contents was directly affected on accumulation of DAG and release of acyl-CoA lead to the synthesis of TAG. Further, this hypothesis will be approved by using quantitative and qualitative analyses of all lipids.

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C026
Effect of Fed and Sprayed Lactobacillus plantarum Strain 545 on Fecal Microbiota in Broilers
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Background: Lactobacilli are local residents of chicken gastrointestinal track, where they may potentially be used as probiotics. The aim of this study was the effects of fed Lactobacillus plantarum 545 and sprayed on the intestinal microbiota of broilers.

Methods: In this study, we raised one-day broilers (4 heads/room and 4 rooms/group) for 40 days without any feed additives (Con), with fed (L. plantarum 545, T1), with sprayed (L. plantarum 545, T2). Fecal microbiota communities were analyzed by sequencing V4 regions of 16s rRNA genes.

Results: Serum IgA and IgG levels and body weight gain in all groups were no significant changes. At the phylum level, all treatment groups (T1 and T2) have fewer Firmicutes than Con (P<0.01). And all treatment groups have higher Bacteroidetes and Synergistetes than Con (P<0.01). At the genus level, all treatment groups have fewer Clostridium, Proteus, Pseudomonas and Streptococcus than Con, and higher Akkermansia, and Enterococcus than Con, but no significant changes were observed. And T2 has the highest level of Bifidobacterium and Leuconostoc (P<0.1).

Conclusions: These results indicate that feeding or being spray could change intestinal microbiota in broilers and that L. plantarum 545 may improve the intestinal microbiome. This study may provide basic information on how we can modulate chicken gut microbiota beneficially.

[This study was supported by NRF (NRF-2016R1C1B2016246).]
C027
A Comparative Proteomic Analysis of *Paenibacillus polymyxa* E681 in Phenotypic Variation
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*Paenibacillus polymyxa* E681, a plant growth-promoting rhizobacterium (PGPR) underwent phenotypic variation under natural conditions. According to our previous study, E681 changed from a sporulating (type ‘B’) to a nonsporulating phenotype (type ‘F’) just before autolysis of the majority of the population. In this study, we conducted comparative proteomics of expressing proteins in both wild-type and phenotypic variant. There were approximately 200 differently expressed spots in 2-dimensional electrophoresis (2-DE) profiles. Among these spots, 53 proteins were selected for identification by MALDI-TOF and matched the translation products of 18 different coding DNA sequences. From these, 47% of the identified proteins were involved in glycolysis and other metabolic pathways associated with carbohydrate metabolism. Other up-regulated proteins in the phenotypic variant were involved in flagella assembly, stress resistance and coenzyme production. Among them, 7 proteins were shown to be overexpressed in proteome (2-DE) and transcriptome analyses (RNA-sequencing). Several biocontrol agents including *P. polymyxa* are widely used in conventional agriculture, by contrast, the phenotypic variation of *P. polymyxa* is not studied well. Our findings provide new knowledge on the mechanism of phenotypic variation and insights in agricultural biotechnology.

C028
Hygiene Monitoring of Desiccated Cotton by Changing Operational Conditions
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Pathogenic bacteria on abiotic surfaces including fabrics and patient wears increase the risk of bacterial diseases in infants and the elderly. Desiccation tolerance of bacteria affects their viability in cotton. Thus, it is important to use a dryer machine under conditions that ensure sterilization of bacteria causing the microbial contamination in cotton. Our research was conducted using three pathogenic bacteria commonly presented in contaminated cotton and then two non-pathogenic bacteria. High survival rate of *Acinetobacter baumannii* and *Staphylococcus aureus* on desiccated cotton was observed by Scanning electron microscope and Replicate organism direct agar contact assay. Survival rate of bacteria exposed in desiccated cotton for 8 h was shown A. *baumannii* (15.8%) and S. *aureus* (7.56%) compared with the others bacteria (< 0.5%). Bacteria in this research exposed to temperatures ranging from 40°C to 70°C in phosphate buffered saline. All tested bacteria were eradicated at high temperatures (> 60°C) over 10 min. In condition of a dryer machine at 60°C for 4 h, however, sterilization rate was 93.2%. This level of sterilization was insufficient in terms of energy efficiency. High proportion (> 99.9%) to ensure reliable sterilization was confirmed at 75°C for 3 h. This study can suggest standard conditions of dryer machines to remove microbial contamination in cotton by providing practical data.

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C029
The Roles of a Novel Butyrate-producing Bacteria in Human Gut

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In the human gastrointestinal tract (GIT), the phylum Firmicutes and Bacteroidetes are the core members, which play commensal roles by aiding the digestion of non-digestible fibers and generating beneficial small-molecule metabolites. In particular, Clostridium cluster XIVa (family Lachnospiraceae) has attracted a great deal of attention due to microbial-derived metabolites such as short chain fatty acids (SCFAs). Among SCFAs, butyrate has been reported to reduce inflammation and pathogen colonization, and produce mucins and host antimicrobial peptides.

To research the roles of butyrate producers in human gut, we isolated a novel butyrate-producing bacterium from a healthy Korean faeces and studied its function in diseases associated with gut dysbiosis. Strain KGMB01110¹, which is a novel species of the genus Mediterraneibacter in the family Lachnospiraceae, produced butyrate as major end product of carbohydrate fermentation through conserved two butyrate synthesis pathways. Furthermore, strain KGMB01110¹ showed the anti-proliferation by apoptosis in human colon cancer cells and anti-tumoral effect in murine colorectal cancer model.

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C030
Physicochemical Components of Astragalus membranaceus Bunge Fermented with Lactic Acid Bacteria

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Fermentated Processing Food Science Division, Department of Agro-food Resources, National Institute of Agriculture Science, RDA

The purpose of this study was to investigate the quality characteristics of Astragalus membranaceus Bunge (AMB) fermented with Lactic acid bacteria and applicability of functional materials. It was also carried out to improve the functionality of various products. The physicochemical components such as pH, total acidity, extraction yield, free sugar and isoflavonoid content (calycosin, formononetin) were investigated. The content of isoflavonoid (calycosin, formononetin) in 80% ethanol extract of AMB fermented with Lactobacillus brevis, Leuconostoc mesenteroides and Lactobacillus plantarum were calycosin 4.96, 4.55, 4.23 mg/100 g and formononetin 0.68, 0.69, 0.68 mg/100 g respectively. These results indicate that it can be used to increase the bioactivity through fermentation, and AGNL can be used as a functional materials and edible resource in the industrial areas.
C031
Physicochemical and Active Ingredient of Astragalus membranaceus Fermented with Aspergillus awamori
Da Bin Lee, Bit Na Song, Sheng Hyun Lee, Bo Ram Park, and Shin Young Park

Fermented and Processed Food Science Division, Department of Agro-food Resources, National Institute of Agriculture Science

Medicinal plants have fewer side effects than synthetic drugs and can be taken for long periods of time. Fermentation of medicinal plants increases the body's absorption rate and bioavailability. It is valuable as a health functional food. So far, Astragalus membranaceus root (AR) has been used as a raw material. Moreover, researches on its use as a food material is not sufficient. There is a lack of research on its use as a food material. Therefore, the purpose of this study was to confirm the physicochemical characteristics of AR by fermentation. AR was fermented by Asp. awamori for 4 and 6 days. Samples were extracted using hot water and alcohol. The pH, total acidity, chromaticity and reducing sugar were investigated. The pH level and total acidity decreased during the fermentation. The total acidity level is 3-5%. The reducing sugar content increased with fermentation. It was the highest 4 days of fermentation. Five active ingredient of the fermented AR were analyzed. The active ingredient were calycosin-7-O-ßd-glucoside, ononin, calycosin, Isomucronulato7-O-ßd-glucoside and formononetin. The content of calycosin was the highest in the hot water extraction samples for 4 days of fermentation. The other components were similar to the control group. The results showed that physicochemical components and active ingredient in the fermentation process of AR were improved. These results indicate that fermented AR can be used as a functional food.

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C032
Zearalenone Biosynthesis and Exocytosis Mechanism in Fusarium graminearum
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Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University

Fusarium graminearum is a plant pathogen that causes Fusarium head blight (FHB) in major cereal crops such as wheat, barley, corn, and rice worldwide. Not only does this fungus causes destructive yield losses, it also produces mycotoxins, zearalenone (ZEA) and trichothecene, on infected grains, which pose serious threat to human and animal health. Although ZEA has relatively low prompt toxicity, the structure is similar to estrogen, and it binds to estrogen receptors of mammals and interferes with effect of estrogen, resulting in reproductive dysfunction.

Previous studies have been characterized ZEA biosynthetic genes (PKS4, PKS13, ZEB1, and ZEB2) and their mechanism of action in ZEA biosynthesis of F. graminearum. In this study, green fluorescent protein (GFP) was tagged to Pks4 and Pks13, and both proteins were revealed to localize in cytosol under ZEA inducing condition. We also tried to investigate ZEA secretion mechanism. Supposing that vesicle trafficking is involved in ZEA exocytosis, we deleted SYN2, which encodes a syntaxin required for fusion of secretory vesicle. We found that ZEA is captured in hyphae of syn2 deletion mutants, compared with being ejected out of the cell in the wild-type strain. This study will provide information on where the secondary metabolites are biosynthesized and how they are ejected out of the fungal cell, and let us develop a novel mycotoxin reduction strategy.

[Supported by grants from Seoul National University]
C033
DNA Guided ssDNA-specific Nuclease from Hydrogenophaga intermedia
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Argonaute proteins are effectors of gene silencing system in all domain of life. Several argonaute proteins utilize small DNA or RNA guide to cleave a complementary target. Here, we analyzed argonaute protein of Hydrogenophaga intermedia (Hin) which was purified using E. coli expression system. We observed that Hin argonaute protein was an ssDNA-guided specific nuclease using 5’-phosphorylated guide DNA. Guide-free Hin could bind to and cut double strand DNA with topoisomerase activity. Hin argonaute required only 17-nucleotide-long guide DNA for ssDNA targeting, suggesting that it might have potential for a novel genome engineering tool.

[This work was supported by grants from Samsung Science and Technology Foundation.]

C034
A Method Using Crispr/dCas9 for Cloning and Expression of Highly Toxic Proteins
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Crispr/Cas9 system was originally developed as an RNA-guided nuclease but its applications were expanded to gene regulators, gene editors and molecular recorders. Here Crispr/dCas9 was used to develop a system for the cloning and expression of lethal genes in Escherichia coli. We demonstrated, using several nuclease genes as examples, that the host vector system described in this report was valuable for the controlled expression for purification as well as cloning of lethal genes.

[This work was supported by grants from Samsung Science and Technology Foundation.]
**C035**

**Screening of DDase (Dextran dextrinase) Activity of Acetic Acid Bacteria**

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Dextrin dextranase (DDase), 6-alpha-D-glucosyltransferase (EC 2.4.1.2) is an enzyme that catalyzes the chemical reaction (1,4-alpha-D-glucosyl) \( n + (1,6\text{-alpha-D-glucosyl}) \to (1,4\text{-alpha-D-glucosyl}) \to n-1 + (1,6\text{-alpha-D-glucosyl}) \to m+1. In general, DDase converts maltodextrin into 1,6-alpha-D-glucan as products. To determine DDase activity of acetic acid bacteria (AAB), Gluconobacter oxydans was used for positive control. The bacterial strains were isolated and sequenced using 16s rRNA sequences. Based on sequenced results, phylogenetic tree was showed the homology between AAB. The sequenced bacterial strains were also determined by Polymerization chain reaction (PCR) using a pair of primers targeting partial DDase sequence from Gluconobacter oxydans. To investigate DDase activity of these bacterial strains, the culture mediums of acetic acid bacteria including maltodextrin were analyzed by HPIC (High-performance ion chromatography). TLC (Thin liquid chromatography) analysis was also showed the sugar composition change in culture medium by enzyme secreted from various AAB.

**C036**

**Heterologous Expression of DNAJ-like Chaperone for Enhanced Carotenoid Synthesis in Microalgae**

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The commercial production of microalgal carotenoids is focused on the possible replacement of plants because of high carotenoid productivity and varied ingredients of secondary carotenoids. The DNAJ-like chaperone, also known as ORANGE (OR) protein, have a pivotal role in regulating carotenogenesis and stress tolerance response in plants under extreme conditions. The OR gene mutation in cauliflower, Arabidopsis, melon, and sweet potato induced the accumulation of high levels of lutein, \( \beta \)-carotene or zeaxanthin. Interestingly, a single amino acid substitution, Alanine to Histidine, in wild-type OR gene greatly increased its ability to promote carotenoid biosynthesis in plants. Here, we generated mutants with endogenously overexpressed OR gene in *Chlamydomonas* and *Ettlia* sp. to investigate the functional role in microalgal carotenogenesis. Moreover, Wild-type IbOR and IbOR\( ^{R96H} \) were heterologously overexpressed in both microalgae to increase the carotenoid levels. Through this study, we aim to identify comprehensively the regulatory mechanisms of OR in microalgal carotenoid accumulation and protection against stress and to realize the development of commercial microalgal mutants with enhanced nutritional quality.

[Supported by grants from Ministry of Science and ICT and NRF]
C037
Characterization of a Thermostable Alkaline Mannanase Purified from *Bacillus subtilis* subsp. *inaquosorum* CSB31
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Mannanase (MnB31) from *Bacillus subtilis* subsp. *inaquosorum* CSB31, isolated from fermented food Kimchi and produced in locust bean gum, was biochemically and thermodynamically characterized. MnB31 was purified to 17.92-fold with 21.51% yield using ion exchange chromatography and gel filtration chromatography in successions in order to obtain purified mannanase owing specific activity of 1796.13 U/mg. It was estimated to have a molecular mass of ~47 kDa via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and glactomannan zymography. It was optimally active at 60ºC and thermostable to 65ºC. MnB31 showed maximal activity with KCl/NaOH buffer (pH 12.5) and stable over wide range of pH (5.8–12.5). The N-terminal amino acid sequence was A-L-Y-E-T-I-F-A-L-X. MnB31 had $K_m$ and $V_{max}$ of 0.03885 mg/ml and 1019.33 ± 4.509 U/mg respectively. The activation energy ($E_a$) for locust bean gum hydrolysis was 31.36 kJ/mol with a $K_{cat}$ value of 152.8995x10$^4$ sec$^{-1}$. Other thermodynamic parameters also supported the spontaneous formation of products, greater hydrolytic efficiency and feasibility of enzymatic reaction, which strongly stands out for industrial biotechnological applications. The halo-tolerance, urea stability and protease resistance of MnB31 signifies its potential applications.

C038
A Potent Cationic AMP from *Bacillus* sp. as a Probiotic Food Produced from Kimchi
Jin Cheol Yoo, Yoon Seok Choi, BoMin Kim, Seung Eun Lee, and Md Maruf Khan*

Department of Pharmacy, College of Pharmacy, Chosun University

Survival strain *Bacillus* CBS YD1 in the gut was found as a potential bacteriocin producing a probiotic candidate, which is mostly identical to *Bacillus amyloliquefaciens* sp. *plantarum*. The aim was for the identification of probiotic, characterization and produces the maximum bacteriocid strain *Bacillus* CBSYD1 from fermented Kimchi. The growth of strain decreased after 3 h in MRS media with bile salt, but strain had the ability to adapt to the bile salt condition, and a clear halos zone was observed in bile salt plate assay. Strain cell viability was detected in different conditions of the digestive track. Different culture's broth media were used to produce bacteriocin, and a clear inhibition zone was observed using Muller-Hinton agar plate. Tricine SDS-PAGE and In-situ analysis determined the band and molecular weight. The optimized growth medium was composing of 1% peptone, 2% maltose, and 0.01% CaCl$_2$. YD1 showed maximum inhibition activity against both 14 Gram positive and negative strains out of 33 bacteria with the highest arbitrary unit per milliliter (AU/ml) at 37ºC for 36 hours production that correlated with its total protein. YD1 remained completely stable at pH 4–9 and up to 80ºC and was found stable with different concentration of proteases up to 60 min of incubation. The molecular weight of YD1 is to be approximate ~3.2 kDa.
**C039**

**Effects of ID-CBT5101 in Preventing and Alleviating Osteoarthritis Symptoms in a Monosodium Iodoacetate-induced Rat Model**

Min-Goo Kim, Byeonghun Lee, Jin Seok Moon, Su Hyeon Eun, and Tae-Yoon Kim

*Research Laboratories, Ildong Pharmaceutical Co., Ltd.*

Osteoarthritis is a disease that affects the articular cartilage and osseous tissue, and can be worsened by aging, overweight status, and post-traumatic arthritis. This study aimed to evaluate the effect of ID-CBT5101 (tyndallized *Clostridium butyricum*) on bone metabolism and the inflammatory response in a monosodium iodoacetate-induced rat model of osteoarthritis. We evaluated the treatment effects based on serum biomarkers, mRNA expression, morphological and histopathological analyses of the knee joints, and weight-bearing distribution analysis. Compared with control rats, the ID-CBT5101 treatments significantly reduced the serum concentration of inflammation and bone metabolism markers and significantly increased the concentration of IFN-γ and glycosaminoglycans. In addition, the ID-CBT5101 treatments effectively preserved the knee cartilage and synovial membrane, and significantly decreased the amount of fibrous tissue. The results indicate that ID-CBT5101 prevented and alleviated osteoarthritis symptoms. Thus, ID-CBT5101 may be a novel therapeutic option for the management of osteoarthritis.

**C040**

**Skin Moisturizing and Antiphodamage Effects of Tyndallized *Lactobacillus acidophilus* IDCC 3302**

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Photoaging is generally the result of chronic exposure to the sun and ultraviolet (UV) radiation, which causes skin damage. In this study, we developed a UVB-induced hairless mouse model to determine whether *Lactobacillus acidophilus* IDCC 3302 tyndallizate (ACT3302) can enhance photodamaged skin repair. Mice (6 weeks old) were divided into six groups containing normal, UVB-treated vehicle, and UVB-treated ACT3302 (1·10⁵, 1·10⁶, 1·10⁷, and 1·10⁸ cells). Epidermal thickness was increased by UVB, but the thickening was lessened by ACT3302 as was the transepidermal water loss (TEWL). However, ACT3302 increased capacitance and decreased TEWL. Skin tissue staining to evaluate skin collagen increases in the number of skin collagen bundles in UVB-treated ACT3302 mice. UVB irradiation increased matrix metalloproteinase (MMP) and proinflammatory cytokine expression and activated mitogen-activated protein kinases in hairless mice; these changes were also attenuated by ACT3302. We conclude that ACT3302 effectively suppressed wrinkle formation induced by UVB irradiation through MMP downregulation. Therefore, ACT3302 potentially prevents skin photoaging and wrinkle formation.
The Probiotic, ID-JPL934, Attenuates Dextran Sulfate Sodium-induced Colitis in Mice through Inhibition of Proinflammatory Cytokines Expression

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Despite the increasing prevalence of inflammatory bowel disease (IBD), classified as immune-mediated disorders, the exact biological mechanisms leading to its development are undetermined, and treatment strategies remain elusive. Probiotics have been proposed as potential alternatives for treating IBD. The purpose of this research was to find therapeutic candidates of probiotics for colitis. We adopted dextran sulfate sodium (DSS)-induced colitis model to demonstrate the therapeutic effects of ID-JPL934, a mixture of three live bacterial strains at a 1:1:1 ratio: Lactobacillus johnsonii IDCC9203, Lb. plantarum IDCC3501, and Bifidobacterium animalis subspecies lactis IDCC4301, on IBD. The severity was scored according to the disease activity index (DAI) for colitis by observing body weight (BW) and stool status of each mouse once a day. BALB/c mice given 3.5% DSS in drinking water suffered from symptoms of colitis such as weight loss, diarrhea, and bloody excrement. In our study, administration of ID-JPL934 reduced the DAI scores in a dose-dependent manner, and treatments with ID-JPL934 10^8 and 10^9 colony-forming unit per mouse per day showed similar inhibition compared with those of sulfasalazine 500 mg/kg BW per day. Moreover, the contraction of colon length improved. ID-JPL934 also suppressed inflammatory lesions such as infiltration of immune cells in mucosa and submucosa, severe crypt damage, and loss of goblet and epithelial cells on the histological analysis. These results might be due to downregulation of the expression of proinflammatory cytokines, including tumor necrosis factor-a, interleukin (IL)-1ß, and IL-6. From these results, ID-JPL934 might be an effective therapeutic candidate for IBD.
D001
Study of Modified Amies Media Prepared by Gamma Sterilization to Process Specimen Collection and Preservation to Maintain Viability of Clinically Important Bacteria Including *Haemophilus influenza* and Others
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Modified Amies media have been studied to process clinical specimen collection and preservation to transport viability of aerobic, anaerobic and fastidious bacteria for up to 48 hours at 4°C and room temperature. Suitable specimen transport with the most appropriate device from collection to the laboratory is essential for accurate laboratory diagnostics. Especially, antimicrobial resistant strain is a cross-disciplinary issue, with ground-breaking studies currently bringing together clinicians, microbiologists, veterinary, soil scientists and anthropologists. So, we have studied liquid transport NB Swab™ system with modified Amies medium formulation containing nicotinamide adenine dinucleotide (V factor) and hemin (X factor) as a relatively new system compared to conventional solid gel-tube system. This NB Swab™ system was evaluated viability of *Haemophilus influenza* and others in our laboratories. To prevent chemical damage by Gamma-Irradiation a few radioprotectants were added and effective for the normal growth of these specific bacteria with Gamma-Irradiation as compared to control. The test procedures for quality control are based upon the quality control methods described in CLSI M40-A2 and others. [Support by grants from KHIDI]

D002
Direct Evolution of the Endolysin PlyPH, Active against *Bacillus anthracis*, Towards Higher Proteolytic and Thermal Stability
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The endolysin PlyPH was previously found to be highly active against *B. anthracis* and was proposed to use as a new therapeutic agent. However, a main limitation in the therapeutic application of peptides was their susceptibility to proteases that generally correlated to heat instability. After three rounds of random mutagenesis, we selected the thermostable mutant PlyPH-A11, which displayed a 5°C increased melting temperature ($T_m$) in comparison to the wild-type enzyme, and contained multiple amino acid substitutions: F130L, K136E, E152D, Q196R, Q208R. The lytic activity of thermostable mutant was optimal over the temperature range from 25°C to 57°C in contrast to the wild-type enzyme, which exhibited the optimal lytic activity between 25°C and 50.5°C. At a temperature of 25°C, the lytic activity of the A11 mutant was almost 50% lower than that of the wild-type enzyme. The A11 mutant demonstrated an increased resistance to proteolytic digestion by plasmin and, after substitution of arginine in position 196, by trypsin. Substitution of arginine for glutamate increased lytic activity by 15% at 25°C with keeping the highest activity at elevated temperatures. The A11-E196 mutated enzyme showed an extended half-life compared to the wild-type PlyPH at elevated temperatures 56°C and 59.5°C.

[This work was supported by the grant MGC2100834 of the Ministry of Education, Science and Technology (MEST) Republic of Korea and by a KRIBB Basic Research Grant.]
**D003**

**Exploring the Actin Dynamic Pathway Hijacked by HIV-1 Infection**  
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HIV-1 hijacks the actin dynamics network during the viral entry and migration of the pre-integration complex into the nucleus. Although some inhibitors have been analyzed with regard to HIV-1 infection, their effects are sometimes disputed and the exact mechanisms for actin dynamics in HIV infection have not been well elucidated. Here, the small molecules regulating HIV-1 infection from diverse inhibitors of the actin dynamic network were screened. Chaetoglobosin A and CK-548 were observed to specifically bar the viral infection, while actin inhibitors increased the viral infection without cytotoxicity within a range of ~μM. However, previously known inhibitory compounds of HIV-1 infection, such as Latrunculin A, Jasplakinolide, Wiskostatin and Swinholide A, exhibited either an inhibitory effect on HIV-1 infection combined with severe cytotoxicity or showed no effects. Our data indicate that Chaetoglobosin A and CK-548 have considerable potential for development as new therapeutic drugs for the treatment of HIV infection. In addition, the newly identified roles of Cytochalasins and some inhibitors of Rho GTPase and LIMK may provide fundamental knowledge for understanding the complicated actin dynamic pathway when hijacked by HIV-1. Remarkably, the newly defined action modes of the inhibitors may be helpful in developing potent anti-HIV drugs that target the actin network, which are required for HIV infection.  
[Supported by grants from the KNIH (2019-NI066-00)]

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**D004**

**Effect of Manuka Honey and Its Bioactive Component, Methylglyoxal, on Biofilm Formed by *Escherichia coli* O157:H7**  
Su-Yeon Kim and Seok-Seong Kang*

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Manuka honey (MH) and its bioactive component, methylglyoxal (MGO), exhibit anti-bacterial activity against pathogenic bacteria. However, the inhibitory effects of MH and MGO on biofilm formation by *Escherichia coli* O157:H7 have not yet been investigated. In this study, MH significantly inhibited biofilm formation by *E. coli* O157:H7 (p < 0.05) by reducing bacterial growth and viability. Pre- and post-treatment with MH also significantly reduced the biofilm formation by *E. coli* O157:H7 (p < 0.05). Similar to the inhibitory effect of MH, MGO markedly inhibited the biofilm formation by *E. coli* O157:H7 as well as its growth (p < 0.05). Using confocal laser scanning and scanning electron microscopes, a considerable reduction in biofilm formation by *E. coli* O157:H7 in the presence of MGO was observed. Furthermore, biofilms formed by *E. coli* O157:H7 on the surfaces of stainless steel and beef meat were significantly reduced after exposure to MGO (p < 0.05). Collectively, this study highlights the potential of anti-biofilm properties of MH and MGO which could be applied to control *E. coli* O157:H7 in food matrices and food processing facilities.  
[Supported by a grant from the National Research Foundation of Korea, which is funded by the Korean government (NRF-2017R1D1A1B03028730).]
D005
Anti-biofilm and Anti-inflammatory Properties of Bacteriocin Produced by *Pediococcus acidilactici* against *Enterococcus faecalis*
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Although *Enterococcus faecalis* is known as a commensal microorganism in the gastrointestinal tract, it causes various infections related with foods. Biofilm formation by *E. faecalis* is associated with the infections by exacerbating inflammation. Hence, we demonstrated that bacteriocin produced by *Pediococcus acidilactici* exhibited anti-biofilm and anti-inflammatory activities against *E. faecalis*. Bacteriocins purified from two probiotic *P. acidilactici* K10 and HW01 strains significantly inhibited biofilm formation by *E. faecalis* on surfaces of polystyrene and stainless steel, while both K10 and HW01 bacteriocins slightly inhibited the growth of *E. faecalis* planktonic cells. Exopolysaccharide production by *E. faecalis* was substantially decreased in the presence of both bacteriocins, suggesting that the inhibition of *E. faecalis* biofilm was by the decreased exopolysaccharide production, but not by killing bacteria. K10 and HW01 bacteriocins also reduced the adhesion of *E. faecalis* to human intestinal epithelial cells. Furthermore, both bacteriocins significantly inhibited *E. faecalis*-induced interleukin-8 production in human epithelial cells. These results suggest that bacteriocin of *P. acidilactici* is able to eradicate *E. faecalis* biofilm as well as to inhibit inflammatory response in the intestinal epithelial cells.

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D006
Inhibitory Effect of Bacteriocin Produced by *Pediococcus acidilactici* on the Biofilm Formation of *Salmonella* Typhimurium
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*Salmonella* biofilms are responsible for contamination in food processing environments as well as serious foodborne diseases. In this study, bacteriocins purified from *Pediococcus acidilactici* K10 (bacteriocin K10) and HW01 (bacteriocin HW01) strains were investigated for their potential to inhibit *Salmonella* Typhimurium biofilm. Both bacteriocins significantly inhibited the biofilm formation of *S. Typhimurium* by crystal violet staining method (*P* < 0.05). Fluorescence and scanning electron microscopy analyses confirmed that the *S. Typhimurium* biofilm was reduced in the presence of bacteriocins. After the biofilm formation of *S. Typhimurium* for 1 to 24 h, both bacteriocins K10 and HW01 exhibited similar patterns of decreased viability of *S. Typhimurium* biofilm cells up to 24 h (*P* < 0.05). The growth of *S. Typhimurium* planktonic cells was also significantly inhibited by treatment with bacteriocin K10 at 24 h and by treatment with bacteriocin HW01 at 12 and 24 h (*P* < 0.05). Furthermore, *S. Typhimurium* biofilm on the surfaces of stainless steel and chicken meat was effectively reduced by the treatment with both bacteriocins K10 and HW01. These results suggest that the bacteriocins of *P. acidilactici* could be effective anti-biofilm agents to control *S. Typhimurium* contamination in food matrices and food processing facilities.

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D007
A Simple Method for RNA-Seq From Mixed Microbe/Host Samples
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Analysis of RNA isolated from mixed microbe/host samples can reveal the presence of RNA viruses, the expression of bacterial and/or viral genes, as well as the expression status of the host. While PCR can be an effective method for the measurement of specific sequences, it is limited to identifying only known target sequences and by the level of multiplexing possible. Traditional RNA-Seq provides hypothesis-free data, but is limited by rather high input requirements, typically 100 ng of more of total RNA. In addition, the sequencing data is typically dominated by host reads. Therefore, without deep sequencing of each RNA-Seq library, microbial reads could be missed altogether. Capture based target enrichment RNA-Seq methods can be used to enrich for microbial sequences, but this approach only allows analysis of the targets included in the capture probe set. NuGEN has developed a simple, hypothesis-free method called Trio RNA-Seq that overcomes the above challenges. As little as 500 pg of total RNA is converted to cDNA and amplified with Single Primer Isothermal Amplification (SPIA). After enzymatic fragmentation and NGS library generation, specific unwanted host transcripts are targeted for depletion, resulting in a significant reduction of the number of sequencing reads required to achieve microbial RNA detection as compared to traditional RNA-Seq methods.

D008
Evaluation of Mycobacterium anyangense as a Preventive Vaccine against M. tuberculosis in Mice
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Bacillus Calmette-Guérin (BCG) is the only currently used vaccine against TB. This is known to be effective to infant but it shows also, low or unmeasurable efficacy in many case especially to adults. In this study, we evaluated the vaccine efficacy against tuberculosis of Mycobacterium anyangense (SNUMI-9), which is non-tuberculous mycobacteria (NTM), approved its safety. We used 6 weeks old female C57BL/6, C3Heb/FeJ mice infection model. The mice were vaccinated in two sessions two weeks apart with PBS, M. bovis BCG Tokyo 172, live and heat-killed SNUMI-9. After that they were infected with an average of 100 colony-forming units (CFUs) of Mycobacterium tuberculosis (TB) by the inhalation exposure system. After 6 weeks from TB challenge infection, the CFUs which vaccinated with SNUMI-9 (live, heat-killed) in lung and spleen were significantly lower than PBS control group, and similar to BCG control. Immune factors show also, SNUMI-9 is good vaccine candidate. The innate immune response-related cytokines (TNF, IFN-γ, IL-6) and IgG2a/IgG1 ratio measured higher than BCG group, and the counts of polyfunctional T cells are increased in double positive IL-2+/TNF+ T cell population at lung and IL-2+/TNF+/IFN-γ+ T cell population at spleen. It is mean that SNUMI-9’s protective efficacy against TB is better than BCG at the early stage of infection.

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A ppGpp-defective Enteropathogenic *Escherichia coli* Increases the Expression of Proinflammatory Cytokines and Enhances Bacterial Clearance in a Murine Peritoneal Infection Model

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In bacteria, stringent response is triggered by sensing of the concentration of an alarmone, guanosine 3’, 5’-bispyrophosphate (ppGpp). Since ppGpp can alter the affinity of RNA polymerase towards promoters, a change in its level has a pleiotropic effect on the regulation of bacterial genes, such as genes involved in the biosynthesis of macromolecules and/or virulence, during starvation. However, host immune response towards bacterial pathogens in the absence of ppGpp biosynthesis has not been yet elucidated. In this study, we compared *in vitro* and *in vivo* immune responses towards the wildtype and ppGpp-deficient (ppGpp<sup>0</sup>) enteropathogenic *Escherichia coli* (EPEC) strains. Whole genome-scale transcriptome analyses revealed that proinflammatory cytokine genes were highly induced by the ppGpp<sup>0</sup> strain in porcine macrophages (3D4/31), when compared to the wildtype. Increased protein expression of interleukin (IL)-6 and IL-8 was confirmed using ELISA. Consistently, our *in vivo* murine peritoneal challenge experiment demonstrated significant increases of IL-6 and monocyte chemoattractant protein 1 (MCP-1) in response to ppGpp<sup>0</sup> EPEC, and thus enhanced bacterial clearance. These results imply that ppGpp<sup>0</sup> EPEC elicited a strong and protective immune responses during a host infection, which is unable to be observed with wildtype EPEC. [This study was supported by a grant from National Research Foundation (NRF-2017R1A2B4013056), Republic of Korea]

Extracellular Cascade Activation of Toxic Proteases by Quorum Sensing-mediated Removal of “Safety Pin” in *Pseudomonas aeruginosa*

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*Pseudomonas aeruginosa* secretes multiple proteases that are known to be implicated in pathogenesis as virulence factors, and most of them are quorum sensing (QS)-regulated, such as PIV, LasA, and LasB. Our previous research found that PIV is post-secretionally activated through the extracellular degradation of the propeptide by LasB. In this research, we found that LasA expressed in QS mutant (MW1) has a severe reduction in its activity in culture supernatant. We intended to elucidate the underlying mechanism in this post-secretional activation of LasA by QS. SDS-PAGE analysis showed that most M-LasA (LasA from MW1) was in the form of proLasA, suggesting that some QS-dependent factors are involved in the extracellular maturation of LasA by cleaving the propeptide. The results show that, LasB and PIV are the QS-inducible factors responsible for the cleavage of the propeptide from proLasA. The contribution of PIV to the extracellular processing of LasA appeared greater than LasB. Deletion of *lasB* remarkably reduced the activity of PIV and LasA, indicating that LasB activates both PIV and LasA. LasA activity was reduced more than 60% in Δ*piv*, suggested that PIV more directly contributes to the extracellular processing of LasA. We suggest that the three extracellular proteases, LasB, PIV, and LasA are post-secretionally activated in a cascade manner, in which LasB first activates PIV as a trigger by degrading the propeptide of PIV, and then the activated PIV activates LasA by degrading the propeptide of LasA. Moreover, LasB also can partly activate LasA. In this mechanism, the propeptides of these extracellular proteases function as “safety pin” to inhibit activities of the proteases.
D011
Identification and Characterization of Antibody Isotype Contributing to Human Serum Vibriocidal Assay
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Serum vibriocidal assays have long been used to evaluate the immunogenicity of cholera vaccines. However, the antibody isotypes responsible for the vibriocidal activity are not fully characterized. In this study, we examined 20 clinical serum samples obtained from vaccinees and convalescent sera to determine which isotype antibody is associated with the vibriocidal activity. Antibody isotypes from the convalescent sera were fractionated by size-exclusion column chromatography and the major vibriocidal activity was detected in the IgM fraction. Depletion of IgM antibodies in the sera produced a significant (P<0.05) decrease in vibriocidal activity (16-fold decrease). In addition, anti-LPS IgM antibody showed the highest correlation with vibriocidal activity among antibody isotypes against heat-killed V. cholerae, lipopolysaccharide (LPS), or major outer membrane protein (Omp U). Furthermore, convalescent sera remarkably inhibited the attachment of V. cholerae to HT-29. Interestingly, IgM-depleted sera could not effectively inhibit bacterial adherence (P<0.05). Finally, bacterial adhesion was substantially inhibited by sera with high vibriocidal titer compared with low-titer sera. Collectively, we demonstrated that anti-V. cholerae LPS IgM is highly correlated with serum vibriocidal activity and it could be a surrogate isotype representing protective antibodies against V. cholerae.

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D012
Genomic Analysis of Ketoconazole Resistance in the Dandruff-associated Pathogenic Fungus Malassezia restricta
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Malassezia restricta is an opportunistic fungal pathogen on human skin and is associated with skin diseases including seborrheic dermatitis and dandruff which are commonly treated with the ketoconazole. In this study, we clinically isolated ketoconazole resistant M. restricta strains KCTC 27529 and KCTC 27550. To understand the mechanism, the genome and transcriptome of the resistant 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 KCTC 27529, the result of which was supported by our transcriptome analysis showing an increased expression of the ATM1 homolog in the strain. Furthermore, transcriptome analysis suggested that the PDR5 homolog is significantly up-regulated in KCTC 27529 implying that an increased drug efflux influences the resistance of the strain. The mechanism of ketoconazole resistance in the other resistant isolate KCTC 27550 is different from KCTC 27529. The comparative genome and transcriptome analyses revealed that there is a genomic multiplication of the homologs of ERG11 in KCTC 27550 which are highly expressed compared to the reference strain. Overall, our data suggest 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.
D013
Genomic and Transcriptomic Analyses of *Escherichia coli* FORC_041, Isolated from Beef
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Although serotype O157 is the most responsible for the EHEC-related food-borne outbreaks, the outbreaks caused by non-O157 EHEC are increasing nowadays. Therefore, it is more important than ever to study non-O157 EHEC to understand its hazards. The EHEC FORC_041 was isolated from pre-packaged beef and its genome and transcriptome were analyzed to illustrate hazards of non-O157 EHEC. FORC_041 was shown to carry the stx2a gene and was identified as serotype O163:H19. FORC_041 showed the highest average nucleotide identity value with CFSAN002236 strain among the completely sequenced EHEC clinical isolate strains. Compared with the strain, FORC_041 had additional virulence factors such as type VI secretion system and hemolysin A. To understand the survival of FORC_041 in beef, FORC_041 was exposed to beef and the transcriptome of this pathogen was profiled by RNA-Seq. The transcriptome of FORC_041 showed that the genes associated with glycolysis were down-regulated, whereas the genes associated with long-chain fatty acid degradation, flagella and adhesion were up-regulated while in contact with beef. Therefore, FORC_041 may survive in the beef environment by promoting cell-to-surface contact with beef and utilizing long-chain fatty acid as an energy source. These results led us to understand that survival strategy of non-O175 EHEC in beef and may have applications in food safety.

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D014
Dysbiosis in Antiphospholipid Syndrome Shown by IgA-Seq Study
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The antiphospholipid syndrome (APS) is an autoimmune thrombophilic disorder. Various pathogens have been associated with transient antiphospholipid antibody production. We hypothesized that members of the gut microbiota could represent a chronic trigger and exhibit heightened adaptive immune responses. Stool from 15 APS patients, 5 non-autoimmune thrombotic states, and 12 normal donors (total of 17 controls) was collected. Fecal homogenates were analyzed for the gut permeability marker calprotectin and, in parallel, stained with PE-conjugated anti-human IgA prior to cell sorting. Fecal DNA was isolated and PCR-amplified targeting the V4 region of the 16S rRNA gene. Samples were sequenced on the Illumina MiSeq platform. Fecal calprotectin and IgA-coated fecal bacterial levels were significantly higher in APS patients compared to controls (p < 0.003; p < 0.05). LEfSe analysis of IgA+ fractions showed that the strongest IgA-coated genus is *Blautia* in APS. These data suggest gut barrier dysfunction and aberrant IgA coating of commensals in APS. Markedly enhanced bacterial IgA coating in several APS patients supports a stronger adaptive immune response to the microbiota. Increased IgA coating of *Blautia* might reflect altered gut homeostasis as a *Blautia* species was shown to be part of proinflammatory IgA+ consortium in IBD. To our knowledge, this study represents the first 16S rRNA profiling of IgA-coated gut commensals in patients with non-gut autoimmunity.
**D015**

**Promoter Analysis of the Type VI Secretion System Hcp Gene Z0264 in Enterohemorrhagic *Escherichia coli* O157:H7**

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Type VI secretion system (T6SS) is a novel secretion system found in a number of Gram-negative bacteria, and is known to have potential roles in bacterial competition and virulence. A previous report showed that enterohemorrhagic *Escherichia coli* (EHEC) O157:H7 strain EDL933 contains a single T6SS gene cluster (Z0248-Z0264). In this study, we attempted to define transcription start sites (TSSs) and promoter regions for Z0264, the first gene from the T6SS structural gene cluster.

We identified a guanosine residue located 117-bp upstream of the start codon with the highest frequency using the ARF-TSS method. Transcriptional activity of predicted Z0264 promoter regions (P_{Z0264}) was analyzed by a truncated promoter-lacZ fusion assay, and confirmed that the predicted region contained a working promoter. Notably, a P_{Z0264}-lacZ fusion harboring a 169-bp region showed stronger transcriptional activity than that of harboring a 591-bp region. qPCR assay was performed using overlapping primers, but it showed that RNA transcript from P_{Z0264} does not cover the entire T6SS cluster.

Conclusively, we identified a main TSS and functional promoter regions for Z0264 gene in EHEC O157:H7. Our results also suggest that negative regulation may occur upstream of Z0264 promoter and that multiple promoters within the T6SS cluster may control transcription.

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**D016**

**Attenuating Virulence of *Vibrio* Species by Targeting Conserved Transcriptional Regulator HlyU**

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The inevitable emergence and spread of resistance to current antibiotics have led to the development of new agents inhibiting bacterial virulence rather than viability. In this study, we performed high-throughput screening of 8,385 compounds and identified CM14 that inhibits the activity of HlyU, a key transcriptional regulator essential for the virulence of a life-threatening human pathogen *Vibrio vulnificus*. CM14 reduces the HlyU-dependent expression of virulence genes in *V. vulnificus*, thereby decreasing hemolytic activity against human erythrocytes and impeding cytopathicity and cytotoxicity toward human epithelial cells. Notably, CM14 significantly enhances the survival of mice infected with *V. vulnificus* by alleviating hepatic and renal dysfunction and systemic inflammation. Structural, biochemical, and mass spectrometric analyses demonstrated a mechanism of CM14 that interferes with the DNA-binding activity of HlyU by inducing a conformational change via covalent modification of the Cys30 residue.

Remarkably, CM14 decreases the expression of various virulence genes in other *Vibrio* species and thus attenuates their virulence phenotypes. Since CM14 is not toxic toward bacteria, human cells, and mice, this molecule could be developed as an anti-virulence agent against HlyU-harboring *Vibrio* species with a low selective pressure for inducing resistance.

[Supported by National Research Foundation of Korea and IPET of Ministry of Agriculture, Food, and Rural Affairs]
D017
Antibacterial Effect of Bacteria Isolated from the Korean Traditional Foods against Pathogenic Bacteria
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Aquaculture continues to be an ever-growing sector. However, high-density farming increases disease outbreaks due to deteriorating water quality and internal stress. To prevent disease, the most common method of chemotherapy is using antibiotic administration. In this study, probiotic bacteria were isolated from Korean traditional foods, such as Gochu pickle and cutlassfish salted seafood. Various bacteria were isolated, and their 16S rDNA sequences were analyzed. The antimicrobial activities of four isolates from Gochu pickle and seven isolates from cutlassfish salted seafood were assayed, in addition to the antibacterial activity of culture pellet and supernatant. The antibacterial activity of the pellet was higher than that of the supernatant. Isolate JKM-2 showed the highest antibacterial activity against *Streptococcus iniae* (43 mm), *S. parauberis* (40 mm), *S. mutans* (35 mm), and *Vibrio vuinificus* (26.5 mm). The sequences of the isolated strains were compared with those of *Bacillus subtilis* (97.71%), *B. tequilensis* (97.71%), *Brevibacterium halotolerans* (97.71%). Future through analysis and new strains confirmed the bacterial cell material investigation of JKM-3, and to ensure sufficient stability, it is desired to verify the utility value as a substitute material for antibiotics by application to the form of the industry.

D018
Inhibitory Effect of *Bacteroides ovatus* on *Clostridium difficile* Growth Mediated by Bile Salts Hydrolase
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*Clostridium difficile* infection (CDI) is known to be one of the most common Hospital-acquired infection. The use of broad-spectrum antibiotics has led to the collapse of intestinal microbiota as a major source of infection. For that reason, fecal microbiota transplantation (FMT), including normal flora, has been used as a treatment for CDI. However, FMT has a risk of secondary infection, and it is difficult to standardize for the development of therapeutic agents. Therefore, it is necessary to develop a method for treatment of CDI, such as bacteriotherapy, by searching for the mechanism through which commensal bacteria inhibit the growth of *C. difficile*. In this experiments, we have shown that *Bacteroides ovatus* SNUG 40239 can produce bile salts hydrolase (BSH) and consequently inhibit the growth of *C. difficile* through metabolism of conjugated bile acids. The inhibitory effect of *B. ovatus* SNUG 40239 on the growth of *C. difficile* was enhanced as the concentration of bile acids was increased, and it was confirmed that this effect disappears when cholestyamine, which is known as an adsorbent of bile acid, is treated. This finding has important implications for finding new bacteria that can be applied to CDI treatment. These findings will serve as a catalyst for future development of new bacteriotherapy for CDI treatment.
D019
Modulation of Type I Interferon Pathways by Accessory and Structural Proteins of Middle East Respiratory Syndrome Coronavirus
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Middle East respiratory syndrome coronavirus (MERS-CoV), which is a highly pathogenic emerging virus, caused the outbreak in South Korea in 2015, resulting in 186 infected patients including 38 deaths. However, the pathogenic mechanisms related to the host innate immune responses still remain unclear. The aim of current study is to determine whether MERS-CoV proteins antagonize innate immune activity, especially Interferon-β (IFN-β) production. To this end, each accessory and structural gene was cloned in fusion to 3xFLAG tag at the N-terminus and screened for its inhibitory activities on the RIG-I/MDA5 pathway. Each individual MERS-CoV gene and IFN-β-luciferase expression vector were co-transfected into HEK293T cells and levels of IFN-b promoter activities were assessed by luciferase assay. Protein levels of MDA5/RIG-I and target genes was confirmed by Western blot. Interestingly, Spike and accessory proteins (ORF4a, ORF4b and ORF8b) demonstrated strong antagonistic effect on IFN-β signaling pathways. Currently, subsequent studies are under way to map domains which are responsible for the inhibitory activities. Understanding of specific mechanisms of how MERS-CoV interacts with the host innate immune system will likely pave way for the development of preventive measure and effective therapeutics.

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D020
Genome-wide Screening of Chikungunya Virus Genes for the Modulation of Type I Interferon Responses
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Chikungunya virus (CHIKV) is a single-strand positive-sense RNA virus and belongs to the genus alphavirus of the family Togaviridae. CHIKV is transmitted by two types of mosquitoes: Aedes albopictus and Aedes aegypti. CHIKV causes chikungunya showing symptoms such as acute fever, arthralgia and multiple joint pains. Expression of interferons is induced upon viral infection, exhibiting strong antiviral activities and modulating the host immune responses. Once inside cells, the genomes of RNA viruses are recognized by RIG-I and MDA5 which are pattern recognition receptors. Activation of RIG-I/MDA5, in turn, activates down-stream signaling molecules, such as MAVS, TBKI, IKKe, and IRF3, culminating in the transcription of IFN-β. The goal of this study is to identify CHIKV proteins which modulate type I interferon responses. First, we annotated and cloned CHIKV individual gene in fusion to 3xFLAG at the N-terminus. Among CHIKV genes, nsP2, E2 and E1 dramatically inhibit the transcriptional induction of IFN-β when assessed by luciferase assay. Further studies are warranted to identify the specific cellular target(s) of those CHIKV proteins, which will pave way to develop virus-specific therapeutics as well as preventive vaccines.

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D021
Modulation of Type I Interferon Responses by Zika Virus-encoded proteins
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Zika virus (ZIKV) is an emerging mosquito-transmitted Flavivirus causing severe neurological diseases including Guillain–Barré syndrome and microcephaly. However, mechanisms how ZIKV infection induces diseases still poorly understood. We hypothesized that one or more ZIKV-encoded proteins may be involved in antagonizing type I IFN responses. Each individual ZIKV gene was cloned and screened for its activities to inhibit IFN promoter activity activated by induction of RIG-I/MDA5 signaling pathway. Our results demonstrated that C, NS2A, NS4A and NS4B proteins significantly down-regulate the promoter activity of IFN-β with NS2A and NS4A exhibiting over 90% inhibition. Moreover, both NS2A and NS4A inhibit MDA5-induced IFN-β induction in a dose responsive manner. To investigate whether NS2A and NS4A affect general transcription and/or translation of the cells, NS2A and NS4A were co-transfected with pEGFP vector whose expression is driven by the CMV promoter. Interestingly, MDA protein levels, but not those of EGFP, were down-regulated, suggesting that the two ZIKV proteins specifically target MDA5. In addition, domains of NS2A and NS4A were constructed and mapped for the inhibitory activities. Taken together, our results demonstrate that NS2A and NS4A play a major role in the antagonism of MDA-mediated IFN-β induction.

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D022
Anti-inflammatory Activity of Peptide in RAW 264.7 Cells Induced by LTA and DRSA
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Drug-resistant microorganism infections cause serious disease and can lead to mortality and morbidity. In particular, Staphylococcus aureus induces pyrogenic and toxigenic infections, and drug-resistance occurs rapidly. Multidrug-resistant S. aureus, such as methicillin-resistant S. aureus and methicillin-sensitive S. aureus, can also cause immunodeficiency and immune deficiency syndrome from lipoteichoic acid. However, antimicrobial peptides have strong antimicrobial activity, low cytotoxicity, and high neutralization activity against endotoxin substances from Gram-negative bacteria. The objective of this study was to use a synthetic antimicrobial peptide to evaluate the inhibition of drug-resistance development, antimicrobial activity, and neutralizing activity in S. aureus Gram-positive bacteria. The peptide showed strong antimicrobial activity against drug-resistant S. aureus strains and significantly increased the anti-neutralizing activity of lipoteichoic acid in S. aureus 1630 drug-resistant bacteria. In addition, S. aureus ATCC 29213 did not develop resistance to peptide as with other antibiotic drugs. These results suggest that the peptide is an effective antibiotic and anti-neutralizing agent against multidrug-resistant S. aureus strains.
D023
Skin-infected Bactericidal Activity of Antimicrobial Peptide against Multidrug-resistant *Staphylococcus aureus*
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Antimicrobial peptide is derived from the pharyngeal tissues of the tunicate *Styela clava*. The 23-amino acid peptide is histidine-rich and amidated at the N-terminus. Peptide possesses low antimicrobial and high hemolytic activity at pH 7.4. Therefore, we designed analogs with substituted hydrophobic amino acids to reduce hydrophobic amino acid interactions. These modifications reduced the aggregation and cytotoxicity of the analogs at pH 7.4. The analogs also showed potent antimicrobial activity by accumulating on bacterial cell surfaces and inducing the lytic mechanism against gram-negative and gram-positive cells at pH 5.5 and 7.4. Moreover, exposure to the analog for up to 29 passages did not induce drug resistance in *Staphylococcus aureus*. Application of peptide to inflamed skin of hairless mice infected with drug-resistant *S. aureus* (DRSA) significantly reduced skin infections without damaging dermal collagen or elastin. Topically applied peptide penetrated 25-40 µm in the dermis within 30 min, reducing the levels of Toll-like receptor-2, nuclear factor kappa B (NF-κB), and the pro-inflammatory cytokines tumor necrosis factor-α (TNF-α) and interleukin-1β (IL-1β). These results suggest that peptide could be a promising topical antimicrobial agent for skin diseases caused by DRSA such as *S. aureus* CCARM 0027.

D024
Comparative Pan-genome Analysis Based Pathogenicity Determination of *Vibrio vulnificus* Isolated from Seafood
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*Vibrio vulnificus* is the opportunistic pathogen and it has been subdivided into three biotypes. In general, biotype 1 is responsible for the majority of human infections and it consists of two genotypes: a clinical genotype (biotype 1C; *vcgC*) causing primary septicemia regarding raw or undercooked contaminated food, and an environmental genotype (biotype 1E; *vcgE*) associated with the wound infections. In this study, six strains of *V. vulnificus* were newly isolated from various seafood and sea water and their genomes were sequenced. To determine the clinical characteristics, other 17 complete genome sequences were obtained from the NCBI database and compared with the six strain genome sequences using pan-genome approach to identify their virulence factors and clinical characteristics. Interestingly, average nucleotide identity (ANI) tree analysis showed that all six strains belong to biotype 1C, suggesting that they may be associated with clinical pathogenesis. In addition, subsequent pan-genome analysis revealed that all biotype 1C have *vcgC* gene, but all biotype 1E have *vcgE* gene, suggesting that these genes may be biomarker genes to distinguish biotypes of *V. vulnificus* by simple PCR reaction. In conclusion, most of *V. vulnificus* strains isolated in South Korea belong to biotype 1C, indicating that they may be associated with clinical strains. Therefore, *V. vulnificus* in South Korea needs to be rapidly monitored and controlled to prevent food-borne outbreaks.
D025

**Antibacterial, Anti-biofilm Activity and Mechanism of SHP14 Peptide and Its Analogs Peptide SHP12 against Multidrug-resistant *Pseudomonas aeruginosa***

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SHP14, isolated from the venom of the scorpion *Heterometrus petersii*, exhibited antimicrobial activity with cytotoxicity. In an effort to develop clinically applicable antimicrobial peptides (AMPs), we designed analogs to reduce cytotoxicity and improve activity (deletion of glycine and phenylalanine, substitution with leucine and lysine). The analog peptides comprised 12 amino acids and displayed amphipathic α-helical structures, with higher hydrophobic moments and increased net positive charge compared to the SHP14. The analogs showed little toxicity toward mouse red blood cell and mammalian cell than the SHP14, especially SHP12, which exhibited particularly potent antibacterial and antibiofilm activities against multidrug-resistant *Pseudomonas aeruginosa* (MRPA) strains. The stability of the SHP12 against salt and trypsin than the SHP14. SHP14 binds to lipopolysaccharide and kills the bacteria by disrupting their membranes. SHP12 kills bacteria more rapidly than SHP14 and not only seems to bind more strongly to LPS but may also be able to enter bacterial cells and interact with their DNA. Additionally, SHP12 can effectively killed *P. aeruginosa* in the wounded region in a mouse skin infection model. The results of this study indicate that SHP12 not only displays antimicrobial activity, but is also functional in physiological conditions, confirming its potential use as an effective therapeutic agent against MRPA.

D026

**Antimicrobial Activity and Action of Mechanism of Antimicrobial Peptide and Its Analog Peptides against *Acinetobacter baumannii* and *Staphylococcus aureus***

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The abuse of antibiotics has resulted in the emergence of multi drug resistant bacteria. Therefore, it is urgent to develop therapeutic agents for multi drug resistant strains. Antimicrobial peptides (AMPs) are promising therapeutic agents for treating antibiotic-resistant bacterial infections. In a previous study, HJ, displayed broad-spectrum antimicrobial activity against Gram-negative and Gram-positive bacteria. But it has a high hemolytic effect, which causes problems in safety. In the present study, we designed novel antimicrobial peptides with potent antimicrobial activity against Gram-negative and Gram-positive bacteria and lower hemolytic activity than the parent peptide HJ. Circular dichroism analysis indicated that HJ and its analogs appeared as α-helical structures in mimicking the anionic environment or the hydrophobic environment of the bacterial membranes. We conducted ONPG assay, NPN assay, DiSC³-5 assay and SYTOX green uptake assay to confirm the mechanism of HJ. We investigated the effect of HJ and its analogs on biofilm inhibition and reduction using crystal violet staining and microscopic observation. Thus, analog peptides may be effective treatments for multidrug-resistant *A. baumannii* and *S. aureus*. 

115
D027
Antimicrobial Peptide JHP5 Suppress Inflammation Induced by Carbapenem-resistant Acinetobacter baumannii in Lung Epithelial Cells
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Carbapenem-resistant Acinetobacter baumannii (CRAB) is a rapidly growing resistant strain and has difficulties in treating infections. CRAB is one of the dangerous pathogens threatening humanity as selected by the World Health Organization (WHO). Antimicrobial peptides are alternative to antibiotics because they control the immune response and have a antimicrobial activity. The antimicrobial peptide JHP5 was synthesized from the hybrid peptide CA-MA. Previous studies have shown that JHP5 kills bacteria by membrane disrupting. It also inhibited the inflammatory response induced by TLR2-to-NF-κB signaling when bacteria were infected against mammalian cells. The purpose of this study is to confirm that JHP5 have an antimicrobial and anti-biofilm effect and anti-inflammatory effects against CRAB in lung epithelial cells. We showed that JHP5 does not have cytotoxicity in lung epithelial cells. In addition, JHP5 has antimicrobial activity in 26 carbapenem-resistant Acinetobacter baumannii isolated from hospital patients. Among the 26 strains, biofilm inhibition assay was performed on the strains that produced the most biofilm, and biofilm was effectively inhibited. JHP5 inhibited pro-inflammatory cytokine when CRAB was infected with epithelial cells. A antimicrobial peptide JHP5 has an antimicrobial and anti-inflammatory effects on CRAB and can be an alternative treatment for CRAB infection.

D028
Mpis Has Antibacterial Activity in Multidrug-resistant Bacteria and Synergistic Effect with Antibiotics
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The abuse of antibiotics for disease treatment has led to the emergence of multidrug resistant bacteria. Antimicrobial peptides, found naturally in various organisms, have received increasing interest as alternatives to conventional antibiotics because of their broad spectrum antimicrobial activity and low cytotoxicity. Mpis, isolated from bee venom, exhibited antibacterial and antibiofilm activities against gram-positive, negative bacteria and drug resistant bacteria. Moreover, Mpis did not exhibit hemolytic activity and cytotoxicity to keratinocytes, whereas melittin, as a positive control, showed very high cytotoxicity. Circular dichroism assays showed that Mpis has an α-helical structure in membrane mimic environments. Mpis binds to peptidoglycan and lipopolysaccharide and kills the bacteria by disrupting their membranes. Moreover, the fractional inhibitory concentration index indicated that Mpis has additive and partially synergistic effects with conventional antibiotics against drug resistant bacteria. Our study suggested that Mpis has potential for use of an antimicrobial agent for infectious bacteria, including drug resistant bacteria.
A Study on Cell Selectivity and Anti-biofilm Activity of Antimicrobial Peptide by Residues Substitution
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Antimicrobial peptides (AMPs) are essential components of the innate immune system, offering protection against invading pathogenic bacteria. However, low effective stability in high-salt environments and physiological instability in biological membranes limit the applicability of naturally occurring AMPs as novel therapeutics. We designed short synthetic peptides by substituting key residues in hagdin, an AMP derived from the epidermal mucus of hagfish, with lysine, arginine, and tryptophan. The hagdin analogs exhibited strong antimicrobial activity against both Gram-positive and Gram-negative bacteria, including multidrug-resistant strains, even under high-salt conditions. Moreover, these peptides showed high binding affinity for both lipopolysaccharides and lipoteichoic acids and inhibited biofilm formation by most bacteria, but did not cause lysis of human red blood cells and cytotoxic to normal human keratinocytes. Circular dichroism analysis revealed that hagdin and its analogs assumed the secondary structures within artificial liposomes and bacterial membranes. In addition, bacterial killing and membrane permeation experiments demonstrated that the hagdin analogs permeated through bacterial membranes, leading to cytoplasmic disruption and cell death. These findings suggest hagdin analogs may be promising candidate antibiotic agents for therapeutic application against antibiotic-resistant bacteria.

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Human Vaginal Lactobacillus Isolate Attenuates Development of Allergic Asthma in a Mouse Model
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Development of asthma is affected by the microbiota modulating immune and metabolic functions of host. Epidemiological studies have shown the more frequent incidence of asthma in infants delivered by Caesarean section than in ones delivered by vaginal birth. In this study, we investigated the effect of representative vaginal lactobacilli strain, Lactobacillus crispatus (Lc), on mitigating asthmatic responses induced by house dust mite (HDM) in a mouse model. Lc isolate from a healthy Korean woman was orally gavaged to mice for eighteen days (approximately 1 × 10⁹ CFU/mouse/day). All mice were challenged with HDM on day 0 and day 7-11 through intratracheal injection. The airway hyper-responsiveness (AHR) to methacholine was assessed to measure lung dysfunction. The Lc-administered group displayed a significantly lower AHR level compared to HDM control group. Histological analysis of lung tissue revealed significantly reduced eosinophil infiltration around bronchioles in Lc-administered group compared to control group. There was a significant reduction in total IL-5 and IL-13 and the T cells producing these cytokines in Lc-administered group. We also observed a significantly reduced ST2⁺ T cells in Lc-administered group. Taken together, Lc successfully alleviated HDM-induced asthmatic responses in a mouse model and can be applied to a microbiome-based therapy for asthma.

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D031
Effect on Viral Fitness and RBD Mutation of MERS-CoV Variants by Neutralizing Antibody
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Although a large number of neutralizing antibodies (nAbs) for MERS-CoVs have been developed, viral replication in the presence of nAb is able to emerge various viral mutants. We developed monoclonal Ab (mAb) with high neutralizing activity for MERS-CoVs. Therefore, we investigated the possibility of occurrence of mutants to escape mAb and analyzed effect of those mutations on viral fitness. We passaged serially for MERS-CoVs under selective pressure of nAb. Viral entry was measured by pseudovirus expressing S protein. Unexpectedly, mutations in the receptor binding domain (RBD) emerged rapidly for KNIH_002 strain, all of eight purified isolates mutate into L506H of RBD when passaged two 2nd with nAb. And, for EMC strain, one of six purified isolates mutated into R511S of RBD when passaged 1st with nAb. Until when passaged finally, L506H mutation for KNIH_002 was maintained consistently, whereas EMC strain, interestingly, showed various amino acid change (L506F/T512I/E513A, L506F/R511S/E513A, R511S/T512A) in RBD region. Those mutations in RBD showed significantly reduced viral entry, resulting in delayed viral growth kinetics. In conclusion, our results indicate that MERS-CoVs can readily mutate in the presence of suitable neutralizing antibody and replicate efficiently in host cells, implying that it would be considered to use MAbs as anti-viral drugs.
[This study was supported by intramural funds (2016-NG47002 and 2019-NI-078) of National Institute of Health, Korea CDC]

D032
Evaluation of Cell-based Antiviral Activity of Novel Compounds against Zika Virus
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Zika virus (ZIKV), a member of the flavivirus family, was initially thought to cause only mild, self-limiting symptoms. However, in 2014, ZIKV infection has been reported to be associated with the autoimmune disease Guillain-Barre syndrome and causally linked to a congenital malformation known as microcephaly. In addition, there is no effective treatment at present, so it is treated with symptomatic therapy. In previous study, we optimized a cell a based therapeutic efficacy screening assay using the Immunofluorescence-based biosensor for identify novel antivirals against ZIKV and found four candidates for therapeutic compounds. In this study, we measured for antiviral activity of these compounds in various cell lines such as African green monkey kidney (Vero) cells and human lung carcinoma (A549) cells by plaque reduction assay and western blot. The results showed that these compounds reduced the level of ZIKV-E protein expression and viral plaque reduction titer in a dose-dependent manner. And, in the post- and co-treatment with ZIKV, each compounds showed anti-viral effects in Vero and A549 cell line. These results suggest that these novel compounds could be potential antiviral drug candidates for ZIKV infection.
[This study was supported by intramural funds (2017-NI53001_02) of National Institute of Health, Korea Centers for Disease Control and Prevention.]
D033
 Mutation in pmrB and Production of Outer Membrane Vesicles in Laboratory-evolved Polymyxin B-resistant Strains of Acinetobacter baumannii
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Modification of lipopolysaccharides by polymyxin B (PMB)-induced PmrAB two-component system appeared to be dominant phenomenon in PMB-resistant Acinetobacter baumannii. But, mechanisms of other PMB resistance are still unclear. Whole genome sequencing of laboratory-evolved PMRLow and PMRHigh strains discovered common mutations in four regions including two hypothetical proteins, MlaD (phospholipid ABC transporter-binding protein) and the sensor kinase PmrB. Duplication of the RelBE antitoxin-toxin system occurred only in PMRHigh strain. Point mutations of PmrB were observed in PMRLow (N353I) and PMRHigh (T234I), respectively. Zeta-potential analysis proved that membrane-negative charge decreased in PMR-resistant strains, resulting in resistance to PMB possibly by reduction of PMB binding to cell surface. Interestingly, transmission electron microscopy revealed that outer membrane vesicles (OMVs) were formed on the surface membrane of PMRHigh not on Lab-WT. Cell viability assay using OMVs from PMRHigh supernatant showed that the OMVs protected the Lab-WT cells from PMB-induced death. Our data suggested that not only the mutation in pmrB, but also the unexpected OMVs production play important roles in bacterial survival by reducing PMB binding to bacterial membrane.

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D034
 The Relationship between Gut Microbiota at 6 Months and Persistence of Atopic Dermatitis in Early Childhood
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Background: Several studies have examined the associations between composition of gut microbiota and the development of atopic dermatitis (AD) in infancy, but far less have evaluated the impact of gut microbiota the persistence of AD in early childhood.

Objective: We investigated the relationship between gut microbiota at 6 months and AD symptoms lasting up to 2 years.

Methods: The composition of gut microbiota was analyzed in fecal samples from 110 infants (6-month-old) by pyrosequencing, including healthy infants (n=84) without AD up to 24 months and persistent AD (n=26) with AD up to 24 months. Total serum immunoglobulin E (IgE) levels and percentages of blood eosinophils (%) were measured at 1 year of age. The severity of AD using the Scoring Atopic Dermatitis (SCORAD) index was simultaneously assessed at the time of fecal collection at 6 months

Results: The α-diversity of gut microbiota was no significant difference between the groups (OTUs and Shannon). The composition of the microbiota differed between the AD groups. Lower Clostridium, and higher Streptococcus were found in children with persistent AD compared to healthy control. The relative abundance of Clostridium negatively correlated with eosinophils (%) (r= -0.321, P=.036). However, there was not associated with SCORAD index and serum total IgE.

Conclusion: Different compositions of the early gut microbiome are related to the persistence of AD in early childhood.
D035

Drosophila melanogaster-based Identification of the Pseudomonas aeruginosa Genes for Polymicrobial Interaction with Staphylococcus aureus

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Microorganisms are widespread in natural habitats and human tissues where they coexist and constitute polymicrobial communities. It remains unclear how such polymicrobial interactions are orchestrated to survive the dynamic host environments. Here, we established a Drosophila melanogaster-based infection model to assess the key aspects of polymicrobial interaction between the two important opportunistic pathogens, Pseudomonas aeruginosa and Staphylococcus aureus that commonly coexist in the mucosal layers. This system revealed that the polymicrobial infection enhanced the virulence of P. aeruginosa, not that of S. aureus. This virulence enhancement was still evident in the interaction between the P. aeruginosa lasRmvfR mutant and a virulence-attenuated S. aureus mutant (m6), suggesting that the virulence enhancement did not require the LasR-MvfR quorum-sensing circuitry. To identify the genes required for the virulence enhancement in P. aeruginosa by S. aureus, we have screened ~1,000 transposon clones of the lasRmvfR mutant and isolated three mutants (11E3, 11G10, and 16E12), whose virulence was not enhanced at all by m6 in the Drosophila polymicrobial infection. Their transposon insertion sites were determined: a hypothetical gene (PA14_24300) under the control of MvfR, dgt for the dGTPase, and fleQ for the regulator of flagellar synthesis. These results suggest unexpected interspecies interactions during the polymicrobial infection caused by P. aeruginosa and S. aureus.

D036

Airway-gut Axis: Persistent Allergic Responses in Mouse Airway Affects Intestinal Microbial Ecosystems

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Asthma and allergic airway diseases are common in Westernized country and rapidly increasing their patient population in developing country. A hallmark of allergic airway disease is airway hyperresponsiveness, which is characterized by eosinophilic inflammation and airway remodeling. The host-microbiome interactions have been considered to modulate host immune mechanisms, especially in the mucosal surfaces. Microbiome analysis by next-generation sequencing allows us to gain more information between asthma and commensal microbes. Airway, once believed to be the sterile site, have an estimated number of 10-100 bacteria per 1,000 human cells. However there is little known about the correlation between allergic airway diseases and mucosal microbiome. Herein, we asked whether persistently applied allergic stimulations to the respiratory system would affect intestinal microbial ecosystems. In mouse model, HDM was treated intranasally for 8 consecutive weeks and samples were collected from cecum, feces, lung and airway secretion of each mice. We focused on microbiome change from chronic asthma mouse models induced by house dust mite(HDM), using 16S rRNA gene sequencing. There was an increase of Proteobacteria ratio in airway secretion, however, no significant change was seen in fecal samples. Addressing this question would help us provide clues to understand how an airway-gut axis operates.

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D037
Immunopathological Characteristics of Anaplasma phagocytophilum Clinical Isolate in the Republic of Korea
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Introduction: Human granulocytic anaplasmosis (HGA) is an infectious disease caused by Anaplasma phagocytophilum and is mainly transmitted by tick bites. In 2017, the isolation of A. phagocytophilum strain from HGA patient was reported by our team. In this study, A. phagocytophilum korean isolate was characterized by immunopathological analysis. Methods and Materials: A. phagocytophilum korean isolate was inoculated to C57BL/6 mice. Whole blood, spleen, and liver tissues were collected from the infected mice at 0(4 hours), 2, 4, 7, 10, and 14 days after infection. Immune response of mice caused by A. phagocytophilum infection was analyzed using FACS Verse system, Realtime-PCR, and Hematoxylin & Eosin (H&E) staining. Results: Significant changes such as reduction of CD4 T cell and NK cell population in spleen or increase of IFN-γ were detected. However, IL-10 was not changed and sustained in the normal level. Histological lesions in the both tissues were observed at day 14 when compared to non-infected mice. Discussion: These results suggest that A. phagocytophilum korean isolate affects to host through inflammatory pathways. Further studies were needed to determine association between A. phagocytophilum and inflammatory factors.

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D038
Deletion of opvAB Operon in Salmonella Typhimurium and Its Quantitative Analysis Using DOC-PAGE
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Salmonella Typhimurium (ST) is pathogenic gram negative bacteria that cause water-borne and food-borne disease in humans through the contaminated the meat of the livestock. Among the diverse virulence factors in ST, opvAB operon is reported to modulate O-antigen chain length in lipopolysaccharide (LPS) as epigenetic regulator. It was also reported that alteration of O-antigen length leads to reduce serum resistance and macrophages proliferation. In this study, we constructed opvAB deletion mutant and the LPS quantitation was analyzed by DOC-PAGE and LAL kit [1]. The mutant did not show any significant difference in O-antigen fraction in band ladder when compared to the wild type. Further experiments would be required to analyze opvAB deletion in the pathogenicity of ST.

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D039
A Salmonella Typhi Ghost Vaccine Activates Macrophage Cells via Autophagy Flux Inhibition
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Salmonella Typhi can cause typhoid fever in human. We developed a Salmonella Typhi bacterial ghost (STG) as a non-living bacteria vaccine against typhoid fever. The efficacy of STG vaccine on the macrophage needs to be investigated. In this study, we aim to evaluate the immune activator effect of STG vaccine on murine macrophage cells and the autophagy flux as a possible mechanism to the STG vaccine. Murine macrophage cells were incubated with STG vaccine, which show no cytotoxicity in MTT assay and LDH releasing up to the dose of 2 CFU/cell. Macrophages were activated with STG vaccine, which showed morphological change on light microscope and efficiently activate macrophage as indicated by upregulated pro-inflammation cytokines tumor necrosis factor (TNF)-α, interleukin (IL)-1β and interleukin (IL)-6 mRNA expressions. STG vaccine treated cells showed increasing of p62 protein expression and decreasing of LC-3 protein expression time dependently which indicated inhibition of autophagy flux in macrophages. Inhibition of autophagy flux with 3-methyladenine (3ma) and chloroquine (CQ) enhanced the expression of TNF-α and IL-1β mRNA concured with that of STG vaccine treatment. These results suggest that STG vaccine can effectively activate macrophage and the autophagy flux can be a possible target for successful vaccination.

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D040
Proteus mirabilis, Emerging Pathogenic Agent of Septicemia in Korean Wildlife
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Proteus mirabilis is a rod shape Gram-negative bacteria, facultative anaerob, part of normal flora in human and mouse. This bacteria has a characteristic with its swarming motility, urease production, and can be found ubiquitously in environment. A river otter was rescued from riverside after presenting neurological symptoms. Soon after, a goral was rescued in a mountainous area, showing similar symptoms with the river otter. The animals were given multiple trials of antibiotic treatments and other fluid therapy, resulting in not improving the general condition. The NGS proved the main pathogen as P. mirabilis for both cases. The result of MIC said to be susceptible for imipenem, ampicillin/sulbactam, cephalothin, amoxicillin/clavulanic acid, gentamicin, amikacin, and cefotaxime, and resistant to ciprofloxacin, tetracycline, chloramphenicol, nalidixic acid and trimethoprim/sulfamethoxazole. The result suggested that P. mirabilis act a main causing agent of bacteremia in the wild animals and various antibiotics profiles be presented. Further study remains to determine how best to translate the result into effective intervention measures to prevent wildlife from infection by the ubiquitous bacteria.

[Supported by grants from Technology Development Program (Project No. 1116043-1) for Bio-industry, Ministry for Agriculture, Food and Rural Affairs.]
D041
Role of Host Defense-Cationic Antimicrobial Peptide (HD-CAP) Resistance in Increased Virulence of Healthcare-Associated Methicillin-Resistant Staphylococcus aureus Strains of Sequence Type 5 in Korea
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Methicillin-resistant Staphylococcus aureus (MRSA) is a leading cause of septicemia in the hospital environment. In Korea, sequence type 72 (ST72) MRSA with SCCmec VI (ST72 CA-MRSA-VI) has been spreading in both community (CA) and healthcare (HA) settings along with the ST5 HA-MRSA strains with SCCmec II (ST5 HA-MRSA-II). In this study, potential genotype-specific virulence factors were examined between ST72 CA-MRSA and ST HA-MRSA strains. Using a total of 58 MRSA strains (31 ST5 HA-MRSA-II and 27 ST72 CA-MRSA-IV strains), we determined i) in vitro susceptibilities to host defense-cationic antimicrobial peptides (LL-37, 30 µg/ml); ii) relative surface positive charges using FITC-labeled PLL binding assay; and iii) profiles of enterotoxin genes. ST5 HA-MRSA-II strains exhibited higher levels of resistance to the HD-CAP (LL-37) compared with the ST72 CA-MRSA-IV strains. The ST5 HA-MRSA-II strains also had increased levels of surface positive charges versus the ST72-MRSA-IV strains. In addition, majority of the ST5 HA-MRSA-II strains were positive for tst (100%) and sec (28/31, 90%). None of the MRSA strains harbored pvl, sed, or see genes. Our results indicate that the increased resistance to HD-CAP via charge repulsion mechanism may play an important role in terms of higher virulence in ST5 HA-MRSA strains along with the staphylococcal superantigens. [This research was supported by a grant from the Research of Korea Centers for Disease Control and Prevention (2017NER54060 [S.J.Y]).]

D042
Identification and Functional Characterization of Essential Transcription Factors in Human Fungal Pathogen
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Cryptococcus neoformans is an opportunistic human fungal pathogen that causes cryptococcosis and fatal meningoencephalitis mainly in immunocompromised individuals. The aim of the study is to identify and characterize essential transcription factors in human fungal pathogen, C. neoformans. According to our previous report (Jung et al 2015 Nat. Comm.), 23 transcription factors are suspected to be essential for the growth of C. neoformans as they could not be deleted from the genome. For these genes, we constructed promoter-replaced mutant strains to control their expression levels, by replacing each native promoter with the copper transporter CTR4 promoter. Among 19 transcription factors tested thus far, 9 of them were found to be required for growth, whereas the remaining 10 were dispensable for the growth of C. neoformans. To examine the essentiality of the 9 growth-required transcription factors, we constructed heterozygous mutants in an engineered diploid strain of C. neoformans, and are analyzing basidiospores from these strains to explore the role of these genes in viability. The outcome of this study is to identify and functionally characterize transcription factors essential for the growth and pathogenicity of C. neoformans.
D043

Complete Genome Sequence of a Methicillin-Resistant *Staphylococcus schleiferi* Strain OT1-1 Isolated from Canine Otitis Externa

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*Staphylococcus schleiferi* has been implicated as an opportunistic pathogen of canine skin and ear infections. Recent emergence of methicillin-resistant *S. schleiferi* (MRSS) carrying various genes for multidrug resistance and enhanced virulence has caused concerns in both human and veterinary medicine. In this investigation, the genome of the MRSS strain OT1-1 was sequenced using a Pacbio RSII and an Illumina HiSeq X platform. Complete whole genome sequence data were analyzed along with antibiotic resistance phenotype, virulence phenotype, and antimicrobial resistance genes (i.e. mecA & SCCmec). The genome of MRSS OT1-1 strain had a single circular chromosome of 2,539,409 bp with G+C contents of 35.92%. The sequenced genome revealed 2,397 open reading frames including SCCmec V and various genes associated with pathogenesis and antimicrobial resistance, suggesting their potential role in canine otitis externa. The availability of complete genome sequence of a MRSS strain OT1-1 will contribute to the investigation of related fields, such as epidemiology, ecology, host-pathogen interaction, and genomics of infectious diseases. The complete genome sequence of *S. schleiferi* OT1-1 has been deposited in GenBank (Accession no. CP035007).

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D044

Immunogenicity and Safety of *Salmonella* Typhimurium phoBR Deleted Gene Mutant

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*Salmonella* Typhimurium (ST) is pathogenic Gram-negative bacteria causing food-borne gastroenteritis in human as well as animals. The gene of phoBR is one of the gene Two-component replicator (TCR) systems that expresses phosphate regulon transcriptional regulatory protein. Members of a TCR family are likely to play a role in the regulation of processes involved in intestinal colonization, and therefore, induces pathogenesis. However, the virulence of phoBR in ST has not been clearly understood.

In this study, we constructed a phoBR deletion mutant in ST isolated from pigs, and examined antibody levels in vivo. In addition, the pathogenicity between the mutant type and the wild type was compared. When the phoBR gene in Salmonella typhimurium was deleted in ST, it showed to increase immunity and safety. We suggest that ST mutant with phoBR deletion can be one of vaccine candidates in the livestock industry.

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D045
Immunostimulatory Effects of Blueberry Yeast Fermented Powder against Cyclophosphamide-induced Immunosuppressed Model
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Current studies have been reported that fruits such as berries may contain both antioxidant and antitumor polyphenols that may be important in this regard. We investigated the immunostimulatory effect of fermented blueberry (Vaccinium corymbosum L.) on cyclophosphamide-induced immunosuppression in animal model. Rats were administered blueberry yeast fermented powder (BYFP) at doses 30, 100, and 300 mg/kg for 4 weeks after cyclophosphamide (Cy) treatment, respectively. The immunomodulatory effect of BYFP were measured both in vitro and in vivo, and the changes of blood components were also analyzed. We found that BYFP recovered immunosuppression-mediated decreased liver, spleen, and thymus weights as well as up regulation of white blood cell, lymphocyte, and Neutrophil in blood. Moreover, BYFP up-regulated IL-2, TNF-αa, and IFN-γa pro-inflammatory cytokine production compared to immuno suppressed control group, respectively. According to histological studies, BYFP regenerated significantly on Cy-mediated injured spleen at the high doses (BYFP 300) comparison with Cy-treated groups (immunosuppression). Collectively, these findings suggest that BYFP may have the potential as a dietary immunostimulatory agent.
[This research was supported by the Ministry of Agriculture, Food and Rural Affairs(MAFRA), through the 2019 Healthy Local Food Branding Project of the Rural Resources Complex Industrialization Support Program.]

D046
Streptococcus pneumoniae is Susceptible to Propionate in a Serotype-dependent Manner
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Streptococcus pneumoniae is a Gram-positive, facultative anaerobic bacterium that causes life-threatening diseases such as pneumonia and bacteremia. So far, over 97 distinct serotypes of S. pneumoniae have been identified based on the capsular polysaccharide structure. Due to increasing occurrence of antibiotic resistance, a novel therapeutic method to treat pneumococcal infections effectively is needed. Short-chain fatty acids (SCFAs), such as acetate, propionate, and butyrate, are metabolites produced by gut microbiota, that were recently shown to inhibit the growth of certain bacteria, including Staphylococcus aureus and Escherichia coli. However, little is known about the effect of SCFAs on S. pneumoniae. In this study, we investigated if SCFAs can inhibit S. pneumoniae growth. Propionate dose-dependently inhibited the growth of S. pneumoniae TIGR4 while acetate or butyrate did not show such effect. To test whether the susceptibility is different for each serotype, we treated 50 mM propionate to ten different S. pneumoniae serotypes that are the major vaccine serotypes responsible for invasive pneumonia. Surprisingly, the growth of serotypes 4, 6A, 23F, 9V and 18C was potently inhibited by the treatment of propionate, while that of serotypes 14, 8, 3, 6B and 19F was only moderately affected, or not affected at all. These results suggest that propionate is a potential candidate for serotype-specific, biocompatible therapeutic agent for treating S. pneumoniae infections.
D047
Exploiting Drug Repositioning for Discovery of Novel Compounds Inhibiting HIV-1 Tat-mediated Viral Transcription
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Tat-mediated human immunodeficiency virus type 1 (HIV-1) transcription is essential for viral replication and is considered as a potent therapeutic target for HIV-1 inhibition. We recently developed a dual-reporter screening system to discriminate precisely the inhibition of Tat-mediated transcription from off-target effects. In this study, LOPAC1280 were screened using our system for repositioning as Tat-inhibitory compounds. In the primary screen, seven compounds were identified that exhibited inhibitory effects on Tat-mediated transcription. In a subsequent confirmatory assay, six of these were shown to efficiently inhibit Tat-mediated transcription without off-target effects. Four of these compounds showed potent antiviral effects related to their inhibition of Tat-mediated transcription. Two of these compounds were Gemcitabine and kenpaullone that were newly identified as inhibitors of Tat-mediated transcription. In addition, screening using several analogues, two nucleoside analogues of gemcitabine showed antiviral activity related to their Tat-inhibitory effect. Our results indicated that the dual-reporter screening system was applicable to identification of compounds that inhibited Tat-mediated viral transcription by screening a large number of compounds. The mechanism of inhibition of viral transcription by identified compounds may suggest a strategy to develop a new class of therapeutic anti-HIV drugs.

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D048
Anti-biofilm Activity of Lactobacillus plantarum Lipoteichoic Acid against Multispecies Oral Pathogenic Bacterial Biofilm
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Apical periodontitis, an inflammatory disease in the periradicular region of teeth, results from infection by multispecies bacterial biofilm residing in the root canal system. In this study, we investigated whether Lactobacillus plantarum lipoteichoic acid (Lp.LTA) can inhibit multispecies oral pathogenic bacterial biofilm. Four representative oral pathogens, Actinomyces naeslundii, Lactobacillus salivarius, Streptococcus mutans, and Enterococcus faecalis were co-cultured to form oral multispecies biofilm in the presence or absence of Lp.LTA on culture dishes or human dentin slices. Preformed biofilm was treated with or without Lp.LTA, followed by additional treatment with intracanal medicaments. Multispecies biofilm was detected by confocal microscopic or crystal violet assay. Biofilm on dentin slices was visualized using a scanning electron microscope. Multispecies biofilm formation was reduced by Lp.LTA in a dose-dependent manner. Lp.LTA also dose-dependently inhibited biofilm formation of multispecies bacteria on human dentin slices. Interestingly, Lp.LTA removed preformed multispecies biofilm. Furthermore, Lp.LTA enhanced the effects of intracanal medicaments on the disruption of preformed multispecies biofilm. Collectively, these results suggest that Lp.LTA is a potential therapeutic agent for treatment or prevention of oral infectious diseases, which is caused by multispecies bacterial biofilm.
**D049**

**Relationship of between Iron and Salmonella inside Macrophage**

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Macrophages release iron into bloodstream via the membrane-bound iron export protein, ferroportin (FPN). The hepatic iron-regulatory hormone hepcidin controls FPN internalization and degradation in response to bacterial infection. *Salmonella typhimurium* is capable of invading macrophages and proliferating in the *Salmonella*-containing vacuole (SCV). Hepcidin is reported to increase the mortality of *Salmonella*-infected animals by increasing the bacterial load in macrophages. Here, we assess the iron levels and find that hepcidin increases iron content in the cytosol but decreases it in the SCV through FPN on the SCV membrane. Loss of FPN from the SCV via the action of hepcidin impairs the generation of bactericidal reactive oxygen species (ROS) as the iron content decreases. We conclude that FPN is required to provide sufficient iron to the SCV, where it serves as a cofactor for the generation of antimicrobial ROS rather than a nutrient for *Salmonella*.

**D050**

**A Short-chain Fatty Acid, Propionate, Attenuates the Growth of Enterococci**

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Enterococci are Gram-positive facultative anaerobic bacteria that colonize the gastrointestinal tract and oral cavity. Enterococcal infections, mainly caused by *Enterococcus faecalis* and *Enterococcus faecium*, include apical periodontitis, endocarditis, and bloodstream infections. Recently, vancomycin-resistant Enterococci (VRE) are considered major pathogens that are common but difficult to treat due to antibiotic resistance, especially in nosocomial settings. In this study, we investigated the effects of short-chain fatty acids (SCFAs), such as acetate, propionate, and butyrate, which are metabolites fermented by gut microbiota, on the growth of Enterococci. Propionate had a bacteriostatic effect, inhibiting the growth of *E. faecalis* dose-dependently. Propionate also inhibited the growth of clinically-isolated *E. faecalis*. In addition, propionate had an additive effect with a combination of metronidazole, minocycline, and ciprofloxacin, which are clinically used as triple antibiotic paste to treat *E. faecalis* infection. Moreover, propionate inhibited the growth of clinically-isolated *E. faecium*. Collectively, these results indicate that propionate attenuates the growth of Enterococci and suggest propionate as a potential agent to control Enterococcal infections.
D051
Streptococcal Lipoproteins as a Negative Regulator of Its Bacterial Biofilm Formation
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Lipoproteins are amphipathic molecules composed of a hydrophilic protein moiety and a hydrophobic diacylglycerol moiety. Bacterial lipoproteins play an important role in bacterial growth and virulence. Lipoteichoic acid (LTA) is also an amphipathic molecule that plays an important role in bacterial physiology. In Gram-positive bacteria, lipoproteins are synthesized by lipoprotein diacylglycerol transferase (Lgt) while LTA is synthesized by LTA synthase (LtaS). Streptococcus gordonii is a Gram-positive facultative anaerobe found in the human oral cavity, which plays an essential role as an early colonizer in dental biofilm formation. In this study, we used wild-type (WT), lipoprotein-deficient (∆lgt) and LTA-deficient (∆ltaS) S. gordonii to investigate the role of lipoproteins and LTA in biofilm formation. These mutants were generated as follows. The upstream and downstream flanking regions of each target gene were amplified by PCR and inserted into pC326. The plasmid was introduced by natural transformation. S. gordonii ∆lgt showed increased biofilm formation compared to WT, while there was no significant difference for ∆ltaS. ∆lgt mutants of Streptococcus mutans and Streptococcus pneumoniae also showed an enhanced capacity to form biofilms. Interestingly, there was no difference in biofilm formation between Staphylococcus aureus WT and ∆lgt. These results suggest that lipoproteins in Streptococci might be a negative regulator of the bacterial biofilm formation.

D052
Effect of Short-chain Fatty Acids on Lipoteichoic Acid-induced Inflammasome via Histone Deacetylase Inhibition
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Enterococcus faecalis is a Gram-positive opportunistic pathogen that inhabits the gastrointestinal tract and oral cavity. Its lipoteichoic acid (LTA) is a major virulence factor that induces inflammation. Short-chain fatty acids (SCFAs) are metabolites produced by gut microbiota that regulate immune cells by inhibiting histone deacetylase (HDAC). Inflammasomes are protein complexes recruited after sensing danger signals and result in the secretion of IL-1β. The effect of E. faecalis LTA (Ef.LTA) and SCFAs on inflammasome activation is not fully understood. In this study, we investigated the role of SCFAs on Ef.LTA-induced inflammasome activation in THP-1 cells. Among SCFAs, butyrate markedly enhanced Ef.LTA-induced inflammasome activation. LTAs purified from Streptococcus gordonii and Bacillus subtilis also activated inflammasome in the presence of butyrate. In addition, caspase-4 inhibitor decreased IL-1β cleavage and secretion, suggesting that non-canonical activation of inflammasome is involved. Moreover, prevention of K+ efflux suppressed IL-1β production and caspase-1 activation. Trichostatin A, a HDAC inhibitor, also enhanced Ef.LTA-induced IL-1β secretion, suggesting that HDAC inhibition might be crucial for inflammasome activation. Collectively, these results suggest that butyrate facilitates LTA-induced inflammasome activation in human macrophages via HDAC inhibition and caspase-4 processing, potentially contributing to the modulation of immune responses.
D053
Hsa, a Serine-rich Repeat Adhesin, is an Important Component of Ethanol-killed Streptococcus gordonii Whole Cells for Inducing Maturation of Human Dendritic Cells
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Dendritic cells (DCs) are professional antigen-presenting cells linking innate and adaptive immunity. At vaccination, DCs capture, internalize, and process the antigen to present it to T cells resulting in induction of antigen-specific adaptive immune responses. Killed whole cell vaccines are widely used because it contains various immunogenic antigens and has a simple and inexpensive manufacturing process. In this study, we prepared ethanol-killed Streptococcus gordonii as a whole cell vaccine and investigated its ability to stimulate human monocyte-derived DCs. S. gordonii efficiently adhered to and internalized into DCs. In addition, S. gordonii induced the expression of maturation markers CD80, CD83, CD86, MHC class I/II, PD-L1, and PD-L2 and induced IL-12p70, IL-6, and TNF-α. However, in the absence of a serine-rich repeat adhesin, Hsa, S. gordonii less efficiently bound to and internalized into DCs with weak induction of maturation marker and cytokines. Moreover, DCs sensitized with Hsa-deficient strain weakly induced proliferation and activation of autologous T cells, while DCs sensitized with the wild-type potently induced it. Furthermore, DCs stimulated with recombinant Hsa also induced maturation and activation of DCs with sufficient activation of autologous T cells. Collectively, these results suggest that killed S. gordonii whole cells effectively stimulate DCs and Hsa might be an important component responsible for the induction of DC maturation and activation.

D054
The Mediate Role of Quorum-sensing Signal BDSF in Burkholderia contaminans SK875
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Many species of bacteria use quorum sensing mechanisms to co-ordinate gene expression by measuring local cell concentrations. The most common quorum sensing (QS) signal molecules produced by gram-negative bacteria are N-acyl homoserine lactones (AHL). Signal molecules of the diffusible signal factor (DSF) family have been shown recently to be involved in regulation of pathogenesis and biofilm formation in diverse Gram-negative bacteria. Cis-2-dodecenoic acid, also called BDSF, is a signal molecule found in Burkholderia. Genomic analyses of B. contaminans SK875 showed that the proteins containing a PAS, GGDEF or EAL domain or their combinations are distributed in various regions of the SK875 chromosome. In this study, we have characterized for the DSF synthase and cyclic di-GMP phosphodiesterase genes and constructed the deletion mutants of rpfF and rpfR related to BDSF signal by double-cross homologous recombination. The mutants of rpfF, rpfR, and rpfFR displayed increased biofilm production with reduced swimming and swarming motilities. A longer life of Galleria mellonella was observed after feeding with the deletion mutants as compared with the wild type. These results suggest that the BDSF signal plays a mediate role on QS-based virulence by controlling biofilm formation and promoting bacterial motility.
D055
The Mtb Inhibitory Effects and Mechanism of Action as a Potential Anti-tuberculare Candidate Substance, and Its Immunomodulatory Effects
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This study was carried out to investigate anti-mycobacterial effect and the mechanism of action of a candidate substance against mycobacterium tuberculosis (Mtb), including its potential as a novel anti-tuberculare agent, and also evaluated the immunomodulatory effects of the substance in Mtb-infected immune cells through specific assays. In particular, its anti-Mtb effects and immunomodulatory actions were confirmed through the production of intracellular factors such as nitric oxide (NO), reactive oxygen species (ROS), and cytokines (TGF-β/TNF-α, IL-1β) in Mtb-infected immune complex cells, as well as expression of specific genes that induce the inhibition of Mtb through RT-PCR analysis. The substance effectively inhibited the proliferation/growth of Mtb in the treated group compared with untreated group, which consistently induced anti-Mtb effect. The substance effectively reduced IL-1β and TNF-α as well as strongly increased production of NO, ROS and TGF-β activity in Mtb-infected immune cells. In addition, the major genes of the cell wall including peptidoglycan were markedly decreased in the treated group, and their expressions were significantly inhibited. Therefore, this study demonstrates that the substance can be utilized as a potential anti-Mtb candidate substance for developing novel anti-tuberculare drugs, as well as causes the death of Mtb by activating the immunomodulatory action and blocking bacterial growth through synergic action with immune cells.

D056
Host Susceptibility to Vibrio cholerae Infection is Determined by Intestinal Abundance of Bacteroides vulgatus
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When perturbed, gut microbiota loses its protective capacity, termed ‘colonization resistance’ against incoming pathogens. However, it remains unclear how such perturbations compromise host resistance, especially at the species and metabolite levels. Here, we illustrate how Bacteroides vulgatus, a dominant species of the Bacteroidetes phylum in mouse intestines, suppresses infection by Vibrio cholerae, an important human pathogen. Clindamycin (CL) is an antibiotic that selectively kills anaerobic bacteria, and accordingly Bacteroidetes are completely eradicated from CL-treated mouse intestines. The Bacteroidetes-depleted adult mice developed cholera-like symptoms when subsequently infected with V. cholerae. Germ-free mice mono-associated with B. vulgatus became resistant to V. cholerae infection. CL-treatment induces microbiota compositional changes. Consequently, relative concentrations of V. cholerae growth-inhibitory metabolites including butyric acid and propionic acid were reduced to undetectable upon CL treatment, while levels of compounds that enhance V. cholerae proliferation soared several folds. Furthermore, the intestinal colonization process of V. cholerae was well-simulated in CL-treated adult mice. Together, our results demonstrate that B. vulgatus is a critical determinant for host resistance against V. cholerae infection and that CL pre-treatment of adult mice generates a simple yet useful animal model of cholera infection.
D057
Transcriptional Regulator DksA Influences Production of Quorum Sensing Mediated Virulence Factors and Metabolism in Pseudomonas aeruginosa
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Pseudomonas aeruginosa is a versatile opportunistic pathogen with capability of highly advanced intercellular signaling process called Quorum Sensing (QS). The QS system is composed of signal synthase and signal receptor. P. aeruginosa possesses four QS systems encoded by las, rhl, pqs, and iqs clusters, organizing a complex QS signal network to produce virulence factors and adapt to various environments. On the other hand, to adapt the environments, P. aeruginosa also uses various transcriptional factors and other signaling system to tightly adjust their phenotypes including modification of metabolism and stress management. Since expression of bacterial virulence is closely related to metabolism and response to the environment, we focused on pleiotropic protein, DksA in P. aeruginosa. DksA is reported to bind RNA polymerase and control stringent response with nucleotide alarmone guanosine 5’-diphosphate 3’-diphosphohate

D058
Regulation of P. aeruginosa Elastase by TCA Cycle Enzymes
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Pseudomonas aeruginosa is an opportunistic pathogen that can cause both chronic and acute infections. Quorum sensing is a bacterial communication system that regulates gene expression in a cell density-dependent manner. P. aeruginosa produces many virulence factors, many of which are regulated by QS. One of the major QS-regulated virulence factors is elastase, encoded by lasB. Many studies reported loss-of-function mutations that resulted in reduced or abrogated elastase production. Herein, we sought to identify a mutant that produces higher level of elastase. We postulated that identification of such mutants may provide novel insights into the regulation of elastase production. To this end, we performed a transposon (Tn) mutagenesis screen and isolated a mutant with elevated elastase production. Tn insertion occurred in the coding region of gltA gene encoding a TCA cycle enzyme, citrate synthase. The gltA::Tn mutant grows slowly but produces more amount of elastase than PAO1, its parental strain. We constructed in-flame deletion gltA(△gltA) mutant and confirmed that both gltA::Tn mutant and △gltA mutant show same elastase expression level. We conducted RNA sequencing and interestingly alternative pathway is extremely increased in △gltA mutant which might for compensating the abnormal TCA cycle. Together, these results suggest that (i) TCA cycle activity is associated with bacterial capability to produce elastase and (ii) elastase production can be achieved at low cell density. We are expecting to figure out how TCA cycle-mediated energy metabolism can regulate elastase expression in P. aeruginosa.
**D059**

**Transcriptional Regulation of *Vibrio vulnificus* vvhBA Encoding a Cytolysin/Hemolysin**

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*Vibrio vulnificus*, a causative agent of food-borne illnesses and life-threatening septicemia, possesses numerous virulence factors accounting for the fulminating and destructive nature of its infection. Among them, a cytolsin/hemolysin VvhA is essential for the hemolytic activity of the pathogen and its gene, *vvhA*, is transcribed as a single operon with *vvhB* encoding a chaperon-like protein. VvhA contributes to severe damage of the host intestinal epithelium and subsequent bacterial infiltration into the bloodstream. However, the regulatory characteristics of *vvhBA* at the transcriptional level has not been yet elucidated in detail. Quantitative real-time PCR analysis showed that *vvhBA* is preferentially expressed in *V. vulnificus* exposed to mouse blood. Furthermore, *vvhBA* expression was growth phase-dependent, reaching its maximum during the stationary phase. Examining the influences of global regulatory proteins on the *vvhBA* transcription demonstrated that IscR and HlyU additively activate *vvhBA*, whereas a bacterial histone-like nucleoid-structuring protein (H-NS) represses *vvhBA*. Western blot analyses revealed that the cellular levels of IscR, HlyU, and H-NS were not significantly affected by one another, indicating that the regulatory proteins function cooperatively to regulate *vvhBA* rather than sequentially in a regulatory cascade. Electrophoretic mobility shift assays (EMSAs) and DNase I protection assays demonstrated that the regulatory proteins directly bind to specific sites within the *vvhBA* promoter, *PvvhBA*. Competitive EMSAs indicated that the additive binding of IscR and HlyU to *PvvhBA* alleviates the repression of *vvhBA* by H-NS. Interestingly, upon exposure to nitrosative stress or iron starvation, the *vvhBA* expression was induced by increased cellular levels of IscR. The combined results suggest that IscR, HlyU, and H-NS function cooperatively to precisely regulate the *vvhBA* expression in response to environmental changes that *V. vulnificus* encounters in the host.

**D060**

**Effect of Spicatoside A on Hepatitis E Virus Replication**

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Hepatitis E virus (HEV) is a member of the *Hepeviridae* family and the causative agent of hepatitis E in humans worldwide. Despite its self-limiting nature, HEV infection often triggers severe liver diseases causing high mortality in pregnant women in addition to chronic hepatitis and cirrhosis in immunosuppressed patients. In this study, we investigated the effect of spicatoside A on genotype 3 HEV replication. Spicatoside A suppressed replication of the genotype 3 HEV replicon and HEV genotype 3 strain 47832c. Furthermore, spicatoside A interfered with expression of HEV ORF2 capsid proteins. Our findings clearly support the potential utility of spicatoside A as an effective anti-HEV agent.

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D061
Glutamine Deprivation Induces Apoptosis by Enhancing Reactive Oxygen Species and Protein Phosphatase 2A in skw 6.4 Lymphoma Cell
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Altered glutamine metabolism is emerging target of cancer therapy. Glutamine deprivation has been proposed to induce apoptosis in multiple cancers. Dependency on glutamine metabolism of skw 6.4 lymphoma cell was investigated in vitro and in vivo. Glutamine deprivation induces apoptosis of skw 6.4 cell. Intracellular concentration of metabolites in tricarboxylic acid cycle and glutathione concentration were reduced and concentration of reactive oxygen species (ROS) and expression of PP2A were increased in glutamine-deprived skw6.4 cell. Reduction of ROS by antioxidants and knockdown of PP2A inhibited apoptosis induced by glutamine deprivation. Glutamine antagonist reduces skw6.4 tumor size in mouse xenograft model in PP2A-dependent manner. Overall, these results suggest survival of skw6.4 cells depends on the supply of glutamine in PP2A-dependent manner.

D062
Study on the Cell Function of Cereblon Protein in Psoriasis
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In this study, we investigated the psoriasis etiology, and relationship between CBBN and psoriasis using WT and CRBN KO mouse models that stimulated skin with aldara cream (5% IMQ) and had similar responses to psoriasis. CRBN KO mice showed a significantly higher inflammatory response compared to WT, especially histologically, the number of macrophages infiltrated into the epidermis increased, and the thickness of the epidermis, including the back and ear skin, became much thicker. In back skin, expression level of inflammatory cytokines such as IL-6 and TNF-α was considerably higher in CRBN KO than that of WT. IL-17, known as significant factor in psoriasis etiology was also higher in CRBN absence mouse. Finally, CRBN can modulate IL-17 and macrophage, alleviate the inflammatory response of psoriasis. It also suggests that this role of CRBN may be a key molecule as a new therapeutic agent for psoriasis.
Cereblon Regulates LPS-induced TNF-alpha and MCP-1 through AMPK/ HO-1 Activation in Retina

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Cereblon (CRBN), as a negative modulator of 5' adenosine monophosphate-activated protein kinase (AMPK), is highly expressed in the retina. First, we confirmed the expression of CRBN in ARPE-19, human retina cell line by Western blot. On the other hand, we presented results indicating that CRBN Knockdown (KD) by CRBN silence could effectively downregulate genes and protein levels of IL-6 and MCP-1 in LPS-induced ARPE-19 cells. In addition, CRBN KD increased phosphorylation of AMPK / acetyl-coenzyme A carboxylase (ACC) and expression of heme oxygenase-1 (HO-1) in ARPE-19 cells. Furthermore, CRBN KD significantly reduced LPS-induced nuclear translocation of NFκB p65 and activation of NFκB promoter activity. However, these processes could be abolished by compound C (inhibitor of AMPK) and Znpp-1 (inhibitor of HO-1). In consistently, compound C and Znpp-1 could rescued LPS-induced levels of pro-inflammation cytokines (IL-6 and MCP-1) in CRBN KD ARPE-19 cells. Taken together, our data demonstrate that CRBN deficiency negatively regulates proinflammation cytokines via activation of AMPK/ HO-1.
E001
“Anthranilate Peak” as a Hurdle for Biofilm Formation in *Pseudomonas aeruginosa*
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Anthranilate is an important intermediate for the synthesis of tryptophan and *Pseudomonas* quinolone signal (PQS), and metabolized by anthranilate dioxygenase complex (*antABC* gene products) via TCA cycle. Anthranilate has been reported to cause biofilm dispersal in various bacteria. To elucidate the relation between the anthranilate production and biofilm formation of *P. aeruginosa*, we traced the change of the anthranilate level as *P. aeruginosa* grows, and investigated the time point when *P. aeruginosa* forms biofilm. The production and secretion of anthranilate remain very low until *P. aeruginosa* reaches stationary phase, but it begins to secrete at stationary phase and rapidly accumulate to a high level at late stationary phase. Interestingly, the level of anthranilate rapidly decreased again when the stationary phase persisted longer. We named this transient increase in anthranilate level “anthranilate peak”. Our results demonstrated that this anthranilate peak blocks early biofilm formation and the mature biofilm forms only after the anthranilate peak disappears. In some mutant strains, the anthrnilate peak was modified: in *antABC* mutant, the high-level anthranilate lasted without decrease and in *rhlR* mutant, no anthranilate accumulates without the anthranilate peak. No anthranilate peak caused early biofilm formation and the lasting anthranilate peak delayed the biofilm formation.

E002
*Biofilm Formation by Pseudomonas aeruginosa Depends on Temperature*
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*Department of Pharmacy, College of Pharmacy, Pusan National University*

In response to external cues, bacteria form biofilm that is very protective life mode and adapt to environmental changes. *Pseudomonas aeruginosa*, an opportunistic human pathogen also adopts biofilm as a protective life mode against environmental challenges. During infection into human, *P. aeruginosa* experiences a big difference in temperature between the environment and human body. This temperature change may act as a cue to *P. aeruginosa* for the biofilm formation. In this study, we investigated the effects of temperature on the *P. aeruginosa* biofilm formation. We show that biofilm formation of *P. aeruginosa* at different temperatures (20°C, 25°C, 30°C, and 37°C) in static- and flow cell-systems. We also measured intracellular cyclic di-GMP (c-di-GMP) levels according to the temperature shift by using reporter (*cDrA*-*lacZ* fusion). Our results demonstrated that the lower the temperature, the better the biofilm formed by *P. aeruginosa*. Consistently, the level of intracellular c-di-GMP was higher at lower temperatures. In conclusion, in the temperature range between 20°C and 37°C, the lower the temperature, the more the c-di-GMP is synthesized, and the better the biofilm is formed by *P. aeruginosa*. 
E003  
Fission Yeast LAMMER Kinase, Lkh1, Regulates the Rad3-mediated DNA Replication Checkpoint Pathway  
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*Schizosaccharomyces pombe* is a rod-shaped fission yeast, which has a phenotype that increases the length when the cell grows. Therefore, when a problem occurs in the cell cycle, it is easy to observe the phenotype change. The cell cycle is regulated by cyclin dependent kinase (CDK), which functions in combination with other cyclins at different times in the cell cycle. Recently, CDK inhibitors have been attracting attention as the agents for the treatment of cancer caused by the defects in cell cycle control. Therefore, it is necessary to understand the molecular mechanism for the regulation of CDK activity. The *S. pombe* LAMMER kinase, Lkh1, has various functions in morphogenesis, oxidative stress response and cell cycle regulation. Recently, we found that the Lkh1 is involved in DNA replication stress response. In the spotting experiment for the hydroxyurea sensitivity test, Lkh1 deletion strain was more sensitive than WT. In addition, expression of *rad3*, a gene involved in DNA replication checkpoint pathway, increased in Lkh1 deletion strain compared to WT and protein level of Cds1, which is activated by Rad3, increased similarly in Lkh1 deletion strain. Taken together, our results suggest that Lkh1 is upstream regulator for Rad3-mediated DNA replication checkpoint pathway in *S. pombe*.

E004  
Expression Patterns of Developmental Genes during Mating in *Aspergillus fumigatus*  
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There are presently no studies on the genes for sexual development of an opportunistic fungi *Aspergillus fumigatus* in situ using mating culture, primarily because of challenging experimental conditions that require a significantly long period of induction and produce developmentally heterogeneous culture, harboring few sexual organs. In order to overcome these challenges, we developed an efficient and convenient procedure called ‘vegetative mass mating (VeM)’ for study at a molecular level. The VeM method enabled production of a developmentally homogenous *A. fumigatus* culture, harboring many sexual organs in a plate within a short period (two weeks). Our results revealed that *preA* expression was MAT1-1-dependent and *preB* expression was MAT1-2-dependent in *A. fumigatus*. The *ppgA* expression was consistent, increasing only in the mated culture by 2-fold. The *steA* and *nsdD* expression was MAT1-2 dependent. Unlike the expression pattern of *steA* and *nsdD*, *veA* expression in all three *A. fumigatus* strains showed similar patterns. Here we present, in situ analysis of developmental gene expression during sexual development in *A. fumigatus*—the first study of this kind. The convenience and effectiveness of VeM method, therefore, opens up possibilities for future investigation of sexual development in *A. fumigatus* at a molecular level by using various approaches such as omics.
E005
A Study on the Cultivation Characteristics of Mycelium in *Naematoloma sublateritium*
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This study on the characteristics of mycelium in *Naematoloma sublateritium*. It was excellent, and SADY medium, MMA medium was investigated, but suitable optimum culture medium appeared to mycelium growing of *Naematoloma sublateritium* the first, existing other study to PDA medium it was investigated. Suitable temperature and provisional results regarding ph of *Naematoloma sublateritium*, proper temperature appeared with 25 degrees, and proper ph was investigated to 6.5~7.0. This study showed to excellent hypha growing at Glucose in circular the carbon which was suitable for the third, hypha growing of *Naematoloma sublateritium* provisional results carbon circle regarding a nitrogen circle, and cultures of *Naematoloma sublateritium* looked at malt extract in case of organic nitrogen circles. However, a kind circular carbon nitrogen used to test is restrictive, and provisional shall consist of various elements by a foundation. This study looked in phosphoric acid circle to affect the fourth, mycelium of *Naematoloma sublateritium* to growth and development. Also, If this study added it was investigated p-aminobenzoic acid in vitamin circle so that hypha growing was comparatively good.

[This paper consisted by assistances of a technology development assignment scientific forest]

E006
Acetylation of Housekeeping Sigma Factor in *Streptomyces venezuelae*
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Streptomyces are well known as antibiotics producer and have a complex cell cycle in response to conditions. *Streptomyces venezuelae* ATCC15439, as a pikromycin producer, has a genome of 9.05 Mb encoding 8080 proteins. By domain analysis, it is predicted to encode 43 sigma factors including HrdB as a housekeeping sigma factor. We determined the expression levels of the *hrdB* gene in *S. venezuelae*. The RNA and protein expression levels of *hrdB* were reduced after the stationary phase but transcriptional levels of *hrdB* regulon were substantially maintained. Recently, many studies revealed that transcriptional factors could be post-translationally modified and these modifications would modulate their functions. However, the function of post-translational modification (PTM) on sigma factor remains ambiguous. Thus, we revealed the function of PTM on the house-keeping sigma factor. By using western blotting, we verified that HrdB in *S. venezuelae* was also acetylated. It was also confirmed using LC-MS/MS analysis. Interestingly, most of the HrdB bound in the RNA polymerase holoenzyme is also acetylated. It can be proposed that the Lys-acetylation of HrdB does not impede its binding to core RNAP. The function of lysine acetylation on HrdB during the transcription process is under investigation. Proteomic studies about acetylome in many bacteria verified that the acetylation of sigma factor is widely conserved, and its significance to the functionality of sigma factor.
E007
Functional Analysis of yejM, an Essential Gene Involved in the Biosynthesis of Outer Membrane in *Escherichia coli*

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The increasing prevalence of antibiotic resistance and the lack of new antibiotic drug development has gradually reduced the treatment options for bacterial infections. To combat antibiotic-resistant bacterial pathogens, there is a critical need for the development of novel antibiotics with new antibacterial modes of action to complement existing drugs that inhibit peptidoglycan biosynthesis, DNA replication, or protein biosynthesis. To identify a novel promising target which are previously unexploited by commercially available drugs, we searched a novel essential gene in *Escherichia coli*. Among 10 candidates, a *yejM* gene was identified as an essential gene. YejM was known as a cardiolipin transporter responsible for cardiolipin trafficking to the outer membrane in *Salmonella Typhimurium*. Overproduction of YejM inhibited the growth of *E. coli* cells under various stress conditions. Complementation experiments showed that the N-terminal domain of YejM is indispensable for its essentiality. The essentiality of the *yejM* mutant was suppressed by deletion of the *lapB* gene, encoding a heat shock protein involved in the assembly of lipopolysaccharide. Through these experiments, we investigate the intracellular function of YejM and assess the possibility of the discovery for potent inhibitors targeting YejM.

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E008
Novel Inhibitors of Class B β-Lactamases Identified by a Cell-based Screening Assay

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The emergence and spread of antibiotic resistance in pathogenic bacteria and the consequent failure of antibiotic therapy has led to hundreds of thousands of deaths annually. Especially, the recent prevalence of carbapenem-resistant Gram-negative pathogens, such as *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*, poses a serious threat to public health worldwide. The Centers for Disease Control and Prevention recently designated carbapenem-resistant Gram-negative pathogens an urgent public health threat requiring aggressive monitoring and prevention strategies for effective patient management. Since carbapenem-resistant Gram-negative pathogens has become resistant to nearly all available antibiotics, several β-lactamase inhibitors are currently in clinical development. However, there is no β-lactamase inhibitor acting on class B metallo-β-lactamases, such as NDMs, VIMs, and CphA. In this study, we performed a whole-cell screening assay of 6,600 chemicals from Korea Research Institute of Chemical Technology against class B β-lactamase-producing *K. pneumoniae*, *P. aeruginosa*, *A. baumannii*, and *Escherichia coli*. The *in vitro* screening identified four hit chemicals exhibiting a synergetic effect in combination with imipenem against at least one species of Gram-negative pathogens tested. [This work was supported by a grant the NRF funded by the Ministry of Science and ICT (number NRF-2018R1A1A105023049)]
E009
Characterization of Functional Differences of Two CRP Paralogs in *Mycobacterium smegmatis* by RNA seq
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The genome of *Mycobacterium smegmatis* has two genes (MSMEG_6189, *crp1*; MSMEG_0539, *crp2*) encoding cAMP receptor protein (CRP). To evaluate the function of the two CRP paralogs, the transcriptomes of the Δ*crp1* and Δ*crp2* mutants were compared with that of the wild type strain. In the Δ*crp1* mutant, 405 among 6938 genes were differentially expressed (*p*-value < 0.05, lFold changel ≥ 2) relative to the wild type strain, of which 210 are induced and 195 are repressed. There are 211 differentially expressed genes (DEG, *p*-value < 0.05, lFold changel ≥ 2) in Δ*crp2* mutant relative to the wild type strain, of which 160 are induced and 51 are repressed in the mutant. DEG analysis showed that CRP1 functions as a transcriptional activator and repressor and CRP2 functions mainly as a repressor. 78 genes were identified as common DEGs for the Δ*crp1* and Δ*crp2* mutants. KEGG analysis demonstrated that the DEGs of the Δ*crp1* mutant are significantly enriched in the ABC transporter pathways and fatty acid biosynthesis pathways. The DEGs of the Δ*crp2* mutant are significantly enriched in the ABC transporter pathways and oxidative phosphorylation pathways. Interestingly, the DEGs of Δ*crp1* overlap with 46% of the genes belonging to the known dormancy survival regulator (*dosR*) regulon. These results imply that CRP1 and CRP2 have divergent function in gene regulation.

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E010
Structural Insights into Trehalose 6-Phosphate Phosphatases of *Pseudomonas aeruginosa*
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The bacterium *Pseudomonas aeruginosa* is a leading cause of hospital-acquired infections and possesses a notoriously low susceptibility to antibiotics. Trehalose 6-phosphate phosphatase (TPP) is an enzyme of the trehalose biosynthesis pathway and has recently attracted attention as a potential drug target since its knockdown in bacterial and nematode pathogens results in a lethal phenotype. Therefore, we explored the structural and functional properties of TPP in *P. aeruginosa* in support of future target-based drug discovery. The TPP was produced as recombinant proteins and characterisation of their enzymatic properties confirmed specific, magnesium-dependent catalytic hydrolysis of trehalose 6-phosphate. The three-dimensional crystal structure of the chromosomal TPP revealed a protein dimer arising through β-sheet expansion of the core domains of the individual monomers which possess the overall fold of halo-acid dehydrogenases. Comparison of the crystal structure with a model of the substrate-bound protein suggested that domain movement between the cap and core domains, in contrast to other TPPs, is unlikely to occur, owing to a bent α-helix that provides a rigid connection between both domains. As a consequence, substrate entry into and product exit from the catalytic site is subject to substantial spatial restrictions which is mirrored by the exceptionally low enzymatic efficiency.

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E011
Identification of the Transcriptional Regulator RamB (MSMEG_0906) Related to the Regulation of the Gene Encoding Isocitrate Lyase in Mycobacterium smegmatis
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Isocitrate lyase (ICL) is the first enzyme of the glyoxylate cycle. The glyoxylate cycle is important in terms of anaplerotic reactions of the TCA cycle. Mycobacterium smegmatis, a fast-growing environmental saprophyte, contains two ICL homologs encoded by MSMEG_0911 (ICL1) and MSMEG_3706 (ICL2). Promoter activity analysis revealed that icl1 was highly induced by acetate. Moreover, an icl1 deletion mutant showed an impaired growth compared to the wild type (WT) strain when both the strains were grown on acetate. Previously it was reported that the transcriptional regulator RamB (Regulators of Acetate Metabolism B) in Corynebacterium glutamicum is involved in regulation of genes related to acetate metabolism including the icl gene. Mycobacterium tuberculosis has an open reading frame encoded by Rv0465c with significant sequence similarity to RamB of C. glutamicum. The protein from M. tuberculosis is known to repress the expression of the icl1 gene and negatively autoregulate its own gene expression during growth on glucose. Like M. tuberculosis, M. smegmatis has a homologous gene encoded by MSMEG_0906 with 86% sequence identity to RamB of M. tuberculosis. Moreover, its synteny is similar to that of M. tuberculosis. Using a MSMEG_0906 deficient mutant, it was revealed that MSMEG_0906 positively regulated the expression of the icl1 gene.
[Supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF)]

E012
Regulatory Network of Alternative Sigma Factor SigF in Mycobacterium smegmatis
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Alternative sigma factor sigF is known to be required for Mycobacterium smegmatis to adaptation to stationary phase and resistance to H2O2. It has been shown that anti-anti sigma factors (RsfA and RsfB) and an anti-sigma factor (RsbW) constitute a regulatory network responsible for SigF regulation, and that RsfB is phosphorylated by MSEG_6129. A putative two-component system (MSMEG_6130, sensor histidine kinase; MSMEG_6131, response regulator), which might be involved in the SigF regulatory network, was identified in the genetic locus adjacent to the rsfB gene in M. smegmatis. The effector domain of MSMEG_6131 showed sequence homology to the PP2C phosphatase. Based on these findings, we hypothesized that the regulatory network configured with MSMEG_6129, MSMEG_6130 and MSMEG_6131 might control expression of the SigF regulon by modulating the phosphorylation state of RsfB. To confirm this assumption, we constructed MSMEG_6129, MSMEG_6130, and MSMEG_6131 mutant strains (Δ6129, Δ6130, and Δ6131) of M. smegmatis. Expression of MSMEG_1777, which is a member of SigF regulon, was increased in the Δ6129 and Δ6130 mutants, while it was decreased in the Δ6131 mutant. These results suggest that RsfB is inactivated by phosphorylation through MSMEG_6129 and activated by dephosphorylation through MSMEG_6131 and that MSMEG_6130 as a sensor kinase inactivates MSMEG_6131 by phosphorylation.
[Supported by the Basic Science Research Program through the NRF]
E013
Calcineurin Activation Mediated by Human Prion Protein Induced Neuron Cell Death via Autophagy Flux
Jeong-Min Hong, Honghua Yin, Kazi Mohammad Ali Zinnah, Seong-Goo Kang, Jae-Won Seol, and Sang-Youel Park*
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It is usually accepted that prion peptide induce apoptotic cell death. However, the mechanisms of PrPsc-neurotoxicity effect are not completely clarified. The Ca^{2+}/calmodulin-dependent phosphatase calcineurin may be the link between deregulation of Ca^{2+} homeostasis and apoptotic neuronal death. In this study, we investigated the effect of human prion peptide-induced calcineurin activation that induced AMPK dephosphorylation and autophagy activation. Furthermore, we demonstrated that these peptide reduced the levels of AMPK phosphorylated at threonine residue 172, and Autophagy activation and calcineurin inhibitor, FK506, was prevented this effect. The data obtained showed that PrP-treated neurons had higher levels of AMPK than control neurons. This increase in AMPK levels was matched by an activation autophagy. FK506 prevented the alterations of AMPK and autophagy levels induced by PrP peptide. Taken together, the data demonstrated that prion peptide triggered an apoptotic cascade through calcineurin activation which mediated AMPK dephosphorylation and autophagy activation. Therefore, these data suggest that therapeutic strategies targeting calcineurin inhibition might be valuable for these neurodegenerative disorders including prion disease.
[This study was supported by a grant from the National Research Foundation of Korea (NRF), funded by the Korean government (2016R1A2B2009293).]

E014
Baicalein Prevents Prion Peptide-induced Neuronal Cell Death by Regulating Calcineurin Activity
Jeong-Min Hong, Honghua Yin, Kazi Mohammad Ali Zinnah, Seong-Goo Kang, Jae-Won Seol, and Sang-Youel Park*
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Prion diseases are a group of fatal neurodegenerative disorders characterized by neuronal cell death. Calcineurin activation mediates prion-induced neurodegeneration, suggesting that inhibition of this phosphatase could be a target for therapy. Baicalein has been reported to exert neuroprotective effects on calcium-dependent neuronal cell death. In the present study, we investigated the effects of baicalein on the development of prion diseases using neuron cell. In this study, we investigated whether baicalein could attenuate prion peptide-induced neurotoxicity mainly through the interruption of intracellular calcium homeostasis, which leads to calcineurin inactivation. We found that baicalein protected the cells against prion peptide-induced neuron cell death by inhibiting the production of calcium evaluation. We demonstrated that baicalein treatment regulated the calcineurin by using calcineurin activity assay and western blot analysis. Thus, these data showed that baicalein has a protective effect against prion-mediated neuron cell death and also suggest that baicalein may be effective therapeutic drug against neurodegenerative diseases, including prion diseases.
[This study was supported by a grant from the National Research Foundation of Korea (NRF), funded by the Korean government (2016R1A2B2009293).]
E015
Calcineurin Activation by Prion Peptide Induces a NF-kb-driven Proinflammatory Response in Neuronal Cell
Jeong-Min Hong, Honghua Yin, Kazi Mohammad Ali Zinnah, Seong-Goo Kang, Jae-Won Seol, and Sang-Youel Park*
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Prion diseases are fatal neurodegenerative disorders that are derived from accumulation of an abnormal isoform of the protease-insensitive isoform (PrPSc) of prion protein in the brains. Recent studies have illustrated that calcineurin could play an important role in the calcium-calmodulin pathway to regulate nuclear factor kappa B (NF-kB). Calcineurin is activated by the binding calcium to calmodulin. In the present study, we examined the activation of calcineurin upon exposure to prion peptide and its role in prion peptide-induced upregulation of nuclear factor-kappa B (NF-κB) and proinflammatory cytokines (tumor necrosis factor (TNF)-α, interleukin (IL)-1β and interleukin (IL)-6) in human neuro carcinoma. The results indicate that prion peptide induced calcineurin activation, which subsequently lead to the putative activation of NF-κB transcription factor. Calcineurin activation increased the expression of TNF-α, IL-1β and IL-6, which blocked by treatment with calcineurin and NF-κB Inhibitors. Taken together, prion peptide–mediated neuroinflammation was attenuated by calcineurin Inhibition, and also suggest calcineurin may be a possible target molecule in anti-inflammation of neuron.
[This study was supported by a grant from the National Research Foundation of Korea (NRF), funded by the Korean government (2016R1A2B2009293).]

E016
Reappraisal of Glucose Repression of Lactose Utilization in Escherichia coli
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Carbon catabolite repression (CCR) is a global regulatory mechanism to ensure the sequential utilization of carbon sources. Most organisms prefer glucose to other sugars by the mechanism of CCR. In most bacteria, sugars transported by the phosphoenolpyruvate:sugar phosphotransferase (PTS) are usually preferred to non-PTS carbon sources like lactose. The currently proposed model for CCR in enteric bacteria including Escherichia coli depends on the phosphorylation state of enzyme IIαGlc(EIIAαGlc), glucose-specific PTS component. However, we found some contradictions of the current CCR model for the glucose repression of the lactose operon. Our data suggest that there must be another contributor that regulates lactose metabolism. To establish a proper mechanism for CCR, we isolated mutants that caused ptsH and ptsI mutant strains to be able to grow on glucose as efficiently as the wild-type Escherichia coli strain. We found a point mutation on cra in the glucose-adaptive strain of the ptsH mutant and overexpression of galP in the glucose-adaptive strain of the ptsI mutant. The two adaptive strains and their crr deletion mutant cells who lack the PTS prefer glucose to lactose, suggesting that a general mechanism of CCR in Escherichia coli could be independent of the PTS.
E017
Characterization of the Transcriptional Regulator VC1825 in Vibrio cholerae
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The phosphoenolpyruvate: sugar phosphotransferase system (PTS) is the highly conserved and the most effective sugar uptake system in bacteria. In Vibrio cholerae, the search for PTS components revealed 25 homologs of PTS components, some of which are putative fructose-specific PTSs. VC1826 is also known as putative fructose-specific PTS but the previous studies showed that it seems to be responsible for the uptake of mannose. To confirm the sugar specificity of VC1826 on the fructose or mannose uptake, we investigated the expression level in minimal medium supplied fructose or mannose as a sole carbon source. The expression level of VC1826 was increased in both media. Since the regulatory mechanism of VC1826 expression is poorly understood, we searched transcriptional regulator of VC1826 expression. VC1825, located upstream of and divergently transcribed from the VC1826 gene, encodes an AraC type transcriptional regulator. We found that expression of the VC1826 gene was notably decreased in a VC1825 deletion strain and that growth of the VC1825 mutant was inhibited by mannose, but not by fructose. We performed electrophoretic mobility shift assay (EMSA) and confirmed that the binding site of VC1825 is in the intergenic region between VC1825 and VC1826. Therefore, in V. cholerae, VC1825 is expected to modulate the expression of VC1826. Furthermore, VC1826 seems to be the mannose-specific PTS, and VC1825 is expected to be a transcriptional regulator of the mannose-specific PTS.

E018
Characterization of Staphylococcus aureus SarZ, Cysteine-based Redox Sensor In Vitro
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Staphylococcus aureus is the most common pathogen that can cause serious illness, from skin infections to pneumonia and sepsis. S. aureus SarZ is known as ortholog of OhrR, organic peroxide sensor in Bacillus subtilis. However, there has been no definitive study of the biophysical properties of SarZ about organic peroxide resistance. Therefore, this study aims to understand the physicochemical characteristics of SarZ in comparison with OhrR in vitro. In order to confirm whether SarZ can bind to OhrR DNA binding sequence, OhrR, SarZ, and SarZ (C13S) mutant proteins were cloned and purified. Finally, we observed binding between protein and DNA through fluorescence anisotropy (FA) experiments. As a result, SarZ could bind to DNA binding sequence in vitro and as oxidized by cumene hydroperoxide (CHP), the binding capacity of SarZ with DNA was weakened, and it was less sensitive than OhrR. In the case of SarZ (C13S), it was not dissociated even when treated with CHP. Similar to OhrR, it could be assumed that the 13th amino acid of SarZ plays the role of peroxidative cysteine, which directly detects organic peroxides.

In conclusion, we observed the change of DNA binding ability according to the oxidation of SarZ. In further study, in vivo and additional experiments will reveal the exact defense mechanisms.
[This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (NRF-2018R1A5A1025077)]
E019
**Characterization of Probiotic Properties of Lactobacillus plantarum SRCM101594 Isolated from Kimchi**
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This study was aimed to isolate lactic acid bacteria having probiotics properties from Korean fermented food, Kimchi. 6 isolates were investigated for safety verification by biogenic amine, antimicrobial and antioxidant activities. Especially, SRCM101594 showed higher antioxidant activity (19.98%) than other strains. SRCM101594 was also evaluated to various antimicrobial spectrum and biogenic amines non-producing microorganisms. Finally, SRCM101594 was selected to confirm probability of probiotics strain, and named as *Lactobacillus plantarum* SRCM101594 by 16S rRNA sequencing analysis. Additionally, SRCM101594 was analyzed to their hemolytic, harmful substances and enzyme productivity, coagulation of milk protein, bile salt hydrolase, antibiotic resistance and survival ability of acidic and bile condition. As a result, SRCM101594 was confirmed as safe strain because of its non-hemolytic activity and non-production of harmful substances (Phenyl pyruvic acid and indole) and enzymes (β-glucuronidase and urase). And SRCM101594 Showed 50% and 92% of higher survival rate in acidic condition at pH 2.0 and bile resistance with 0.5% oxgall. In addition, SRCM101594 has resistant to various antibiotics. These results suggest that SRCM101594 has potential for application as probiotic lactic acid bacteria.

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E020
**Hfq and RplT Genetically Interact with BipA at Low Temperature in Escherichia coli**
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BipA is ribosome binding GTPase conserved in bacterial and structurally similar to other translational GTPases. BipA is not required under optimal growth conditions but becomes an essential factor for survival at low temperature, nutrient depletion, and various other stress conditions. Recent studies show that BipA is a cold shock-inducible GTPase participating in 50S subunit assembly by incorporating the L6 ribosomal protein into the 44S particle. In this study, to found the genes genetically interacting with *bipA*, we constructed genomic library from Δ*bipA* strain and screened suppressors for the cold-sensitive growth of Δ*bipA* strain. Then, we isolated and identified two suppressors, Hfq and RplT. Hfq has key roles in the control of gene expression and participates in 30S subunit assembly. Mutational analysis revealed that ribosome assembly activity of Hfq is responsible for suppression. Furthermore, Hfq bound to 50S subunit accumulated in *bipA*-deletion strain at 20°C. RplT, ribosomal protein L20, is a component of 50S subunit. The N-terminal domain of RplT, important for ribosome assembly, restored cold sensitivity of Δ*bipA* strain, whereas the C-terminal domain of RplT involved in post-transcriptional regulation could not restore. Our findings imply that Hfq and RplT directly suppressed ribosome assembly defect of Δ*bipA* strain by facilitating assembly of 50S subunit.

[Supported by grants from NRF]
F001
The Ku Complex Repairs Unresected Double-strand Breaks during Meiosis in *Saccharomyces cerevisiae*
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Double-strand breaks (DSBs) are repaired by two pathways for cell viability and genome stability. Non-homologous end joining (NHEJ) pathway mediate the ligation of DNA ends during G1 phase. Whereas, Homologous recombination (HR) pathway that are required for genetic diversity during S and G2 phase. Meiotic recombination requires diverse recombinase proteins and regulatory factors involved in the formation of crossovers (COs) and non-crossovers (NCOs). In NHEJ pathway, The Ku complex binds to these DSB ends, inhibiting additional DSB resection and mediating end joining with Dnl4, Lif1, and Nej1, which join the Ku complex and DSB ends. Here, we propose the role of the Ku complex in DSB repair using a physical analysis of recombination in *Saccharomyces cerevisiae* during meiosis. We observe that the Ku complex is not essential for meiotic progression, DSB formation, joint molecule formation, and CO/NCO formation during meiosis. Surprisingly, the absence of the Ku complex and functional MRX complex, a large portion of meiotic DSBs was repaired via the recombination pathway to form COs and NCOs. Our data suggested that DSB resection channel, MRX complex was impaired regulation from meiotic recombination to the NHEJ pathway, which is also required for the maintenance of genomic integrity.

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F002
Redox Potential Dependent Reduction of a Reducing System for SoxR in the Cytoplasmic Membrane of *Escherichia coli*
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SoxR is a Fe-S containing transcription factor whose activity is modulated by redox-active molecules. A reducing system of SoxR has been proposed in *Escherichia coli* through genetic studies. It consists of a putative electron transfer system encoded by the *rsxPABCDGE* operon and *RseC* encoded from the unlinked *rpoE-rseABC* operon. We found *ApbE*, known to function in Fe-S maintenance in *Salmonella*, is an additional component of the reducer system. *RsxC*, the only cytoplasmic component of the system, interacts with SoxR, and is likely to link it with the rest of the complex via *RsbB*. Membrane fractions containing the wild type complex, but not the mutant complex, reduced purified SoxR, using NADH as an electron source. However Streptomyces type SoxR was not reduced by SoxR reducer complex. This demonstrates the electron-transfer capability of membrane-bound SoxR-reducer complex, and opens the possibility of transferring electrons to other suitable substrates.
F003
Comparative Genomic Analysis of Human Intestinal Mucin-degrading Bacterium Akkermansia muciniphila Isolated from Korean Feces
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Akkermansia muciniphila is a well-known mucin-degrading bacterium distributed in the mammalian intestinal tract. A. muciniphila exerts beneficial effects during metabolic disorders, inflammation, obesity, and obesity-associated complications. Although genetic data on Akkermansia have increased recently, data on the strains isolated from humans are yet lacking and there have been no reports for Akkermansia genomes from Koreans. This study aimed to analyze the genome of A. muciniphila CBA5201 isolated from fecal samples of a Korean individual, owing to its high value as an intestinal microorganism, and compared it with 55 other A. muciniphila genomes. A. muciniphila CBA5201 comprises a circular chromosome of 2,860,407 bp with 55.32% G+C content, contains mucin-degrading enzymes and Amuc_1100 protein. Pan-genome analysis of 56 A. muciniphila genomes revealed that the genomes have 1,241 core genes and A. muciniphila CBA5201 has four unique genes. The complete genome sequence of A. muciniphila CBA5201 determined herein helps understand the genetic characteristics of Akkermansia strains.
[Supported by grants from World Institute of Kimchi (KE1902-1 and KE1902-2) funded by the Ministry of Science and ICT.]

F004
Genomic Analysis of Salmonella enterica Serovar Virchow FORC_080 Isolated from Human Stool in South Korea
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Salmonella enterica serovar Virchow is a foodborne pathogen causing gastroenteritis and systemic infections in host. S. Virchow invades epithelial cells and replicates within macrophages by using type III secretion system (T3SS) encoded on Salmonella pathogenicity islands (SPIs). S. Virchow FORC_080, isolated from human stool in South Korea, was analyzed at the genomic level to understand its pathogenesis. The genome of FORC_080 contains important virulence genes within SPIs and also several genes encoding T3SS effector proteins. The invasion activity of FORC_080 was comparable to that of S. Typhimurium SL1344, an invasive strain. Comparative genome analysis between FORC_080 and SL1344 revealed that FORC_080 harbors three additional fimbrial gene clusters, which may account for the higher abilities of FORC_080 to adhere to the epithelial cells and to form biofilm than those of SL1344. FORC_080 also contains antibiotic resistance genes which are not present in SL1344, resulting in the resistance of FORC_080 to several antibiotics including chloramphenicol, tetracycline, and trimethoprim. All these results provide enhanced knowledge on the pathogenesis of S. Virchow and its potential risk to public health.
[This research was supported by a grant (14162MFDS972, 19162MFDS037) from Ministry of Food and Drug Safety in 2019.]
F005
Unraveling the Molecular Mechanism of Zur Oligomerization in Streptomyces coelicolor
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Metal ions are important for central reactions such as respiration, photosynthesis, and nitrogen fixation, but excess metals can be toxic. As metals cannot be degraded or synthesized, bacterial metalloregulators regulate the expression of genes involved in metal transport, metal storage, and metal usage when metal levels deviate from optimal set point. These metalloregulators are generally multimeric DNA-binding proteins whose DNA-binding activity is modified upon metal binding, causing changes in gene expression either via co-repression or co-activation. The Zn(II)-specific sensor Zur (Zinc Uptake Regulator) is known to express its regulons in two phases in response to zinc concentration in Streptomyces coelicolor. Dimeric Zur binds to the Zur-box motif at sub-femtomolar zinc concentration resulting in the low zitB expression while dimeric Zur binds to Zur-box motif and forms oligomerization toward the upstream of the Zur-box motif at micromolar zinc concentration resulting in high zitB expression. Here, we aim to elucidate the mechanism of Zur oligomerization. We performed electrophoretic mobility shift assay (EMSA) and ChIP-qPCR with DNA fragment containing Zur box and identified a Zur variant that showed different binding patterns compared to wild type Zur. The Zur variant was unable to form oligomerization and could not either activate or fully repress Zur regulons. Further experiments regarding this topic are underway.

F006
Identification of Microbial Taxa Associated with Gastric Carcinogenesis through Microbiota Analysis
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Gastric cancer, which is the leading cancer in Korea, occurs through stages of atrophic gastritis, intestinal metaplasia, and gastric cancer. Gastric carcinogenesis is initiated by Helicobacter pylori infection and it has been confirmed by many studies since first proposed by Correa. However, recently many studies have suggested that H. pylori is not the only cause of gastric cancer. Therefore, we aim to characterize microbiota structures of the stomach in relation to disease states. We conducted 16S rRNA sequence analysis of gastric biopsy samples from several disease states including gastritis, atrophic gastritis, intestinal metaplasia and gastric cancer and from normal states including superficial chronic gastritis. The gastric microbial structure varies depending on individuals, however, mostly constitutes of five phyla: Actinobacteria, Bacteroides, Firmicutes, Fusobacteria and Proteobacteria. Among several factors that shape the bacterial community structure, H. pylori infection is a leading one. The results of beta diversity analysis and network analysis suggest that gastric microbiota composition can be clustered into several groups depending on the disease states. This study allows us deep understanding on the gastric microbiota structure and may provide us clues to the identification of culprits which are responsible for each disease state besides H. pylori.
F007
RNase G-mediated Control of the tpiA mRNA Abundance Contributes to Transition between Respiration and Fermentation in Escherichia coli
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Previous reports have shown association of RNase G with expression levels of many enzymes involved in carbohydrate metabolism in E. coli. However, mechanisms of RNase G action on this phenomenon have not been characterized. Here, we show that tpiA mRNA, encoding a glycolytic enzyme, triosephosphate isomerase, is cleaved by RNase G in its 5' untranslated region, determining the mRNA stability. In addition, we discovered that expression levels of tpiA increased, which coincided with decreased RNase G expression, under the microaerobic condition compared to the aerobic condition. Our findings suggest that RNase G contributes to modulation of expression of glycolytic enzymes in response to oxygen availability in E. coli.

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F008
Functional Analysis of the Putative Transcription Factors Involved in the Process of Differentiation in Aspergillus nidulans
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In this study, we characterized a novel putative TF ; AN1536, AN2826, AN5775, AN7343, AN7346. over-expression strains of these genes showed decreased conidiation and fluffy morph. The mRNA level was checked to confirm that these genes were over-expressed in the strains. Also, the amounts of sterigmatocystin were measured to investigate whether these genes are involved in secondary metabolism. As a result, the amounts of sterigmatocystin in OE AN5775 and OE AN7343 were lower than WT. Also, RT-qPCR was performed to investigate the relationship between the genes involved in secondary metabolism and these genes. As a result, the levels of aflR and stcU mRNA in OE AN7343 were lower than WT. Deletion strains of these genes showed increased conidiation on the whole. The conidia number of each strain was measured. As a result, AN5775, AN7343 and AN7346 deletion strains show increased conidiation. AN1536 deletion strain shows similar level conidiation. AN2826 deletion strain shows decreased conidiation. In summary, it appears that AN5775 and AN7343 are all involved in the secondary metabolism and differentiation in Aspergillus nidulans.

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F009

Function Analysis of the Candidates Presumed to be Transcription Factors Involved in the Process of Differentiation in *Aspergillus nidulans*

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*Aspergillus nidulans* research has advanced the study of eukaryotic cellular physiology, contributing to metabolic regulation, development, cell cycle control, morphogenesis and human genetic diseases. During asexual development, several morphological changes generate to form conidiophores and asexual spores called conidia. In addition, mycelial mass are formed from which Hülle cells and cleistothecia are developed for sexual development. Several genes involved in asexual development have been genetically characterized and interactions between them have been investigated. In contrast, the 'sex-related' genes have not been well dissected. We have performed transcriptome analysis of *A. nidulans* throughout the whole life cycle from vegetative growth to asexual differentiation, and selected fifty-one genes of putative transcription factors (TFs) exhibiting significant stage-dependent variation in their transcription levels. In this study, we characterize the novel putative regulator TFs asexual and sexual development in *A. nidulans*. The overexpression AN9025 AN7516 AN3356 strains has increased asexual development more than WT but overexpression AN6295 strain has decreased asexual development more than WT. In addition, the amount of biosynthesis of ST, which is a secondary metabolite, is significantly lower than that of WT. Thus, qRT-PCR was performed to investigate the relationship between genes involved in the ST biosynthetic process.

F010

Functional Analysis of the Putative C2H2 Transcription Factor RocA in *Aspergillus nidulans*

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We characterize the novel regulator RocA with C2H2 domain regulating asexual and sexual development in *A. nidulans*. The *rocA* (repressor of conidiation) mRNA specifically accumulates during the late phase of asexual development and the early to middle phase of sexual development. The deletion of *rocA* leads to increased number of conidia and delayed production of sexual fruiting bodies (cleistothecia). In the *rocA* deletion mutant, mRNA levels of the *brlA*, *abaA*, and *wetA* genes that regulate sequential activation of asexual sporulation increased. On the other hand, mRNA levels of the genes that positive regulators of sexual development decreased. Overexpression of *rocA* causes reduced conidiation and increased forming sexual structures. Accordingly, mRNA levels of the genes increased. These results suggest that RocA functions as a negative regulator of asexual development and a positive regulator of sexual development. Additionally, *rocA* deletion caused increased production of the secondary metabolites, such as sterigmatocystin (ST), penicillin (PN) and terrequinone (TQ), as well as expression of their biosynthetic genes, such as *stcU* and *qflR* for ST, *ipnA* and *acvA* for PN, and *tdiA* and *tdiB* for TQ. On the other hand, overexpression of *rocA* negatively affected not only production of ST, PN and TQ, but also expression of the relevant genes. It thus appears that RocA functions as a negative transcriptional modulator of the secondary metabolic genes involved in ST, PN and TQ biosynthesis.
F011
Analysis of the Genome Sequence of the *Lentibacillus* sp. CBA3610 Isolated from Human Feces
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*Lentibacillus* is a Gram-variable, aerobic, and halophilic bacterial genus of the family Bacillaceae and phylum Firmicutes. In the present study, *Lentibacillus* sp. CBA3610 was isolated from a fecal sample collected in Korea, and its whole genome sequence was analyzed using various computational tools. With the use of Pacbio RSII sequencing platform, genomic DNA was assembled into one contig of 4,035,571 bp in length and GC content of 42.04%. The contig is predicted to contain 4142 CDS, 63 tRNA genes, and 17 rRNA genes (six 16S rRNA, six 23S rRNA, and five 5S rRNA). Analysis of 16S rRNA gene sequences showed that *Lentibacillus* sp. CBA3610 was closely related to *Lentibacillus salicampi* and *Lentibacillus salarius*. The ortho-average nucleotide identity values among other *Lentibacillus* species range from 70.69 to 79.75. In addition, 1821 SEED database proteins were identified in the RAST annotation. Finally, the PHASTER and CRISPRFinder tools detected one incomplete prophage gene and five putative CRISPR genes. These genomic data offer insights into the unique physiological characteristics of *Lentibacillus* sp. CBA3610 and may help to elucidate possible mechanisms involved in the interactions with the host gut.

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F012
Dynamic Transition of Gene Essentiality According to Growth Phases through CRISPRi System Introduction to *Escherichia coli*
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The cells determine the hierarchy of gene essentiality for cell surviving and maintaining in a nature. Consequently, cells control the transcription and translation for cellular fitness. Here, we investigated the transition of gene essentiality according to growth phases, colony, exponential, and saturation as introducing CRISPRi library system into *E. coli* for whole CDS. Consequently, the list for the gene essentiality of *E. coli* were created according to the growth phases. It showed a high correlation over 95% with KEIO collection. Further, the distribution of gene essentiality by Clusters of Orthologous Groups was variable. The gene essentiality in core proteins such as transcription and translation was sustained regardless of growth phases, but some proteins, for example, lipopolysaccharide, peptidoglycan biosynthesis, biofilm, and adhesion proteins were more essential in colony phase. And our essentiality index reflected the core enzyme with high essentiality in the essential central metabolic pathway, glycolysis, TCA cycle, and pentose phosphate pathway. Our gene essentiality index determined by knockdown inhibition of transcription, will enable to support more broad interpretation for gene function according to the various environmental conditions.

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F013
Evolution of the Potyvirus Polyprotein Cleavage Sites
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Potyvirus, which causes a significant yield loss in a wide range of crop plants, is the largest genus of plant RNA viruses with 186 recognized species. The potyvirus genome encodes a single large polyprotein with about 3000-4000 amino acids. The polyprotein undergoes proteolytic cleavage to produce 10 mature proteins (P1, HC-Pro, P3, 6K1, CI, 6K2, VPg, Nla-Pro, Nlb-RdRp, and CP). The first 2 junctions, P1/HC-Pro and HC-Pro/P3, are cleaved by the P1 and HC-Pro, respectively. The other 7 cleavage sites are processed by the Nla-Pro. The consensus recognition sequences are \([VILMFWC]X[HQ][FY]/S\) for P1, \(YX-VG/G\) for HC-Pro, and \(VX-HQ/[AGS]\) for Nla-Pro, where ‘/’ is the cleavage boundary and ‘X’ any amino acid. In this study, about 2000 full-length potyvirus polyproteins were analyzed to find out if the processing consensus sequences are conserved in all potyvirus lineages. As a result, the P1/HC-Pro and HC-Pro/P3 junction sequences were strictly conserved in all potyviruses. In contrast, some Nla-Pro cleavage sites had a distinct and lineage-specific consensus sequence different from the previously known sequence, suggesting that the cleavage site sequence may change during potyvirus evolution. Interestingly, a subclade containing 18 potyviruses showed novel consensus sequences in almost all the Nla-Pro recognition sites, implying that the active site sequence of the Nla-Pro protease itself may have evolved in this lineage.

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F014
Division of Labor among Oxidative Stress Response Regulators in Streptomyces coelicolor
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Streptomyces coelicolor, a model actinomycete, has a 8.67 Mbp genome and a complex life cycle. This soil-dwelling bacterium interacts with neighbor organisms and is exposed to diverse stress. Aerobic growth of these bacteria severely faces oxidative stress through reactive oxygen species (ROS). ROS can damage metalloenzymes, DNA integrity, and membrane potential, and cause cell death. S. coelicolor has several transcriptional regulators that modulate gene expression to defend oxidative stress. Among these regulators, OxyR, CatR, and OhrR are well studied in other bacteria. These regulators bind their target region and directly activate or repress their few target genes characterized in S. coelicolor. However, it is unknown why S. coelicolor has many regulators to cope with oxidative stress compared with other bacteria. In this work, we present transcriptome-based approach to reveal the targets of OxyR, CatR, and OhrR respectively, and confirmed each direct regulation through DNA binding.
F015
Searches for Apoptosis Regulatory Factors by Overexpression Assay in Candida albicans
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Candida albicans is an opportunistic fungal pathogen in humans. C. albicans is capable of switching morphologies among yeast, pseudohyphal, and hyphal forms. It is known that pathogenicity of C. albicans is accompanied by a morphological switch to hyphal form. Farnesol, recently described as a molecule that is able to prevent yeast-to-hyphal transition, induces apoptosis in C. albicans. So, we are interested in correlation of apoptosis with pathogenicity in C. albicans.

In C. albicans, apoptosis can be induced by various environmental stimuli and characterized by ROS accumulation and increased caspase activity. H$_2$O$_2$-induced apoptosis in C. albicans is accompanied by activation of CaMca1p, which is known for a key regulator of apoptosis.

In this study, we identify candidate apoptosis regulatory factors by overexpression system in C. albicans. Overexpressed mutant strains were analyzed for apoptotic markers after treatment of H$_2$O$_2$ stress. While OECaBIR1 showed decreased level of ROS accumulation, OECaNMA111 and OECaYBH3 showed increased level of ROS accumulation in H$_2$O$_2$ stress condition. Each overexpression mutant strains showed similar caspase activity. We suggest that CaBir1p inhibits the apoptosis and CaNma111p and CaYbh3p promote the apoptosis in C. albicans. To further investigate relationship between CaMca1p and apoptosis regulatory factors, expression level of CaMca1p will be analyzed in each apoptosis regulatory factor overexpressed mutant strains.

[Supported by the NRF.]

F016
Phosphorylation Analysis of mRNA Decapping Activator Dhh1 in Translation Regulation and P-body Formation in Saccharomyces cerevisiae
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DEAD-box RNA helicase Dhh1 has well-conserved ATPase motif, RNA binding motif, and RNA helicase motif. These functional domains are crucial for Dhh1’s roles in mRNA decay, translation repression, and the formation of P-body. Our previous studies also confirmed that it has an important influence on the regulation of Ste12 protein expression. However, little is known about the N-terminal domain and the C-terminal domain except for the functional domain. Phosphoproteomic analysis previously identified three phosphorylation sites of Dhh1; Thr10, Ser14 and Thr16. The Q / P rich region involved in p-body aggregation is known to exist in 427-506 amino acids of Dhh1. However, it is not known what role phosphorylation of Dhh1 plays. Also, Dhh1 was found to be functionally connected with Loc1 and Puf6 in the context of Ste12 expression. Therefore, in this study, we would like to confirm the effect of regulation of Ste12 protein expression and formation of P-body by using phosphorylation site mutants of Dhh1. Furthermore, we investigated the expression of phosphorylated protein of Dhh1 and how other proteins interacting with Dhh1 are affected by phosphorylation site mutants of Dhh1.
F017
Prophase Roles of Cohesin-related Molecules in Meiotic Recombination and Chromosome Morphogenesis during Yeast Meiosis
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Cohesin is ring-shaped multifunctional protein complex, which has 3 main subunit, Smc1, Smc3 and kleisin subunit, Scc1. Cohesin regulates stabilization of chromosome structure and allows proper segregation of chromosomes during cell division. During meiosis, cohesins not only mediate sister chromatid cohesion but also are prominent components of chromosome structural axes and important mediators of the local DNA events of recombination. In this study, we explore the roles of cohesion-associated protein, Pds5, during meiosis, and its functional relationships with the meiosis-specific α-kleisin, called Rec8, and Rad61/WAPL which negatively regulates cohesin functions. First, we analyzed Zip3 focus which interacts initiation of synapsis to meiotic recombination. In the presence or absence pCLB2-PDS5, rec8Δ or rad61Δ. Rec8 and Pds5 have affected in formation of COs but Rad61/WAPL has not affected in formation of COs. We further observe formation of synaptonemal complexes. pCLB2-PDs5, rad61, and pCLB2-PDS5 rad61 double mutant exhibits very short synaptonemal complexes, suggesting that Pds5 and Rad61/WAPL are involved in axis length determination.

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F018
Multiple Roles of Cohesin-associated Factors in Meiotic Recombination in Saccharomyces cerevisiae
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The cohesin complex is important role in these cell divisions that contains at least five core subunits: two Structural maintenance of chromosomes proteins (Smc1, Smc3), alpha-kleisin subunit (Mcd1/Scc1/Rad21 at mitosis and Rec8 at meiosis), Scc3 (Irr1/SA1, 2), and accessory factors (Rad61, Pds5). Previous studies show that Rec8 localize chromosome axis and is important role in homolog bias maintenance, and Pds5 plays a roles in homolog pairing and synopsis. Here in this study we show that Pds5 is important roles to promoting meiotic recombination. To investigate meiotic recombinants, intermediates and final products, we analysis DNA physical analysis system that is well-characteristic HIS4/LUE2 hotspot. The pds5-mn delayed in completion of pre-meiotic DNA replication and double-strand break (DSB) formation, and interhomolog JM levels were reduced with delaying turnover of the JM. In addition, the crossover and non-crossover formation were delayed with reduced NCO levels compared to wild type. Thus, Pds5 might affect CO-designated DSB repair and proper JM resolution in a tightly controlled meiotic cohesion dynamics.

[This work was supported by grants to K.P.K. from the National Research Foundation of Korea (NRF) funded by the Korean Ministry of Science, ICT and Future Planning (MSIT; NRF-2017R1A2B2005603; NRF-2018R1A5A1025077) and the Next-Generation BioGreen 21 Program (SSAC; No. PJ01322801), Rural Development Administration, Republic of Korea.]
F019
Synapsis Elongation Factors Ggulate Recombination and Pachytene Checkpoint during Meiosis
Min-Su Lee, Eui-Hwan Choi, and Keun Pil Kim*
Chung-Ang University

The synaptonemal complex (SC) is a meiosis-specific chromosome structure that links between homolog chromosomes that is essentially required for crossover recombination during meiosis. The Ecm11-Gmc2 heterodimeric complex localizes at the synapsis initiation sites with SIC and promote synapsis elongation to form the full synapsis by stabilization and polymerization of zipper like protein, Zip1 during meiotic prophase I. The roles of Ecm11-Gmc2 complex in the formation of SC but the roles in meiotic recombination is unknown. We investigated the roles of Ecm11-Gmc2 complex in meiotic recombination process using DNA physical analysis during meiotic prophase I. Physical analysis reveal that inter-homolog crossover were specifically reduced and meiotic progress were delayed in the absence of Ecm11 and Gmc2. We detected that joint molecules were accumulated in the cells without Ecm11 and Gmc2 using 2D physical analysis. These phenomena imply that Ecm11-Gmc2 complex regulate pachytene exit and its function is liked with CO appearance. Moreover, we found that meiotic progress delay caused by absence of Ecm11 and Gmc2 is alleviated by defecting of Pch2.

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F021
Comparison of Illumina Sequencing Output and Data Assembly Efficiency According to the Sequencing Library Size
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NGS sequencing is one of the most important and key technology in modern biology. Among the NGS sequencing platforms, illumina technology has become the dominant platform for gene amplicon or genome sequencing in microbial genomics and ecology studies. However, various technical concerns, such as library size effect on data output or assembly efficiency, still exist.

In this study, we have tried to find out how the size of the library affects sequencing and data analysis efficiency. For this purpose, we have constructed libraries with average library sizes of 500-bp, 700-bp, and 1000-bp, respectively, and performed paired-end sequencing with the Illumina MiSeq platform for bacterial genome sequencing. The resultant data were analyzed for comparison of sequencing output and de novo assembly efficiency between them. In conclusion, the results suggest that the longer library size produced more data output and assembly efficiency for genome sequencing work.
**F022**

**Morphological Phenotype and Genetics of *Streptococcus mutans* Fluoride Resistant Strain**

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Fluoride is an inorganic, monatomic anion and is widely used as an anticariogenic agent for dental caries. However, prolonged exposure to fluoride has been suggested to induce the emergence of fluoride-resistant strains. The aims of this study were to identify genetic changes in genome of a *Streptococcus mutans* fluoride resistance (FR) strain and to compare how genetic alterations affect its gene expression and cell morphology. When morphology was observed using a scanning electron microscopy, a FR strain was relatively smaller cell size than the wild-type (WT) strain and had a rounded shape. Using the whole genome sequencing analysis, DNA of the FR strain was found to include single nucleotide substitutions in *glpF*, *pykF*, *murC2*, and *smu.2059c*, single nucleotide substitutions in intergenic region of *smu.1289c* and 1290c, and nucleotide insertion in *hsdS*. While the FR strain had a higher expression of *hsdS*, *smu.1289c*, and *smu.1290c* to 2.84, 5.73, and 5.53 folds than that of the WT, respectively (*P*<0.01). The expression level of *glpF* and *smu.2059c* in the FR strain lowered 0.59 and 0.7 folds, respectively (*P*<0.01). Expression level of *pykF* was 1.01 fold higher and *murC2* was 0.78 fold lower than that of the WT. Therefore, the genes containing nucleotide alterations can play an important role in the achievement of fluoride resistance trait, possibly related to changes in gene expression and cell morphology.

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**F023**

**CodY Acts as a Negative Regulator of Transcription of CRISPRs in *Streptococcus mutans***

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Clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated (Cas) genes function to cleavage specific sequence in genomes of invading viruses and bacteriophages, so are known as an adaptive immune system in many prokaryotic organisms. This study was to investigate expression regulations of two CRISPR loci (CRISPR 1, CRISPR 2) in *Streptococcus mutans* UA159. Through the sequence analysis of these CRISPR arrays, we found a potential promoter for each CRISPR locus. Moreover, possible binding sites for CcpA and CodY proteins, transcriptional regulators that modulate carbohydrate and amino acid metabolisms, respectively, were identified in predicted promoter regions. Reverse transcriptase PCR and β-galactosidase assays demonstrated that transcription of the individual CRISPRs was driven by the potential promoter. The CcpA and CodY proteins could directly bind to the promoter region. Notably, the qRT-PCR results indicated that cas genes were differentially expressed in the absence of CcpA or CodY. All four *cas* in CRISPR 1 and the *cas3* in CRISPR 2, enhanced the expression level to 13, 34, 18, 42 and 4.2 folds in the *codY* mutant background, respectively. However, there was no difference in the expression level, in *ccpA* mutant. Thus, CodY protein negatively regulates transcription of CRISPRs in *S. mutans* that controls optimal expression of CRISPRs in response to certain environment conditions.

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F024
Genome-wide Functional Profiling of Phosphatase Networks in the Human Fungal Pathogen Cryptococcus neoformans
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Cryptococcus neoformans causes fatal cryptococcal meningoencephalitis mainly in immunocompromised patients. Despite its clinical importance therapeutic options for treatment of systemic cryptococcosis are highly limited. Here, to further elucidate complex signaling networks regulating the virulence of C. neoformans, we aimed to identify and functionally characterize the 139 putative phosphatases, which are major signaling components. We selected putative phosphatases based on annotation in the C. neoformans var. grubii genome database provided by NCBI and performed a BLAST search with their protein sequences to identify any corresponding orthologs in S. cerevisiae, A. nidulans, C. albicans, F. graminearum and human. We classified putative phosphatases into 16 groups based on InterPro phosphatase domain annotation. Thus far, we have successfully constructed 230 signature-tagged gene-deletion strains representing 114 putative phosphatases through homologous recombination methods. We are in the middle of examining their phenotypic traits under 30 different in vitro conditions including growth, differentiation, stress response, antifungal resistance, virulence-factor production and in vivo virulence potential in insect and mammalian hosts. Along with our previous functional genetic studies for C. neoformans transcription factors and kinases, this study will provide a comprehensive insight into the fungal pathobiological signaling networks.

F025
Unraveling the Role of Pseudouridylation in Opportunistic Fungal Pathogen Cryptococcus neoformans
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Cryptococcus neoformans is a fungal pathogen that causes systemic cryptococcosis and meningoencephalitis mainly in immunocompromised individuals. Due to its clinical importance, revealing the factors that can affect its life cycle is critical for development of novel antifungal drugs. Among the various factors, pseudouridylation of RNA is the most abundant type of post-transcriptional modification. Pseudouridylases isomerize uridine into pseudouridine, which subsequently affects the stability of RNA structure. In S. cerevisiae, eight proteins exist as stand-alone pseudouridylases, and each protein has specific pseudouridylation sites and roles. To unravel the biological functions of pseudouridylases in C. neoformans, we identified six putative pseudouridylases in C. neoformans by performing BLAST search in the FungiDB database with protein sequences of the known S. cerevisiae pseudouridylase genes. To characterize the role of pseudouridylases, we constructed more than two independent strains for 5 putative pseudouridylase genes and examined their phenotypic traits under various in vitro and in vivo conditions. CBF1, which is essential gene in S. cerevisiae, is also suspected to be essential in C. neoformans. Among the proteins, DEG1 and PUS7 seemed to have major roles in stress responses and virulence of C. neoformans. By using pseudouridylation RNA-sequencing, we will identify pseudouridylated mRNA transcripts and characterize their role in pathogenicity of C. neoformans.
F026

Genome-based Reclassification of Bacterial Species
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Currently, similarity value of the 16S rRNA gene sequence and relatedness value of DNA-DNA hybridization between two species are major criteria for bacterial species identification. However, the 16S rRNA gene analysis is not enough for tens of thousands of bacteria identification due to the short length of gene size, about 1500bp, and DNA-DNA hybridization experiment is highly labor intensive and has a lot of errors. In this study, we determined genome sequence of several bacteria species, which have more than 99% of 16S rRNA similarity with closely related species, and analyzed the phylogenetic relationship using orthoANI, UBCG pipeline, and TrueBac reference database of ChunLab Inc. The results indicated that some species have more than 95% of average nucleotide identities (ANI), which is higher than the cutoff proposed for bacterial species boundary, with phylogenetically close other species. Therefore, we suggest that bacterial taxonomic identification should be conducted based on genome sequence level analysis.

F027

Genome Based-identification of a Novel Lactobacillus Species Using ChunLab’s TrueBacTM ID System
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The strain EH110, which is a lactobacilli isolated from fecal sample of Korean baby, showed high level of 16S rRNA gene similarity (99.9%) with Lactobacillus gasseri ATCC 33323T. To analyze the taxonomic relationship between the strains EH100 and ATCC 33323T, we determined genome sequence of the strain EH110 and bacterial identification was conducted with TrueBac™ ID platform in ChunLab, Inc. Results from TrueBac™ ID platform showed that an average nucleotide identity (ANI) value between the strains EH110 and ATCC 33323T was 93.5%, which is clearly higher than the cutoff proposed for bacterial species boundary. Therefore, we suggest that the strain EH110 should be classified as a novel species in the genus Lactobacillus.
F028
Comparative Genomics of the Canine Gut *Lactobacillus reuteri* Reveals Genetic Feature and Lifestyle Adaptation
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*Chon-buk National University, The Animal Molecular Genetics and Breeding Center*

In bacteria, *Lactobacillus reuteri* is a Gram-positive, catalase-negative species that has been used as a model to describe the ecology and evolution of vertebrate gut symbionts and some strains of *L. reuteri* are used as probiotics. However, the genetic features and evolutionary strategies of *L. reuteri* from the canine remain unknown. Therefore, we isolated and sequenced one *L. reuteri* strain from dog feces in this study. A comparative genomic approach was used to assess genetic history and gain insight into the distinguishing features related to the different hosts based on other published vertebrate genomic sequences. Genome size, G + C content, and average nucleotide identity values of the *L. reuteri* strains from the dog indicated that the strain was similar to human, omnivorous animal. The pan-genome of 28 *L. reuteri* strains contained 7,371 gene families, and the core genome contained 1,070 gene families. Some functional genes may be attributable to host-specific of the dog. Moreover, the numbers of genes encoding Cell wall/membrane/envelope biogenesis (M in COG database) and Replication, recombination and repair (L in COG database) were higher than other hosts. This study provides new insight into the adaptation of *L. reuteri* to the intestinal habitat of the dog, suggesting that the genomic feature of *L. reuteri* from the dog origins is closely associated with its living environment.

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F029
Algicidal Effects of *Pseudoruegeria sabulilitoris* on *Alexandrium tamarense* Based on Transcriptome Analysis
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*Alexandrium tamarense* is a dinoflagellate which produces paralytic shellfish poisoning (PSP) neurotoxin, causing worldwide harmful algal blooms (HABs). In previous study, algicidal bacteria for *A. tamarense*, *Pseudoruegeria sabulilitoris* was screened from Namhae seawater. Here, to understand the algicidal mechanism of *P. sabulilitoris* for *A. tamarense*, we co-cultured *A. tamarense* with *P. sabulilitoris* for 2, 6, and 12 hours and further the changes of their cellular transcriptomes were examined using RNA-seq. For *A. tamarense*, about 50,000 unigenes were identified by de novo assembly and their functions were annotated from NR, NT, KEGG, Swissprot, Pfam, GO, and KOG. Especially, in *A. tamarense*, core proteins of photosystem, light detection system, carbon fixation, and microtubule-related genes was down-regulated from 2 hour, whereas preferably in *P. sabulilitoris*, energy production-containing TCA-electron transfer system, several secondary metabolite productions, and transport system-related genes were up-regulated after 12h. The comprehensive metatranscriptome analysis between algicidal bacteria and harmful algae may suggest a clue to solve the HAB problem.

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F030
CHA-ud, a Novel Genetic Element Which Originates Multiple cagA Genotypes in Helicobacter pylori
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Helicobacter pylori is arguably the most genetically diverse bacteria causing gastric carcinoma due to CagA oncoprotein. In our previous study, we found that some of the H. pylori strains including PMSS1 underwent a dynamic expansion and contraction of cagA copy number which correlates with the disease development. Moreover, we have suggested that the cagA homologous area located both the upstream and downstream of cagA (CHA-ud) would be likely important for this numerical gene variation. We hypothesized that the genetic elements of two CHA-ud sequences which flanking cagA at the adjoining ends are functioning a critical role in the generation of multiple cagA repeats via homologous recombination. The loss of function of CHA-ud was postulated by generating PMSS1 isogenic mutants having only a single CHA-ud at either upstream or downstream of cagA. The gain of function was postulated by generating G27 isogenic mutant with two CHA-ud at both upstream and downstream of cagA with contrast to G27 wild type which has one copy of cagA. Then large-scale single colony derivatives were isolated and screened for the detection of multiple cagA genotypes which further verified via DNA sequencing. The results showed that G27 isogenic mutants were able to undergo recombination for cagA duplication and deletion with contrast to the PMSS1 isogenic mutants.

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F031
Comparative Genomic Analysis of Four Probiotic Lactobacillus Species, L. acidophilus, L. helveticus, L. rhamnosus, and L. casei
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Lactobacillus species are members of lactic acid bacteria and are widely used as a starter culture in the manufacture of fermented food products or probiotics for health improvement, because of its high metabolic function to produce various bioactive compounds. Here, we report the genome sequence of Lactobacillus helveticus LHS and Lactobacillus rhamnosus LRS, each of which had been isolated from a healthy Korean adult. DNA sequencing was performed using the PacBio platform to assemble the genomes and Illumina MiSeq to improve the sequence accuracy. The genome sequences of L. helveticus LHS and L. rhamnosus LRS were compared with those of other strains in the species, along with those of Lactobacillus casei, Lactobacillus acidophilus. Using the genomic information, we underwent a comparative genomic analysis of factors that might be involved in adaptation to the host intestinal conditions, S-layer proteins, antioxidants, and bacteriocins. We found that strains possessing a high ratio of strain-specific genes tend to have more genes for adaptation in different environments. In the same context, S-layer gene clusters and antioxidant genes were more wildly distributed among habitat-versatile strains. A number of bacteriocin gene clusters were identified using a combination of in silico prediction tools.
F032
OipA Functions in H. pylori-induced Cell Elongation and IL-8 Secretion
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*Helicobacter pylori* is a bacterium to cause gastric diseases. Outer inflammatory protein A (*oipA*) plays a critical role in proinflammatory reactions of *H. pylori*. However, how *oipA* involved in inflammatory function is unclear.

To investigate *oipA* function in inflammatory reaction, we constructed isogenic deletion and complementation mutants of 3 *H. pylori* strains including G27, PMSS1, and K74. G27 and PMSS1 are Western strains while K74 is East-Asian strain. Interestingly, G27 and PMSS1 have one *oipA* gene and K74 has identical *oipA\textsubscript{1}* and *oipA\textsubscript{2}*, at different loci. *OipA* status of all mutants were checked by PCR and DNA sequencing, and expression level were determined by Western blot. AGS cells were infected by *H. pylori*, cell elongation and IL-8 secretion level were observed. G27\textDelta\textit{oipA} and K74\textDelta\textit{oipA\textsubscript{1}}\textDelta\textit{oipA\textsubscript{2}} (K74\textDelta\Delta) showed significant reduction in cell elongation, IL-8 induction and phosphorylated CagA in AGS cells, while K74\textDelta\textit{oipA\textsubscript{1}}, K74\textDelta\textit{oipA\textsubscript{2}} and PMSS1\textDelta\textit{oipA} didn’t. However, K74\textDelta\Delta\textit{oipA\textsubscript{2}}, K74\textDelta\Delta\textit{oipA\textsubscript{1}}\textit{oipA\textsubscript{2}} and G27\textDelta\textit{oipA} showed similar phenotype to K74\textDelta\Delta and G27\textDelta\textit{oipA}, but didn’t show complementation of phenotypes to their wild-type.

Thus, we have to be aware of the controversial functions of *oipA*, which may result from strain-specific different functions or unexpected secondary mutations related with *oipA* deletion.

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F033
Identification of Five Novel Amalgaviruses from Plant Transcriptome Data
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Transcriptome data obtained from plants often contain sequences derived from infected RNA viruses. These virus reads can be assembled into novel RNA genomes. Five novel RNA viruses were identified from four different plant hosts: Spinach amalgavirus 1 (SpAV1) from the spinach (*Spinacia oleracea*), Zostera marina amalgavirus 1 (ZmAV1) and Zostera marina amalgavirus 2 (ZmAV2) from the common eelgrass (*Zostera marina*), Cistus incanus RNA virus 1 (CiRV1) from the hoary rockrose (*Cistus incanus*), and Salvia hispanica RNA virus 1 (ShRV1) from the chia (*Salvia hispanica*). The sequence similarity and phylogenetic analyses using proteins containing RNA-dependent RNA polymerase (RdRp) motif indicated that SpAV1, ZmAV1, ZmAV2, CiRV1, and ShRV1 are novel viruses belonging to the genus *Amalgavirus*. Amalgaviruses contain two partially overlapping open reading frames (ORFs) and the ORF1+2 fusion proteins are produced by the +1 programmed ribosomal frameshifting (PRF) mechanism. The conserved sequence motif sequence, UUU\_CGN, where the +1 PRF occurs, was identified. Interestingly, a comparison of the 31 amalgavirus ORF1+2 fusion proteins showed that only three positions were repeatedly used for the +1 PRF, suggesting that the ORF1/ORF2 boundary is under selection for proper folding and function of the fusion protein. The five RNA virus genome sequences may be useful for studying evolution of plant amalgaviruses.

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F034
MpkB MAP Kinase Pathway, Which is Required for Sexual Development, is Dispensable for Mycotoxin Production in Aspergillus nidulans and Aspergillus flavus
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In most eukaryotic systems, MAP kinase pathways regulate stress responses as well as growth and development. MpkB MAP kinase in a filamentous fungus Aspergillus nidulans has been known to coordinate sexual development and secondary metabolism, including sterigmatocystin (ST) production. In this study, however, the results of the ST production analysis of wild type and mpkB deletion mutants showed that the mutation did not affect the ST production and ST related gene expression. Furthermore, ST production of ΔmpkB, ΔmkkB, and ΔmpkBΔmkkB mutants in the veA+ background was similar with wild type. Also, MpkB constitutive activation or inactivation mutants showed no significant effect on the ST production. Interestingly, ST production of mpkB and mkkB mutants was remarkably delayed in the veA1 background, suggesting that the ST production is affected primarily by the veA gene. Similarly, in Aspergillus flavus, MpkB ortholog AflmpkB mutant couldn’t produce any sclerotia, but it produced aflatoxin B1 normally. Taken together, the mpkB gene alone does not affect mycotoxin production such as ST in A. nidulans or aflatoxin B1 in A. flavus, indicating that the signaling of MpkB MAP kinase and mycotoxin production were governed by independent pathways.

F035
Spore-specific Gene Expression in Aspergillus nidulans
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A genetic model filamentous fungus, Aspergillus nidulans, is a homothallic ascomycete that has been studied sexual and asexual developmental processes in molecular level for many years. Previous studies showed that a GATA-type transcription factor, NsdD, plays a pivotal role in activating sexual development of A. nidulans. The nsdD deletion mutants failed to form the sexual structures, cleistothecia, even under conditions where sexual development preferentially occurs in wild type. Over-expressors of the gene formed larger numbers of cleistothecia than wild type, even under conditions where wild type strains form little sexual structure, indicating that the nsdD gene is positive regulator of sexual development. To identify the direct and/or indirect target genes of NsdD, ChIP-seq and RNA-seq analyses have been performed. As a result, NsdD Responsible Element, or NRE, has been identified as CMGATCT and many possible target promoters have been elucidated. Moreover, since physiological and genetic studies of ascospores are remained to be characterized, we also performed RNA-seq analysis from conidia and ascospores RNA samples in A. nidulans for obtaining more information about ascospore biology. Comparative analysis of transcription profiles revealed many genes that are expressed specifically in ascospores. Detailed investigation of the differentially expressed genes will be discussed.
F036

TORC1 and cAMP/PKA Signaling Converge on CK2 to Control Sir2 Activity for PMA1 Expression Regulation in Saccharomyces cerevisiae

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Target of rapamycin complex 1 (TORC1) signaling is a central regulator of cell growth, and inhibition of TORC1 signaling increases lifespan from yeast to high eukaryotes. Sir2, a NAD+-dependent protein deacetylase, negatively regulates the transcription of PMA1, encoding an ATP-dependent proton pump, through the cAMP/PKA-CK2 axis in Saccharomyces cerevisiae. In this study, we demonstrate that TORC1 signaling controls Sir2 activity through CK2 to regulate PMA1 expression. Deletion of TOR1 decreased the amount of Pma1 on the plasma membrane, resulting in low cytoplasmic and vacuolar pHs, and deletion of SIR2 in the tor1Δ mutant returned the altered phenotypes to those of wild-type. Further genetic analyses indicated that TORC1 signaling controls Sir2 phosphorylation at Serine 473 that is regulated by the cAMP/PKA-CK2 axis. Moreover, we uncovered that Sit4, a PP2A-like phosphatase, and Kns1, a LAMMER kinase, link TORC1 signaling to the Sir2 phosphorylation. Finally, we show that the lifespan extension caused by inhibition of TORC1 signaling is achieved, at least in part, through Sir2 activity for PMA1 expression regulation. Taken together, this study suggests that signals from active TORC1 and cAMP/PKA converge on CK2 to phosphorylate Sir2, which increases PMA1 expression and cytoplasmic and vacuolar pHs. Supported by grants from NRF.

F037

In Vivo Transcriptional Profiling of Signalling Pathways in Fungal Meningitis Pathogen

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Cryptococcus neoformans is a causative agent of global fungal meningoencephalitis. Nevertheless, its treatment option is limited mainly due to a lack of complete understanding on how the pathogen interacts with the host during infection and disease progression. Although a number of signalling components involved in the pathogenicity of C. neoformans have been characterized past years, it remains elusive how complex signalling pathways are coordinated and regulated during the whole infection process. Previously we performed NanoString-based in vivo transcription profiling of 183 kinases, 178 transcription factors, and 139 phosphatases during the whole infection process of C. neoformans. Here we focused on 8 transcription factors, including GAT204, STB4, ZFC1, HOBS, PDR802, FZC5, FZC38 and FZC39, of which in vivo expression were highly induced during host infection but deletion mutants did not exhibit evident in vitro phenotypes. To elucidate their in vivo functions, the expression level of the 8 genes were measured in host mimic condition (HMC): RPMI media supplemented with 10% fetal bovine serum at 37°C under 5% CO2. We found that all of them were highly induced by HMC. Next we further dissected the HMC signals that trigger the induction of the 8 genes. We found that PDR802 and GAT204 were highly induced by body temperature and carbon starvation. In conclusion, we provided further insight into complex signalling pathways modulating the pathogenicity of C. neoformans.
F038
The Velvet Regulators in *Aspergillus flavus*
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Fungal development and secondary metabolism are intimately associated via the activities of the fungus specific transcription factor velvet that are conserved in Aspergillus species. In this study, we investigated the roles of the velvet genes in the aflatoxicogenic fungus *Aspergillus flavus*. Distant from *A. nidulans* or *A. fumigatus*, the *A. flavus* genome contains five velvet genes, *veA*, *velB*, *velC*, *velD*, and *vosA*. The newly identified gene *velD* (velvet-like protein D) is required for aflatoxin production. Importantly, the VosA and VelB proteins are crucial for sporogenesis in *A. flavus*. Expression analyses revealed that *vosA* and *velB* mRNAs accumulated at high levels during the late phase of asexual development and in conidia. The absence of *vosA* or *velB* decreased the content of conidial trehalose and β-glucan and the tolerance of conidia to the thermal and UV stresses. In addition, double mutant analyses demonstrated that VosA and VelB play an inter-dependent role in trehalose biosynthesis and conidial stress tolerance. Transcriptome analyses demonstrated that VosA and VelB are required for appropriate expression of certain genes which are associated with trehalose biosynthesis, β-glucan biosynthesis, and sporogenesis. Overall, these results suggest that VosA and VelB play the conserved and vital role in sporogenesis, conidial trehalose biogenesis, stress tolerance, and β-glucan biosynthesis in *A. flavus*.

F039
Genome-wide Analysis of Velvet Target Genes in *Aspergillus nidulans*
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The Velvet proteins are fungal specific transcription factors that regulate fungal development and secondary metabolism in *Aspergillus* spp. In this study, we investigated the direct and/or indirect target genes of the VosA-VelB hetero-complex that is a key regulator for conidia maturation, cell wall integrity, dormancy, and germination. Genome-wide analysis revealed that both VosA and VelB are necessary for proper expression of a total of 3,648 genes in *Aspergillus nidulans* conidia. In both asexual and sexual spores in *A. nidulans*, 2,306 genes showed significant differential expression between the ΔvosA and WT. The combination of ChIP-seq and transcriptome analyses identified 111 potential direct target genes of the VosA-VelB complex. The VosA-VelB complex represses certain genes associated with cell wall integrity (*fksA, chsC, gclC, agsB*) and fungal development (*brlA* and *veA*). However, this complex induces mRNA expression of spore-specific genes and trehalose biosynthesis genes. Among the VosA-VelB target genes, we further characterized two VosA/VelB-inhibited developmental gene *vidA* (AN2498) and *vidB* (ANS859). VidA is a transcription factor containing C2H2 zinc finger protein that is required for proper asexual and sexual development. The *vidB* gene encodes a Zn2Cys6 transcript factor that is ortholog of Saccharomyces cerevisiae PDR8 (pleiotropic drug resistance). Phenotypic analysis demonstrated that VidB is essential for fungal growth, development, conidiation and sensitivity by stress conditions in *A. nidulans*. Overall, these results imply that the VosA-VelB complex regulates mRNA expression of certain targets, thereby affects fungal growth and development in *A. nidulans*.
Zinc Regulates Gliotoxin Biosynthesis in *Aspergillus fumigatus*

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*School of Life Sciences and Biotechnology, Korea University*

Gliotoxin is a member of the epipolythiodioxopiperazine class of toxins and one of the secondary metabolites which *A. fumigatus* produces. In *A. fumigatus*, a cluster of 13 genes is required for gliotoxin biosynthesis. The expression of these genes was down-regulated in *zafA* deletion strain (Δ*zafA*) and recovered by *zafA* introduction (*zafA_comp*) at the transcription level. Gliotoxin was not detected in Δ*zafA* strain. Gene expression of *zafA* is up-regulated in low zinc condition, and the genes involved in gliotoxin biosynthesis were also up-regulated in low zinc condition.

*GliZ* encodes transcription factor to up-regulate gliotoxin biosynthesis, and we found two ZafA binding sites (5'-'CAAGGT-3') from *gliZ* promoter region. Through EMSA, it was confirmed that ZafA binds to the *gliZ* promoter regions, but failed to bind to the *gliZ* promoter region when two ZafA binding sites were deleted (M1M2). β-Galactosidase assay also showed that ZafA protein binds to M1, M2 and M1M2 sequence weaker than wild type sequence. Furthermore, we found that M1M2 strain is more susceptible to macrophage cells derived from HL-60 than wild type. Virulence test with mouse model also showed that M1M2 strain was weaker virulence activity than wild type. Taken these results together, we suggest that zinc regulates gliotoxin biosynthesis via regulating gene expression of *gliZ*.
G001
Strategy for 4-Hydroxyvalerate Production Enhancement in Pseudomonas putida KT2440
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Levulinic acid (LA) is one of starting material for valuable C5 chemical. Because LA has a commercially high potential because it has a relatively low price and a growing market. Thus, many bacteria including LA catabolic pathway is very attractive as industrial host strain. Pseudomonas putida KT2440 is also one of them. P. putida KT2440 has high resistance to toxicity of organic solvent and oxygen stress, less side pathway and relatively low maintenance energy for growth. Above all, LA catabolic operon was already identified, and it includes 4-hydroxyvaleric-Coa, which can be converted to 4-hydroxyvalerate, which is a precursor of Gamma-valerolactone. Because Gamma-valerolactone is platform chemical that is convert to other valuable product such as green solvent or bio-fuel, we determined 4HV as the target product and regulated metabolic pathway of P. putida for accumulation of 4HV. We also tried to maximize the production of 4HV by detection and strengthening the side pathway involved in 4HV production by adaptive laboratory evolution and developing novel genetic engineering system for P. putida. As a result, we could construct fast growing P. putida strain in minimal media include LA, and increased 4HV production in P. putida.

[This work was supported by the Industrial Strategic technology development program (2.180034.01, A 300 L Pilot-scale Biological Production of Gamma-lactones) funded By the Ministry of Trade, Industry & Energy (MOTIE, Korea)]

G002
Introducing Combinatorial Metabolic Engineering to Improve Free Fatty Acids Production
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Microbial production of fatty-acid-derived chemicals has been studied due to its promising substitute for some petroleum-based chemicals. Many studies have attempted to engineer microbes for increased production of FFA through metabolic engineering and synthetic biology. Here, we constructed a high FFA-producing Escherichia coli (E. coli) strain by combinatorial combinations of previous positive results; 1) heterologous expression of the methylomalonyl-CoA carboxyltransferase (MMC) and overexpression of phosphoenolpyruvate carboxylase (PPC) to increase malonyl-CoA pool from oxaloacetate (OAA), 2) expressing a mutant acyl-CoA thioesterase I (TesA) with high specific enzyme activity, and 3) deletion of FFA transport-related genes. The manipulation of E. coli increased the FFA production by 5.4-fold compared with control strain. Additionally, employing transcriptional activator of fatty acid synthesis (FadR) further increased the TRY in our strain, resulting in 9.5- and 1.4-fold increases in FFA production, compared with the control strain expressing only the wild-type thioesterase and the positive control strain overexpressing FadR, respectively.

[Supported by the Next-Generation BioGreen21 Program funded by the Rural Development Administration, Republic of Korea (SSAC, Grant#: PJ013457)]
G003
High Production of 4-Hydroxyvalerate by Coexpressing a 3HBDH Mutant and a NAD+-Dependent Formate Dehydrogenase in Escherichia coli
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4-Hydroxyvalerate (4HV) is an important compound that is a necessary intermediate for sustainable solvents such as gamma-valerolactone (GVL) as well as plastic additives. However, currently, the 4HV production method using the levulinic acid (LA) degradation pathway of Pseudomonas putida has a disadvantage of using a large amount of ATP. Since ATP over-consumption can affect cell growth and bio-production, it is not suitable for mass production of 4HV. Here we report alternative bio-based method of 4HV production. High production and yield of 4HV was obtained from LA, a cheap and renewable biomass source. 4HV production was performed by expressing 3-hydroxybutyrate dehydrogenase (3HBDH) that can convert LA into 4HV and formate dehydrogenase (CbFDH) that regenerates NADH in E. coli. In the first stage of cultivation, the cells were cultured at a high concentration in a pH-stat-glycerol fed batch under aerobic conditions and the enzyme was expressed. In the second stage, conditions were changed to anaerobic, 4HV was produced by fed batch of LA, formate, and glycerol. As a result, about 100 g/L of 4HV was produced, which corresponds to a 95 % molar production yield. In conclusion, this conversion yield can have the potential to stimulate the development of carbon-based chemicals and promote economic access to the commercial scale of GVL.

[This work was supported by the Industrial Strategic technology development program funded By the Ministry of Trade, Industry & Energy.]

G004
Improving Azelaic Acid Production in Escherichia coli via Adaptive Laboratory Evolution
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Azelaic acid, a medium-chain dicarboxylic acid (DCA) with nine carbons, has been used in plastics and acne medication. Its use in cosmetics is emphasized as it is known as a tyrosinase inhibitor that reduces melanin synthesis and for its antibacterial and anti-inflammatory effects which lead to improvement of the skin. Azelaic acid has been produced from grains such as wheat, rye, and barley.

In general, wild-type Escherichia coli cannot effectively uptake the medium-chain fatty acids. In this study, we constructed an E. coli MG1655 mutant in order to improve the uptake of medium-chain fatty acids by with fadR deletion to retain gene expression of β-oxidation pathway. Then we obtained an E. coli strain that grows faster than the wild type on nonanoic acid (C9 fatty acid), which is the precursor to produce azelaic acid through ω-oxidation pathway, by evolutionary engineering. According to previous studies, ω-hydroxyacids were converted to dicarboxylic acids by the action of an engineered ω-oxidation pathway. Using this approach, the Pseudomonas putida alkane monooxygenase system, encoded by alkBGT, was introduced to the evolutionary engineered E. coli with fadE deletion to produce the C9 DCA. The mutant strain showed approximately 3-fold increased production of azelaic acid in comparison with wild type strain.

[Supported by the Next-Generation BioGreen21 Program funded by the Rural Development Administration, Republic of Korea (SSAC, Grant#: PJ013457)]
G005

Development of Engineered Redox Regenerator Escherichia coli Mutant and Its Application to 3-Hydroxypropionic Acid Production
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Redirection of the central carbon metabolism is one of the most promising strategies to supply redox cofactors for efficient biosynthesis of value-added chemicals in microbial cell factories. However, the strategy is often confined by theoretical limit of metabolic landscape but also impeded cell growth. Here, we aim to explore metabolic bottlenecks upon flux redistribution and to propose engineering tactic for developing a redox regenerator mutant. Deletion of two genes encoding phosphofructokinase-1 in wild type Escherichia coli enables the Pentose Phosphate pathway to operate in partial cyclized manner while intensively regenerating NADPH. To overcome severe defect of the double knock-out mutant in growth with glucose as sole carbon source, from growth-based selection an evolved mutant showing enhanced cell growth was isolated. By relating genotype and phenotype changes of the evolved mutant key contributors in improving cell fitness and a metabolic control point were identified. The evolved mutant was further modified at the control node. Its application to production of 3-hydroxypropionic acid showed improved production performance compared to the unevolved strain but also two widely used redox regenerator mutants.

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G006

Construction of 3-Hydroxypropionic Acid Inducible Reporter System in Escherichia coli
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3-hydroxypropionic acid (3-HP) is an important platform chemical that can be converted to acrylic acid, malonic acid and other chemicals valuable in the industry. Recently, construction of enhanced 3-HP production pathway in recombinant strains has drawn attention. Escherichia coli is an appealing host for production of such value-added compound because it has short doubling time as well as its database and toolkits such as mutant library construction have already been well established. To engineer and discover a 3-HP overproducing mutant, a biosensor reporting intracellular 3-HP concentration facilitates screening of mutant with high 3-HP producing ability. In this study, two 3-HP inducible reporter systems based on HpdR and MmsR transcriptional factor originated from Pseudomonas putida KT2440 were constructed in wild type E. coli so that it can be a starting point for further development of 3-HP biosensor. To enhance promoter strength and inducibility, further improvement of the system is required by engineering promoter and 5'-UTR elements of both LysR-type transcriptional regulator (LTTR) family protein and reporter protein.

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G007
Secretion of Lignin Peroxidase H8 via the Flagellar Secretion Apparatus in Pseudomonas putida KT2440
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Producing useful chemicals from lignin, the second most abundant natural polymer, has been spotlighted for decades. However, only few microorganisms are known to have an ability to depolymerize lignin and utilize it. Among them, white rot fungi produce an enzyme lignin peroxidase H8 to decompose lignin into various chemicals including vanillin. We found out that Pseudomonas putida KT2440 has own unique metabolic pathways for aromatic compounds such as vanillin for carbon source. Here, we tried to express lignin peroxidase H8 in P. putida KT2440 and secrete directly via modified flagella to avoid forming inclusion body and achieve convenient whole-cell biotransformation of lignin. We deleted the fliC-D gene to construct modified flagella for secretion of FliC tagged lignin peroxidase H8.

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G008
Improved Genome-based 2,4-Dinitrotoluene Biosensor by Modulating Genes Related with DNT Metabolism
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Landmines deployed around the world cause countless deaths and environmental pollution. Therefore, there is a need for a method to efficiently search various types of mines. In this context, many researches have been done on how to find landmines using biosensors. For example, in 2013, a biosensor was developed using an yqjf promoter-based reporter system that responds to DNT leaked from landmines based on E. coli [1]. However, since the E. coli-based biosensor is plasmid-based biosensors, contamination by gene transfer tends to occur, and continuous abuse of antibiotics is necessary. Therefore, it is necessary to use a genome-based biosensor to solve these problems, but the intensity of the biosensor became significantly lower than that of the plasmid-based biosensor. In this study, we used transposon-based mutagenesis and a biosensor based on yajf promoter to find genes that are related to DNT metabolism in E. coli and found some mutants that show high or low GFP signals in the presence of DNT. By controlling the expression of these genes, we have succeeded in increasing the intensity of genome-based biosensors by up to 30 percent.
G009
Enhanced Production of 4-Hydroxyvalerate by Engineering the Iva Operon in Pseudomonas putida KT2440
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Monomeric 4-hydroxyvalerate (4HV) is a versatile chemical used to produce various commodities and fine chemicals. Conventional productions of 4HV suffer from various shortcomings, including low yield, use of harsh conditions, catalysts, and organic solvents, need for chemical modification, and incomplete depolymerisation. Therefore, in the present study, we deleted the ivaAB gene from the iva operon in Pseudomonas putida KT2440 and overexpressed tesB under the control of the iva operon system in a levulinic acid (LA) and 4HV inducible expression system to produce 4HV from LA. The ivaAB deleted strain showed almost complete conversion of LA to 4HV, compared with 24% conversion in the wild type strain. In addition, under optimized culture conditions, the final engineered strain produced a maximum of 50 g/L of 4HV with 97% conversion from LA. The system presented here could be applied to produce high titers of 4-hydroxyvalerate in a cost-effective manner at a large scale from renewable cellulosic biomass.

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G010
Phage Display Screening of Anti-dengue Virus NS1 Affibody and Application of ELISA
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Infection with dengue virus (DENV) is a serious health issue that causes severe dengue fever and occasionally lethal complications, such as dengue hemorrhagic fever. Here, we developed a highly sensitive enhanced enzyme-linked immunosorbent assay (ELISA) for dengue NS1 using affibody-functionalized gold nanoparticles (AuNPs). First, we screened NS1 antigen-specific affibody molecules (ZNS112, ZNS116, and ZNS146) from the affibody phage library. The affibodies were then expressed and purified from Escherichia coli. Among them, the ZNS112 affibody showed the highest equilibrium binding constant (Kd) of 1 μM. This affibody was functionalized on AuNPs measuring 20 nm in diameter. The developed anti-NS1 affibody-functionalized AuNPs ((ZNS112)2-AuNP) were used as carriers to achieve amplification of the signal. (ZNS112)2-AuNP showed good properties, such as easy synthesis, high number of affibodies conjugation on AuNPs, and excellent stability under harsh conditions with high salt concentrations and temperature. In addition, this nanoparticle-based enhanced ELISA resulted in a 14.2-fold signal amplification performance for dengue NS1 detection in comparison with conventional ELISAs. This novel and sensitive method using (ZNS112)2-AuNP may have applications in the detection of DENV in infected patients at an early stage and for the detection of other pathogens in clinical diagnostics.

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**G011**

**Production of 2,3-Butanediol Production via Eco-friendly Process and Its Safety and Efficacy Evaluation as a Cosmetic Ingredient**

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2,3-Butanediol (2,3-BDO, C₆H₁₀O₂), synthesized as one of the fermentation products, has potential applicability in a broad range of industries for cosmetics, agricultures, food additives, plasticizers, fumigants, pharmaceuticals, and etc. 2,3-BD exists in three stereoisomers, the (2R,3S)-, (2R,3R)-, and (2S,3S)-forms, and each stereoisomer has different physiochemical properties. We developed microorganisms by mutation method and eco-friendly process for 2,3-BDO production (Especially, (2R,3S)-BDO) as a cosmetic ingredient. To evaluate the applicability and functionality of (2R,3S)-BD for a cosmetic ingredient, we carried out several tests such as patch response test, MIC test, and etc.. (2R,3S)-BD has non-skin irritation and excellent antiseptic, antimicrobial, and moisturizing properties.

[This work was supported by the Biochemical Industry Promoting Technology Development Project (No. 10050407) funded by the Ministry of Trade, Industry & Energy (MOTIE, Korea).]

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**G012**

**Biological Production of 2,3-Butanediol by Using Newly Isolated *Bacillus licheniformis* Strains**

Chan Woo Song, Jong Myoung Park, Chelladurai Rathnasingh, and Hyohak Song*

*GS Caltex Research and Development Center*

Biologically produced 2,3-butanediol (2,3-BDO) has diverse agricultural applications such as plant growth promotion, disease control, and drought stress resistance. In this study, schematic isolation and screening procedures were designed to obtain efficient 2,3-BDO producing *Bacillus* strains. The candidate strains were isolated by pretreatment and enrichment, and the isolated *Bacillus* strains were further screened by morphological, biochemical, and genomic analyses. The screened strains were then used to test the utilization of common carbon and nitrogen sources for the economical production of 2,3-BDO. Two-stage fed-batch fermentation was finally carried out to enhance 2,3-BDO production. In consequence, a newly isolated *B. licheniformis* GSC3102 strain produced 92.0 g/L of total 2,3-BDO with an overall productivity and yield of 1.40 g/L/h and 0.423 g/g glucose, respectively, using a cheap and abundant nitrogen source.

[This work was supported by the Biochemical Industry Promoting Technology Development Project (No. 10050407) funded by the Ministry of Trade, Industry & Energy (MOTIE, Korea).]
G013

Complete Genome Sequence of *Pantoea intestinalis* SRCM103226, a Microbial C40 Carotenoid Zeaxanthin Producer

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The bacteria which produce carotenoids have been studied significantly for their potential applicability in terms of microbial sources in the industrial field as cosmetics ingredients, antioxidants, and food or feed additives. Amongst various types of carotenoids, zeaxanthin is a major yellow pigment in the plants such as corn. Zeaxanthin is used in food – it is a base material for the color of egg yolk, meat or skin of poultry. In addition, the zeaxanthin and lutein have various implications for human health such as their involvement in the maintenance of eye health and for their antioxidative qualities. A novel species, *Pantoea intestinalis* SRCM103226, isolated from edible insect mealworm overproduces zeaxanthin as a main carotenoid. The complete genome of *P. intestinalis* SRCM103226 was sequenced using the Pacific Biosciences (PacBio) RS II single-molecule real-time sequencing technology. The genome of *P. intestinalis* SRCM103226 comprises a 4,784,919bp circular chromosome (53.41 % G+C content), and is devoid of any extrachromosomal plasmids. Annotation using the RAST server reveals 4,332 coding sequences and 107 RNAs (22 rRNA genes, 85 tRNA genes). Genome annotation analysis revealed that it has five genes involved in the carotenoid pathway. The genome information provides fundamental knowledge for comparative genomics studies on the molecular evolutionary events of the zeaxanthin pathway.

G014

Biocatalytic Resolution of Styrene Oxide and Styrene Oxide Derivatives Using an Epoxide Hydrolase from a Marine Bacterium, *Spingorhabdus* sp. YGSMI21

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Enantiopure epoxides and vicinal diols are versatile synthetic intermediates for the preparation of enantiopure bioactive compounds. One of the most promising ways for preparing such chiral synthons under environmentally gentle conditions is the enantioselective hydrolysis of racemic epoxides using cofactor-independent epoxide hydrolase (EHase). EHases are ubiquitous enzymes that have been isolated from a wide variety of sources such bacteria, yeast, fungi, insect, plant and mammalian. A gene encoding a putative EHase was identified by analyzing an open reading frame (ORF) of the genome sequence of *Spingorhabdus* sp. YGSMI21, retaining the conserved catalytic residues such as the catalytic triad (Asp179, Glu331 and His358) and the oxyanion hole. The recombinant EHase (rSHEH1) was purified by metal affinity chromatography and further characterized. We could demonstrate that the rSHEH1 was highly enantioselective toward racemic styrene oxide and styrene oxide derivatives (2, 3, 4-chlorostyrene oxide). Enantiopure styrene oxide derivatives are a valuable epoxide intermediate for preparing optically active pharmaceuticals. The rSHEH1 could be applied to bioprocess for providing valuable pharmaceutical intermediates.

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CRISPR/Cas9-coupled Recombineering System for Scarless Knockout of Genes in *Corynebacterium glutamicum*

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*Corynebacterium glutamicum* is an important strain for industrial production of amino acids. Genome engineering of *C. glutamicum*, however, has relied on random mutagenesis and inefficient double crossover methods. Here we report a rapid and iterative genome engineering system for scarless knockout of multiple genes in *C. glutamicum*. Recombinase RecT of this system incorporates synthetic single-stranded oligodeoxyribonucleotides into the *C. glutamicum* chromosome and Cas9-sgRNA ribonucleoprotein complex introduces double-stranded break to unedited target locus and counter-selects unedited cells. Subsequent curing of the CRISPR/Cas9 and RecT vectors generate the final strain free of plasmids and antibiotic markers. To demonstrate performance of the system, seven different mutants were generated within two weeks using through the rapid and iterative genome engineering system and were used to study effects of deleting three different genes on the production of γ-aminobutyric acid. This scarless genome engineering tool will facilitate generation of high-performing *C. glutamicum* for industrial applications.

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RecET Recombineering System for Markerless Integration of Heterologous Biosynthetic Genes to *Pseudomonas putida* Chromosome

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*Pseudomonas putida* is a promising workhorse for producing valuable natural products. While integration of genes is an essential strategy to construct stable industrial strains producing heterologous bioproducts, current methods for *P. putida* rely on time-consuming homologous recombination techniques and transposon-mediated random insertions. Here we developed a RecET recombineering system for markerless integration of heterologous genes to the *P. putida* chromosome. Knockout of various chromosomal loci spanning 0.6-101.7 kb demonstrated the efficiency and capacity of the recombineering system. Subsequently, biosynthetic gene clusters for four proof-of-concept bioproducts were successfully integrated to the target locus of *P. putida* chromosome using the RecET recombineering. Cre/lox system and efficient plasmid curing system was combined to the RecET recombineering system to complete the markerless recombineering system for generating final strains free of antibiotic markers and plasmids. This markerless recombineering system will expedite metabolic engineering of *P. putida*, a bacterial host strain of increasing academic and industrial interest.

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G017

**Metabolic Engineering of* Escherichia coli* for Secretory Production of Free Heme**

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Heme is used in diverse applications in healthcare and food supplement industries. Small amount of heme has been produced intracellularly by engineered *Escherichia coli* through the C4 pathway, requiring subsequent extraction for applications. Here we report metabolic engineering of *E. coli* for secretory production of free heme. To enhance the biosynthesis of heme, the endogenous C5 pathway and the downstream heme biosynthetic pathway was optimized. Furthermore, knockout of the *IdhA, pta* and also *yfeX*—encoding a putative heme-degrading enzyme—genes results in 7.88 mg/L of total heme with 1.26 mg/L of extracellular heme in flask cultivation. Subsequent overexpression of a heme exporter CcmABC in the engineered *E. coli* strain enabled secretion of 73.4 mg/L extracellular heme (63.5%) out of 115.5 mg/L total heme from glucose in fed-batch fermentations. Supplementation of L-glutamate during the fed-batch fermentation allowed secretion of 151.4 mg/L heme (63.3%) out of 239.2 mg/L total heme produced. The engineering strategy reported here will be useful for microbial production of free heme.

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G018

**Characterization of Citrulline and Ornithine Production of Kimchi Isolated Lactic Acid Bacteria**

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Kimchi is a representative fermented vegetable food. It composed of diverse ingredients, such as cabbage, garlic, ginger, and pepper. Lactic acid bacteria (LAB) are important component in the kimchi fermentation. LAB converts raw materials into numerous metabolites, which contribute to the taste of fermentable food. Arginine is known as an energy source in the bacteria. To validate the consumption of arginine by LAB, its content in LAB culture media was monitored. The LAB were isolated from home-made kimchi and investigated to identify the arginine consumption, citrulline, and ornithine production. The arginine content was correlated with the growth of LAB. Interestingly, the addition of extra arginine in the media also showed the enhancement of cirulline and ornithine production except *L. lactis*. This result was well consisted with existence of arginine deiminase gene among the bacteria. Addition of arginine also effected on the pHs in the culture media by production of ammonia ion. This results suggested that arginine may play an important role in the lactic acid bacteria growth and have effect on the acid resistant of lactic acid bacteria during the fermentation.

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G019
Potential of Phenyllactic Acid Produced from Kimchi-originated Lactic Acid Bacteria for Food Safety
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Kimchi is representative Korean vegetable fermented food and easily available on the market. Phenyllactic acid (PLA) is a well-known natural antibacterial compound derived from phenylalanine catabolism. In this study, we investigated the PLA contents from kimchi and its relationship with kimchi-derived lactic acid bacteria (LAB) using liquid chromatography-mass spectrometry. PLA was detected in all the kimchi samples to different extents depending on the initial glucose concentration and fermentation stage. PLA content in the kimchi was 12.0–21.1 μg/ml at the early stage and decreased to 4.8–9.5 μg/ml at 3 or 4 weeks. PLA production in LAB was managed by the presence of lactate dehydrogenase gene. LAB lacking D-lactate dehydrogenase gene did not produce PLA. The addition of LAB to kimchi resulted in enhanced PLA production during the fermentation, especially, Lactobacillus plantarum caused a 1.7-fold increase of PLA content in kimchi. Lactobacillus brevis and Leuconostoc lactis increased a 2–4-fold of PLA content in kimchi compared to the control. These results suggested that addition of specific LAB to kimchi has great potential to enhance the food safety.

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G020
Internalized Prebiotics Nanoparticles Enhanced Antibacterial Property of Probiotics against Pathogens
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To replace antibiotics, one of the most challenging aspects of probiotics is to enhance their antimicrobial activity. Given that prebiotics is only digested by gut microbes of mammals, and stimulates the growth and activity of the advantageous bacteria. Moreover, since polymeric nanoparticles have been used for biomedical application because of their interesting characteristics to overcome various biological barriers. In this study, we developed prebiotic nanoparticles (PN) as prebiotics by conjugation with hydrophobic groups with hydrophilic prebiotics. We compared antimicrobial activity of probiotic bacteria against pathogens between prebiotics and PNs. The PNs were able to internalized into probiotic bacteria according to size, energy and transporter dependently. The internalized PNs were able to enhance antimicrobial property of probiotics against on both Gram-positive and Gram-negative pathogens than prebiotics-treated probiotics or probiotics itself through the intracellular stimulation. Our results identify that prebiotic nanoparticles can regulates the probiotic bacterial metabolism demonstrating a new avenue for probiotics modulation and their potential use in many gut diseases.

[Supported by NRF (No. 2016936920)]
G021

Push-and-pull Strategy of Acetyl-CoA Flux for Enhancement of ß-Carotene Production in *Yarrowia lipolytica*

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*Yarrowia lipolytica* is an oleaginous, non-conventional yeast that is known for its unique ability of storing large amounts of hydrophobic compounds, such as lipids and carotenoids, in its lipid bodies. Here, a new strain of *Y. lipolytica* that produces a significant amount of ß-carotene was engineered. Heterologous genes, *crtI* and *crtYB* from *Xanthophyllomyces dendrorhous*, as well as native genes regulating the rate limiting steps, *GGS1* and *tHmg1*, were introduced into the genome by targeting multiple sites of rDNA regions using CRISPR-Cas9 mediated system. To further increase the ß-carotene production level, various heterologous and endogenous genes were overexpressed to enlarge the Acetyl-CoA flux, the main precursor of ß-carotene. Of those genes, *Cat2* has shown the best performance in improving ß-carotene production. Lastly, to increase the cytoplasmic Acetyl-CoA pool by accumulation of citrate in the mitochondria, transcription of *IDP* gene was repressed by targeting the *IDP*-promoter using CRISPRi system, resulting in improved ß-carotene production by almost three folds (up to 900 µg/g DCW).

[This work was supported by the National Research Foundation of Korea (NRF) Grant funded by the Korean Government.]

G022

Enhanced 5-Aminovaleric Acid Production by Metabolically Engineered *Corynebacterium glutamicum*

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In this report, we demonstrate the development of 5-Aminovaleric acid (5AVA) producing *Corynebacterium glutamicum* strain. 5AVA is widely used for synthesis of polymers and other industrially valuable chemicals. Overexpression of lysine 2-monoxygenase (*davB*) gene and 5-aminovaleramidase (*davA*) gene has been successful for enzymatic conversion of L-lysine to 5AVA. In addition, a recombinant *Escherichia coli* strain expressing the *davB* and *davA* genes has been developed for 5AVA bioconversion from L-lysine. Direct fermentative production of 5AVA from glucose by metabolically engineered *E. coli* strains were examined to use glucose and xylose derived from lignocellulosic biomass instead of L-lysine as substrates. However, the recombinant *E. coli* strains’ yield and productivity of 5AVA remain very low. As an efficient L-lysine producer, *Corynebacterium glutamicum* is highly promising to develop direct fermentative production of 5AVA. Here, we report metabolic engineering strategies of *C. glutamicum* to enhance fermentative production of 5-Aminovaleric acid (5AVA) from glucose.

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G023
High-level Astaxanthin Production by Metabolically Engineered Escherichia coli
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Astaxanthin is a powerful antioxidant red carotenoid pigment. Here, we report metabolic engineering of Escherichia coli high-level and high productivity of astaxanthin production. First, the crt genes (crtE, crtY, crtI, crtB, and crtZ) from Pantoea ananatis and the truncated BKT gene (trCrBKT) from Chlamydomonas reinhardtii were employed to the strain. To have stable expression and efficient guiding to the membrane, 8 different fusion tags were tested on trCrBKT. Among them, the signal peptide OmpF and TrxA that were tagged to trCrBKT produced 12.90 mg/L of astaxanthin, 2.08-fold higher than without tags. After optimizing the culture condition, the production was increased to 332.23 mg/L by fed-batch cultivation. Through in silico FVSEOF analysis, two target genes, ispD and ispF, was employed to further improve the production level to 377.10 mg/L of astaxanthin with 9.20 mg/L/h productivity. When IPTG concentration was reduced from 1 mM to 0.5 mM, the titer increased to 432.82 mg/L with a productivity of 9.62 mg/L/h. To improve plasmid stability, hok/sok system was introduced and 385.04 mg/L of astaxanthin with a productivity of 7.86 mg/L/h was produced with this system.

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G024
Metabolic Engineering for High-level L-Arginine Production in Corynebacterium glutamicum
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We report the metabolic engineering of Corynebacterium glutamicum for the L-arginine production. To increase the tolerance to L-arginine, random mutagenesis was done on C. glutamicum strain. This strategy resulted in inactivation of Arginine operon repressor proteins. Then, PPP flux was increased by the downregulation of pgi gene and overexpression of opcA, pgl, tal, tkt, and zwf genes. Next, to channel L-glutamate to L-arginine, inactivation of the Ncgl1221 gene encoding L-glutamate exporter was done followed by optimizing the gene expression levels of argF and carAB to convert L-ornithine to L-citrulline effectively. Lastly, argGH operon was overexpressed to strengthen the L-arginine flux. The final developed strain resulted in 81 g/L of L-arginine in fed-batch fermentation of 1,500 L bioreactor. The approaches used in this study will be useful in developing strains of Corynebacterium glutamicum for L-arginine production and its derivatives.

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**G025**

**Novel Metabolic Pathway for Microbial Production of Four-, Five-, and Six-carbon Lactams**

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In this work, we demonstrate the construction of a new and efficient platform of metabolic pathway for the microbial production of four-carbon (butyrolactam), five-carbon (valerolactam) and six-carbon (caprolactam) lactams. In this pathway, the synthesis comprises of two steps conversion from ω-amino acids. The first step is the activation of ω-amino acids catalyzed by the *Clostridium propionicum* β-alanine CoA transferase (Act). The second step is the spontaneous cyclization. The pathway was validated both by *in vitro* and *in vivo* experiment. Three metabolically engineered *Escherichia coli* strains were developed by introducing the synthetic metabolic pathway followed by systems-level optimization, which resulted in the production of butyrolactam, valerolactam and caprolactam from renewable carbon source. Particularly, the final engineered *E. coli* strain produced 54.14 g/L of butyrolactam in fed-batch fermentation using glucose minimal medium. These result showed the high efficiency of the novel pathway and strategy employed in this study.

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**G026**

**Significance of the N-Terminal Domain of Ralstonia eutropha Polyhydroxyalkanoate Synthase along with the Proposed Structure and Whole Enzyme Mechanism**

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The polyhydroxyalkanoates (PHAs) are natural biodegradable polyesters produced in bacterial cells, and also potential outstanding alternatives to petroleum-based plastics. In this study, demostrating 3D reconstructed models of *Ralstonia eutropha* PHA synthase, key enzyme in PHA biosynthesis, and the complex with PhaM (PHA granule associated protein) was aimed by using small angle X-ray scattering (SAXS) analysis. The catalytic C-terminal domain of RePhaC1 dimer located at the center leads to the enzyme catalysis while its N-terminal domain is not directly involved because of its opposite localization to the dimerization subdomain of C-terminal domain. On the other hand, the localization studies showed that the appropriate localization of enzyme on PHA granules and stabilization of growing PHA polymer near active site are mainly led by that N-terminal of PHA synthase during PHA polymerization. Also, the further study based on serial truncation of N-terminal domain indicated requirement of the predicted five a-helices for the proper folding and granule binding function of N-domain.

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G027
Sacbrood Virus (SBV)-infection Effect on Gut Microbiome in Adult Honeybee (Apis cerana) and Larvae
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Sacbrood virus (SBV)-infected honeybee larvae often results in failure to pupate and death, while SBV-infected adult honeybee shows little clinical signs. In this study, the bacterial communities in the guts of the adults and larvae of SBV-infected Asian honeybee (Apis cerana) in Korea was investigated by using 16S rRNA gene amplicon sequencing to explore correlation of gut microbiome and SBV-infection. The numbers of operational taxonomic units (OTUs) were much lower in the SBV-infected larval guts than in the SBV-infected adult guts. For the larvae infected by SBV, the diversity was significantly less than in healthy ones with remarkable domination of the genus Gillimella (99.07%) of the family Orbaceae. Also, the genus Lactobacillus, which is known to play a beneficial role in honeybee’s health, was significantly reduced when compared to normal larvae. Most of the adult honeybee gut bacterial 16s rRNA gene sequences were highly similar to the known honey bee-specific ones and affiliated with the genus Gilliamella, Lactobacillus, Apibacter, Bifidobacterium and Snodgrassella. The results showed that the relative abundances of OTUs could be markedly changed depending on the developmental stage of the honeybee and larvae. For further study, the effect of the different microbiomes on the pathogenesis of SBV will be elucidated through culture-based approach in the future.

G028
Biosynthesis of Short-chain Alkanes in Metabolically Engineered Escherichia coli
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Escherichia coli is one of the industrially important microorganism to produce bio-based chemicals as alternatives to petroleum-derived chemicals. In this study, an engineered E. coli strain was developed to be capable of producing short chain alkanes (gasoline) through the fatty acyl-[acyl carrier protein (ACP)] in fatty acyl-CoA pathway. For the development of new microbial platform, fadE gene was deleted to prevent β-oxidation that degrades fatty acyl-CoAs into acetyl-CoA. By the deletion of fadR gene, the activity of 3-oxoacyl-ACP synthase (FabH) was triggered to enhance the initiation stage of fatty acid while its activity is inhibited by unsaturated fatty acyl-ACPs. Thus, to convert short chain fatty acyl-ACPs to the corresponding free fatty acids (FFAs), a mutated thioesterase was employed. The further conversion of short chain FFAs led to the biosynthesis of desired alkanes by the sequential reactions catalyzed by E. coli fatty acyl-CoA synthetase, Clostridium acetobutylicum fatty acyl-CoA reductase, and Arabidopsis thaliana fatty aldehyde decarboxylase.

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G029
A Study on the Removal of Cesium from Aqueous Solution by Photosynthetic Bioaccumulation of Green Microalgae
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This present study investigated the feasibility of using an isolated novel microalga, Desmodesmus armatus SCK, for treating cesium (Cs⁺) and radioactive ¹³⁷Cs from aqueous solution with effects of different temperature, potassium (K⁺)-starvation of seed cells, and organic substrate including volatile fatty acids (VFAs) on bioaccumulation of the Cs⁺. The obtained results revealed that D. armatus SCK accumulated a relatively higher Cs⁺ than other green microalgae, yielding uptake of 2.08 nmol Cs⁺ 10⁶ cells⁻¹ at 25° C under illuminated condition. At lower temperature, 3.7-fold higher Cs⁺-accumulation than that observed in 25° C was also obtained, probably due to excessive accumulation phenomena of exterior K⁺ by inhibitory effect of chilling stress. The biologically engineered D. armatus SCK grown in K⁺-depletion condition allowed to increase 26% of its maximum uptake capability observed in K⁺-sufficient condition. Furthermore, the capability of Cs⁺-uptake by D. armatus SCK was significantly enhanced when the VFAs are added as organic substrates in algal culture. The result of radionuclide experiment in this study also indicated that this strain can eliminate a wide level of the radioactive ¹³⁷Cs ranging from very lower (10 Bq mL⁻¹) to higher level (1000 Bq mL⁻¹) of its radioactivity.

G030
Introduction of Xylose Metabolic Pathway Drives Methanol Utilization in Engineered Saccharomyces cerevisiae
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Methanol is an increasingly appealing carbon source for the biological synthesis of valued chemicals, due its low price and richness. Some methylotrophic microorganisms can metabolize methanol, but there is a growing interest in developing synthetic methylotrophy in model organisms. Here, a set of methylotrophic genes from Pichia pastoris were introduced into Saccharomyces cerevisiae, a eukaryotic model organism. S. cerevisiae expressing 4 key genes encoding alcohol oxidase (AOX), dihydroxyacetone synthase (DAS), dihydroxyacetone kinase (DAK), and catalase (CTA) could consume 0.56 g/L of methanol when 10 g/L of methanol and 2 g/L of glucose were fed simultaneously. During methanol assimilation, methanol is first converted to formaldehyde by AOX and then DAS-mediated transketolase reaction converts formaldehyde and xylulose-5-phosphate (X5P) to glyceraldehyde 3-phosphate and dihydroxyacetone. Therefore, the XSP supply is important for methanol assimilation. As an effort to provide more XSP pool, we also used xylose-assimilating S. cerevisiae strain integrated with genes for xylose reductase (Xyl1), xyitol dehydrogenase (Xyl2), and xylulokinase (Xyl3). When four methylotrophic genes were introduced into the strain fed with xylose, methanol consumption increased by around 2 folds. [This work was supported by the National Research Foundation of Korea (NRF) Grant funded by the Korean Government.]
Degradation of Poly(ethylene terephthalate) via Unraveling Molecular Mechanism with Crystal Structure

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Plastics, i.e., poly(ethylene terephthalate) (PET) are remarkable and highly useful materials because of their favourable characteristics. However, these non-biodegradable materials cause serious environmental problems due to their durability. With the recently found PET-degrading bacterium \textit{Ideonella sakaiensis}, its potential use can make degradation and/or recycling of PET possible. In this study, the crystal structure of \textit{I. sakaiensis} PETase (IsPETase) with high resolution was reported. This crystal structure allowed to confirm that IsPETase has a Ser-His-Asp catalytic triad at its active site and contains an optimal substrate binding site for four monohydroxyethyl terephthalate (MHET) moieties of PET. By using structural-based protein engineering with the knowledge of its crystal structure, a new variant of IsPETase was attained with more enhanced PET-degrading activity. Also, the structural and site-directed mutagenesis related studies showed how PET is degraded into MHET, terephthalic acid, and ethylene glycol. Thus, PET degrading activity of IsPETase was determined with 3D structure and biochemical studies-based new phylogenetic tree analysis of PETase-like proteins.

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Malonyl-CoA is a key metabolite in the biosynthesis of various natural compounds. In this study, a type III polyketide synthase RppA was repurposed as a colorimetric malonyl-CoA biosensor being applicable in microorganisms, i.e., *Escherichia coli*, *Pseudomonas putida*, and *Corynebacterium glutamicum*. Colorimetric screening of cell was achieved through the conversion of malonyl-CoA into red-colored flaviolin by RppA activity. For biosensor targeting, 1,858 synthetic small regulatory RNA library was screened, and then performed to figure out 14 knockdown genes improving malonyl-CoA level in *E. coli*. These knockdown targets were applied to produce natural compounds such as polyketides (6-methylsalicylic acid and aloesone) and phenylpropanoids (resveratrol and naringenin). Knocking down these genes with different strategies enabled engineered strains to be capable of producing 6-methylsalicylic acid, aloesone, resveratrol and naringenin to 440.3, 30.9, 51.8 and 103.8 mg/L, respectively.

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G033
Characterization of Acetic Acid Bacteria Strain SRCM102383 Isolated from a Fermented Vinegar
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In this study, we tried to screen Acetic acid bacteria, which have commercially available benefits, from 40 kinds of traditional fermented vinegar. We used acetic acid bacteria-selected medium for first screening, and isolated 6 strains of acetic acid bacteria-like strains. Finally, 1 isolate was selected as acetic acid bacteria with excellent resistance against the toxicity of ethanol and sulfite. This strain grew even in the presence of 350 mg/L of potassium metabissulfite used as a preservative and have resistance against 10% ethanol. It was named as Acetobacter pasteurianus SRCM102383 by 16S rRNA sequencing and biochemical characterization. To optimize temperature for increasing acetic acid productivity, Acetobacter pasteurianus SRCM102383 was incubated at various temperature, pH and EtOH concentration conditions for 10-20 days and Acetic acid was measured by means of a high-performance liquid chromatography (HPLC system) that was equipped with an Aminex HPX-87H Column and RI detector. As a result, optimization of the temperature was 30°C and this strain was able to utilize the ethanol completely and produce acetic acid. Also, optimization of the pH and EtOH concentration was pH 3.0 and 7% ethanol concentration. Further study, we will establish high-concentrated acetic acid production vinegar.

G034
Characterization of Zygosaccharomyces rouxii Isolated from Fermented Food at Soy Sauce
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Zygosaccharomyces rouxii, an osmotolerant food-grade yeast, plays crucial role in the formation of flavor compounds in soy sauce production. Among the 32 Z. rouxii strains, 6 strains with superior tolerances to salt, sugar and ethanol were selected. Growth of the strains were compared by plate assay and determination of specific growth rates in soy sauce medium. In addition, production of flavor compounds in soy sauce medium were compared by GC-TOF/MS. Z. rouxii MBY2178 showed the highest specific growth rate of 0.85 ± 0.02 1/h. [This work was supported by the National Research Foundation (2017M3C1B5019250) of the Ministry of Science and ICT, Republic of Korea.]
G035
Development of Novel Platform *E. coli* Strains for Cellodextrin-based Production of 3-Hydroxypropionate (3HP)
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The biomass utilization into platform chemicals would economically support the petrochemical industries. The US Department of Energy displayed 12 platform chemicals derived from biomass-based sugars, which can be transformed into new molecules in emerging industrial applications. For present work, selected 3HP has very high global demand of 8 million tons/year in 2020. Recently, the price of glycerol is gradually increasing due to the rapid growth of industrial biodiesel. Therefore, the development of bioprocesses from low-cost cellulosic biomass is required. However, the development of industrial strains that can use cellodextrin, a partial hydrolysis product of cellulose in the hydrolysis process of cellulose, is insufficient. Development of artificial microorganism platform technology suitable for making biochemical products by fermenting various sugars produced from biomass. To solve the above problems, customized artificial microorganisms capable of simultaneously metabolizing complex sugars such as glucose and xylose, which are the degradation products of cellulose and hemicellulose, as well as cellodextrins, a partial decomposition product of cellulose is required. Malonyl-CoA is a precursor for 3HP biosynthesis and produced by carboxylation of acetyl-CoA with ACCase enzyme. The resulting malonyl-CoA is converted to 3HP via the MCR enzyme. In general, the overproduction of acetyl-CoA / malonyl-CoA biosynthetic genes, elimination of competitive pathways and elimination of the malonyl-CoA degradation pathway increase the concentration of malonyl-CoA, a precursor of 3HP in *E. coli*. The overall contribution of this project to design an ideal *E.coli* strain for consolidated bioprocessing of 3HP production from biomass.
H001
Structural and Physiological Exploration of Salmonella Typhi YfdX Uncovers Its Dual Function in Bacterial Antibiotic Stress and Virulence
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YfdX is a prokaryotic protein encoded by several pathogenic bacteria including Salmonella enterica serovar Typhi. YfdX is a product of the yfdXWUVE operon and is known to be under the control of EvgA, a regulator protein controlling the expression of several proteins involved in response to environmental stress, in Escherichia coli. Nevertheless, unlike other proteins encoded by the same operon, the structural and physiological aspects of YfdX have been poorly characterized. Here, we identified a previously unknown pH-dependent stoichiometric conversion of S. Typhi YfdX between dimeric and tetrameric states; this conversion was further analyzed via determining its structure by X-ray crystallography at high resolution and by small-angle X-ray scattering in a solution state and via structure-based mutant studies. Biologically, YfdX was proven to be critically involved in Salmonella susceptibility to penicillin G and carbenicillin. Furthermore, by using Galleria mellonella larvae as an in vivo model of Salmonella infection, we demonstrated that Salmonella virulence was remarkably enhanced by YfdX deficiency. The present study work provides direct evidence regarding the participation of YfdX in Salmonella antibiotic susceptibility and in the modulation of bacterial virulence, providing a new insight into this pathogen’s strategies for survival and growth.

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H002
A Phylogenetic Analysis Program Applying Artificial Neural Network Technique
Dong Su Yu
National Institute of Ecology

When taxonomically analyzing some bacterial species, traditional methods using 16S rRNA have often shown a relatively low confidence because 16S rRNA cannot exactly represent functional features of the species even though it is stable in phylogeny. Nevertheless, many researchers still have used similarity based on 16S rRNA in early phase of species identification because of the simple study. Since high-tech methods such as NGS and 3rd-generation sequencing were developed to sequence genomes, species identification based on protein function has been more useful than by 16S rRNA. In taxonomic analysis using proteins, selecting functionally equivalent proteins is highly important because of the high accuracy. We developed TaxonFEP system that identifies taxonomically species based on FEP-B algorithm that can predict functionally equivalent proteins with artificial neural network technique. By FEP-B algorithm, TaxonFEP can predict functionally equivalent proteins against UniProt Knowledgebase and identify species by equivalent protein function.
H003
Potent Inhibitory Effect on UV Induced Oxidative Stress by Deinococcal Exopolysaccharide (DeinoPol)
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The bacterium, *Deinococcus radiodurans* shows remarkable resistance to a range of extreme stress damages, such as ionizing radiation, desiccation, UV radiation, oxidizing agents, and electrophilic mutagens. These characteristics were the impetus for investigating the ongoing development of its use for bioremediation of radioactive wastes and the production of biomolecules. Outermost Deinococcal cell envelope consists with the fragile soft layer containing carotenoids, lipids, proteins, and EPS. Most of *Deinococcus* sp. has clusters of gene implicated in EPS biosynthesis which might facilitate biofilm formation to protect from extreme extracellular stress. However, the mechanisms underlying whether it has protective capacities against ROS induced cellular damages remain poorly understood.

The present study optimized the conditions for isolation of EPS from *D. radiodurans* R1 strain, characterized their chemical compositions, and antioxidant activities including scavenging effects on hydroxyl radical and anti-apoptosis activities in human macrophages and keratinocytes. We found here Deinococcal EPS (DeinoPol R1) had high potent to inhibit caspase mediated cell death pathway by scavenging intracellular ROS.

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H004
Using Metagenomic Analysis to Explore Seasonal and Spatial Microbial Diversity and Co-occurrence Patterns of Bacterial Community on Beef in South Korea
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Beef is one of the most consumed food around the world, and foodborne outbreaks steadily occur due to the consumption of contaminated beef. Analyzing microbial composition of beef can help understand the risk of such food poisoning. Beef samples were collected from three different sites in South Korea in winter and summer. The composition of the microbiota in beef differed depending on the region and the season in which the sampling took place, and was also different in ground beef. *Clostridium* was prevalent in beef sampled during the winter, and *Serratia* was easily found in ground beef. Also, this analysis showed that the potential human pathogen which was most prevalent but low in proportion would be *Shigella dysenteriae*, while *Serratia liquefaciens* was the most abundant species. Co-occurrence network analysis revealed some ecological patterns. *Macrococcus caseolyticus*, one of the most prevalent species in beef, had strong correlation with *Shigella*. *Staphylococcus equirum* and *Staphylococcus saprophyticus* were frequently found to have positive correlations with many pathogenic species. Lastly, possible keystone species of each sample measured by betweenness centrality(BC) varied greatly among samples but mainly belonged to the phylum Proteobacteria. These results provide an extended understanding on microbial ecology, and would be helpful for prevention of foodborne outbreaks.

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H005
Possible Functions of the C-terminus of RapC during Development in Dictyostelium
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Ras proteins are small GTPases of diverse signaling pathways including cell migration and differentiation. RapA is a key regulator of cell motility in Dictyostelium. Recently we have demonstrated that loss of RapC, which is a Ras subfamily protein with the highest homology to RapA, resulted in severe defects in cytokinesis leading to multinucleation; decrease of migration speed in chemoattractant-mediated cell migration, likely through increased cell adhesion; and aberrations in multicellular development producing abnormal multiple tips from one mound and multi-branched developmental structures. Interestingly, these phenotypes of rapC null cells are similar to those of the cells expressing the constitutively activated form of RapA, suggesting that RapA and RapC might play opposite functions in cell spreading and cell migration. To investigate the mechanism by which RapC has such an activity, we prepared cells expressing the C-terminal truncated RapC (RapCΔtail) and examined the phenotypes in cell spreading and development. rapC null cells expressing wild-type RapC showed completely rescued phenotypes in cell spreading and multicellular development. In contrast, rapC null cells expressing the C-terminal truncated RapC displayed the spreaded morphology and multiple tip-formation during multicellular development similar to those in rapC null cells. These results suggest important roles of the C-terminus of RapC in cell spreading and development.

H006
Phenotypes of Cells Overexpressing RapA and RapC in Dictyostelium
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Cell migration is one of the most essential biological processes involved in immune response, development, and cancer metastasis. Ras family proteins are small GTPases and play as major regulators of diverse signaling pathways. 19 Ras subfamily proteins are found in Dictyostelium, a good unicellular model organism that has been used to study cellular and molecular biological processes. Recent our study demonstrated that RapC, which is highly homologous to RapA, shows opposite functions to RapA in cell spreading, cell adhesion, development, and cell migration. Here, to investigate the opposite functions of RapA and RapC, we prepared cells expressing RapA or RapC, and compared the phenotypes of the cells in cell spreading, growth rate, and development. RapA OE and rapC null cells were bigger than wild-type cells, while RapA DN and RapC OE cells were smaller than wild-type cells. The growth rates of RapA OE and rapC null cells were lower than wild-type cells, whereas those of RapA DN and RapC OE cells were higher than RapA OE and rapC null cells. Similar phenotypes were found in multicellular development; RapA OE and rapC null cells showed slightly delayed development, while RapA DN and RapC OE cells exhibited similar or accelerated development, compared to wild-type cells. These results confirm that RapA and RapC have opposite functions in cell spreading, growth, and development. Further studies on the relationship between RapA and RapC are in progress.
H007
Metagenomic Analysis of Microbiota in Beef Stored at Different Temperature over Storage Time to Understand the Risk of Food Poisoning and Improve Product Management
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Outbreaks of foodborne illnesses in fast-food chains are commonplace nowadays and controlling foodborne pathogens is becoming crucial for food safety issues. Even beef processed in a completely sanitary environment can get exposed to foodborne pathogens during delivery. Therefore, analyzing the microbiome of beef may help understand the risk of food poisoning and offer a better way to manage beef products. A controlled infection experiment was conducted with Escherichia coli FORC_044, an Enterohemorrhagic E. coli strain isolated from the stool of a food-poisoned patient. The proportion of E. coli in infected beef decreased over time at 4°C but increased at 25°C. Co-occurrence network analysis conducted by SAS and Cytoscape showed that Escherichia has a positive correlation with the genera dominant in beef. Shifts of possible functions, assigned using Qiime and Picrust based on the KEGG Orthology system, were observed over storage time. This analysis showed predicted contributions of Escherichia and other genera, especially those that have a positive relationship with Escherichia, to shifts of virulence factors. These results suggest that the interaction between Escherichia and other microbiota in beef will increase the potential risks of food poisoning over time even at a proper temperature. Thus, any prolonged storage time of beef products is ill advised in light of food safety.

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H008
Evolution of Escherichia coli for Optimal Growth in a Rich Medium
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Escherichia coli is the most widely used model organism for scientific research and a platform cell factory for industrial application, because it grows quickly and is easy to edit the genome. Experimental evolution is a powerful tool for adapting bacteria to a specific environmental condition. Bacterial fitness increases along the evolutionary process and an evolved strain can reproduce better than ancestral strains in the adapted condition. Previous experimental evolution studies were limited to minimal media and defined media under stressed conditions, such as nutrient deficiency, pH, heat, and metabolite stress conditions. Here, we present a phenotypic and genome sequence alterations after adaptation of E. coli K-12 W3110 in LB medium. Nine clones were isolated from three evolved populations. At the physiological level, evolved strains grew faster than the ancestral strain in LB medium. Also, almost all evolved strains lost their motility except for one clone. Illumina HiSeq 2000 was used to identify the genome sequences of ancestral and evolved strains. In descendant strains, SNPs and Indels were identified compared with the ancestral strain. Mutated genes were involved in motility, transcription, metabolism, and DNA repair. Reverse genome engineering using TM-MAGE technique revealed key mutations contribute to rapid growth. The results of this study shed light to several mechanisms that drive the adaptation process in a rich medium.
H009
Characterization of RasY Overexpressing Cells in Dictyostelium
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Ras proteins are small, monomeric GTPases that act as crucial regulators of a number of cellular signaling pathways including proliferation, cell migration, differentiation, and apoptosis. The Dictyostelium genome database contains 19 Ras subfamily proteins, 15 Ras, 3 Rap, and 1 RheB protein. The functions of most of these Ras proteins in development and cell migration have not been studied yet. Here we have investigated functions of RasY in Dictyostelium. Multiple alignments of the amino acid sequences of Ras proteins show 76% and 56% homology of RasY with RapA and RasG, respectively. To investigate the functions of RasY, we prepared cells expressing wild-type (OE), constitutively activated (CA), or dominantly negative (DN) forms of RasY, and rasY knock-out cells are under preparation by homologous recombination. RasY-CA cells were bigger than wild-type cells, whereas RasY-DN cells were smaller, suggesting that RasY might be involved in the regulation of cell size. All RasY cells including RasY-CA and DN showed a slightly delayed multicellular developmental process. GFP-RasY was found on the plasma membrane and intracellular vesicular membranes. Cell migration and adhesion are under examination.

H010
Analyses of Terpene Synthase in a Tomato
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Plants emit volatile organic compounds as terpenoids constituting a large class of secondary metabolites in plants, some of them are inducible in response to various stimuli. These volatile organic compounds play important roles in defense, protection and ecological communications such as antimicrobial, antioxidant, and signaling agents for tritrophic interactions. In order to screen tomato terpene synthase, we found 39 full length terpene synthase sequences and annotated in silico from tomato genome database. Furthermore, we analyzed the volatile compounds are released. Among them, limoene terpene was capable of significantly suppressing the Ralstonia solanacearum growth.

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H012
Identification of Viruses and Viroids Infecting Major Peach Cultivars in Korea
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Peach is one of popular stone fruits belonging to the genus *Prunus*. Most popular peach cultivars are co-infected by diverse viruses and viroids. In order to identify viruses and viroids in major peach cultivars in Korea, we conducted metatranscriptome analyses for six major peach cultivars by RNA-Seq. Six different libraries for six peach cultivars were paired-end sequenced by HiSeq2000 system. *De novo* transcriptome assembly followed BLAST search revealed five known viruses belonging to the family *Betaflexiviridae* and a novel virus referred as *Peach virus T* in the family *Tymoviridae*. Moreover, we identified two viroids including *Peach latent mosaic viroid* and *Hop stunt viroid* infecting peach. Each peach cultivar was infected by at least one virus to six viruses. In addition, we assembled 18 complete genomes for identified viruses and viroids. Single nucleotide polymorphism analyses revealed the mutation frequency of identified viruses and viroids. Comparative virome analyses revealed that each peach cultivar possesses a unique virome. Moreover, we provide RT-PCR primers to diagnose the identified viruses and viroids. In summary, this is the first comprehensive peach virome study revealing a viral population in a single peach tree.

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H013
Identification of Crucial Amino Acid for Interaction of NbCPIPa with Coat Protein of Potato Virus X
Yeonhwa Jo and Hoseong Choi

Previously, we identified several *Nicotiana benthamiana* proteins interacting with coat protein (CP) of *Potato virus X* (PVX). Of them, NbCPIP2a is a positive regulator of PVX replication by interacting with PVX CP. In this study, we characterized important residues in NbCPIP2a required for interaction with PVX CP. NbCPIP2a contains two important domains referred as DnaJ and DnaJ_C. To determine an important domain required for interaction with PVX CP, we generated six different constructs. Bimolecular fluorescence complementation (BiFC) assay in *N. benthamiana* plant revealed that DnaJ_C domain in NbPCIP2a is important for interaction with PVX CP. Next, we further characterized motifs in DnaJ_C domain of NbCPIP2a using three different deletion constructs derived from the DnaJ_C domain. As a result, 183 to 223 amino acids (aa) region of NbCPIP2a was necessary to interact with PVX CP. To find important residues in 133 to 223 aa region, we generated two constructs containing five and six alanine substitutions, respectively. Only, the construct containing six alanine substitutions showed interaction with NbCPIP2a. Taken together, we identified essential residues in NbCPIP2a required for interaction with PVX CP using BiFC assay.

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H014
Three-dimensional Label-free Imaging of Individual Bacteria Using Holotomography
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Imaging three-dimensional shapes of bacterial cells and subcellular structures are crucial for the study of microbiology and related medical diagnosis. Although conventional microscopic techniques such as phase contrast microscopy or fluorescence microscope have been extensively used to provide morphological and molecular specific information about bacteria, conventional approaches do not provide three-dimensional quantitative imaging of live bacteria at the individual cell level.

Here, we present the three-dimensional label-free imaging of live bacteria using Holotomography (HT). HT provides an unprecedent capability at observing microscopic transparent objects, such as biological cells and their intracellular organelles. The lateral resolution of 110 nm is suitable to observe bacterial species whose sizes are several microns. The 3D image acquisition speed is 2.5 fps, which prevents the blurring effect from the Brownian motion and swimming of bacteria. From the RI tomograms of live bacteria, the dynamic 3D structures of E. coli, B. subtilis, and biofilms were readily retrieved, respectively. We also acquired quantitative information about an individual bacterial cell, such as volume, surface area and dry mass, based on the linear relationship between RI values and the local protein concentration. We expect the present method can find diverse applications to the study of microbiology. [Grants from Tomocube]

H015
Melanin Synthesis Inhibition Effect of Fermented Adlay Bran by Lactobacillus brevis
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Coix lacryma-jobi var. ma-yuen has been used as a food and traditional medicine for treating to invigorate the spleen function and promote urination, alleviate arthritis, arrest diarrhea, remove heat and facilitate the drainage of pus, especially known as “Adlay” in Korea. The aim of this study was melanin synthesis inhibition effects of fermentation extract made from the adlay bran. Lactobacillus brevis was isolated from Korea traditional food. For adlay bran fermentation, the adlay bran was mixed with distilled water in the ratio of 1:4 (w/w) and mixed thoroughly before sterilized at 121°C for 20 min. Lactobacillus brevis was inoculated in MRS broth and cultured for 24 h. Then the seed culture was inoculated into adlay bran medium (1%) as prepared above, and incubated at 37°C for 48h. After fermentation, total fermentation product was extracted with 70% Prethanol for 24 h. The extracted broth was filter and the supernatant was dried to dryness under vacuum. The dried extract was used for evaluation of melanin synthesis inhibition assay.
Metabolomics and Metagenomics Approach to Evaluate the Effect of Jakyakgamcho-tang on Chronic Colitis

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Chronic colitis was induced by giving rats 3% DSS dissolved in drinking water for 7 days. They were treated with 5-ASA and JGT dissolved in drinking water for 3 days. This process was carried out in four cycles. The severity of chronic colitis symptoms was alleviated by JGT treatment. Induction of colitis and JGT treatment changed compositions of inflammatory cytokine levels of TNF-α, IL-6, IL-10, IL-12 and IFN-γ. PLS-DA score plots derived from serum metabolites showed a clear separation among groups. Propionic acid, lactic acid, alanine, glycine, 2-aminobutyric acid, valine, leucine, glycerol, serine, threonine, asparagine, phenylalanine, glutamine, tryptophan and glycerol monostearate were identified as variables contributing to the separation of samples in the PLS-DA score plot. There was no significant difference in gut microbial community between induced group and positive control group (5-ASA treatment group). However, as the concentration of JGT was increased, gut microbial communities including Actinobacteria, Verrucomicrobia, and Bacteroidetes became similar to the those of control group. This study highlights the applicability of metabolomics and metagenomics study for evaluating anti-inflammatory effects of a new functional herbal medicine as a therapeutic agent for colitis.

Metabolite Markers for Sasang Constitution Type Classification through Metabolomics Study

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GC-MS and 1H NMR-based metabolic analyses were conducted to find marker metabolites in serum and urine according to different SC types. A total of 93 subjects were assessed for the classification of sasang constitution using sasang constitutional analysis tool. Although some samples were overlapped on OPLS-DA score plots, serum samples showed separation patterns between different SC types. Levels of lactate, glutamate, TG, and FAs of Tae-Eum type were higher than those of So-Eum and So-Yang type. FAs, TG, and lactate levels were also found to be metabolites related to BMI, indicating that marker metabolites for the diagnosis of SC type could be associated with obese. However, Tae-Eum type showed higher lactate levels in serum than So-Yang type for both normal weight and overweight groups. These results suggest that metabolomics analysis could be used to determine SC types.

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H018
Central Administration of Biochanin A Rescues Metabolic Dysfunction in a Cancer Cachexia Model
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Cancer cachexia leads to reduce appetite and loss of body weight which is implicated insufficient calorie intake. Cancer anorexia, induced by the inadequate response of hypothalamus to peripheral signals, is a major cause of decreased survival rate in cancer patients. Biochanin A, 5,7-Dihydroxy-4'-methoxyisoflavone, has been reported to effect on metabolic regulation in hypothalamus and activation of G coupled protein receptors (GCPR). In this study, we showed that change of hypothalamic metabolism contributed to increase food intake in cancer cachexia model. Male C57BL/6N mouse were exposed to intracerebroventricular (i.c.v.) injections of biochanin A or vehicle for 28 days every other day. Lewis lung cancer (LLC1)1 cells were subcutaneously inoculated after a week from the first injection (1x10⁵ cells). Body weight, food intake and blood glucose were weekly measured. Mice, which were treated with biochanin A, exhibited increased food intake and decreased body weight loss compared to the vehicle injected mouse. These results suggest that biochanin A might be a therapeutic drug to interrupt progress of cancer-induced eating disorder and mitigate morbidity and mortality.

[Supported by grants from Korea Institute of Science and Technology]

H019
HA2-enveloped Baculovirus Based DNA Vaccine against Middle East Respiratory Syndrome Coronavirus (MERS-CoV)
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Middle East respiratory syndrome coronavirus (MERS-CoV) is a beta coronavirus infecting humans, major outbreak in the Republic of Korea in 2015. Infection of humans by MERS-CoV, which mainly occurs through the lower respiratory tract, causes severe respiratory symptoms, leading to failure of the respiratory system and/or other organs. But for which no vaccines are available. Here, we produced and evaluated the MERS-CoV vaccine used a recombinant baculovirus whose surfaces were modified to express hemagglutinin2 (HA2). Using the HA2-modified baculovirus (AcHA2) as a delivery vector, we constructed major antigen spike protein(S)-encoding DNA vaccine system, AcHA2- MERS-CoV S using recombinant baculovirus encoding MERS-CoV S protein. In vivo test, we confirmed that AcHA2- MERS-CoV S induced strong IgG as well as neutralizing antibody and IFN-γ. These result supports that the recombinant baculovirus vaccine AcHA2- MERS-CoV S, may serve as a potential MERS-CoV vaccine which can elicit not only humoral but also cellular immune response.

[Supported by grants from KHIDI]
H020

*Enterococcus Phage vB_EfaS_HEf13 as an Anti-biofilm Agent against *Enterococcus faecalis*

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*Enterococcus faecalis* is a Gram-positive bacterium commonly found in root canals of patients with refractory apical periodontitis. It easily invades dentinal tubules and forms biofilm often leading to treatment difficulty and failure. Recently, bacteriophages are known to penetrate biofilm and infect bacteria inside biofilm. In this study, we isolated a novel *Siphoviridae* phage vB_EfaS_HEf13, which inactivates *E. faecalis* growth for up to 24 hours, and investigated its effect on *E. faecalis* biofilm. When *E. faecalis* biofilm was formed in the presence of the phage, the phage interfered with biofilm formation in a dose-dependent manner. Interestingly, the phage could also disrupt the pre-formed *E. faecalis* biofilm. Furthermore, the phage cooperatively enhanced the anti-biofilm effect of clinically used anti-bacterial agents (e.g. chlorhexidine, penicillin, and triple antibiotics) on both biofilm formation and pre-formed biofilm. Collectively, these results suggest that vB_EfaS_HEf13 could be used as a potential anti-biofilm agent for the treatment or prevention of *E. faecalis*-associated diseases.

H021

*Microbial Reduction and Quality Changes in Red Pepper Powder*

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Microbiological quality control of red pepper powder is important because the high levels of microbial contamination in red pepper powder reported by many studies reviewed suggests a need for control of the production to prevent potential foodborne illnesses. According to the result, microbial contamination level was not reduced after decontamination step by HACCP. To reduce microbial contamination level, several treatments were applied at washing and drying of red pepper and drying and UV irradiation of red pepper powder. In washing step, twice or more repeated washing was effective in reducing microorganisms. In drying step, the general drying temperature of red pepper was 55°C, but as the temperature was increased up to 70°C, microbial contamination decreased. However, since the high temperature changes the color of the red pepper to dark, it has established a drying condition that does not change color even though it has a microbial reduction effect. The last step was reducing of microbial level. *E. coli* was decreased by UV treatment. Level of aerobic bacteria was decreased by heat treatment or UV treatment. Combination treatment of heat and UV reduced contamination level of *E. coli* about 3 log CFU/g. Aerobic bacteria were also reduced about 1 log CFU/g by combination treatment. The treatment of heat and UV did not affect the color and capsaicin content of red pepper powder. [This work was supported by a grant (PJ01267603) from the Rural Development Administration)]
H022
Plant Disease Caused by *Xanthomonas* Promotes *E. coli* Growth on Lettuce

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Plant pathogen infection was reported a critical factor for the persistence of foodborne pathogen like *Samonella enterica* in plants. Generally *E. coli* rarely grows on healthy plants, but its survival could be influenced by depending on the presence of bacterial plant pathogens. To study the interactions between plant pathogen and foodborne pathogen on plant, growth of *E. coli* O157:H7 and *Xanthomonas campestris* pv. *vitians* (a lettuce bacterial leaf spot pathogen) in the plant was tracked. *Xanthomonas campestris* pv. *vitians* infection did not induce but supported *E. coli* growth in lettuce. *E. coli* populations in healthy lettuce that were not inoculated with *Xanthomonas* decreased gradually. These results indirectly support that *E. coli* can be replicated and proliferated by necrosis of lettuce caused by *Xanthomonas campestris* pv. *vitians*. The finding that damaged parts caused by plant pathogen affects the fate of *E. coli* populations in diseased plants suggests that targeting of plant pathogen disease is important in controlling *E. coli* populations on plants.

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H023
Molecular Characterization of a Novel dsRNA Mycovirus of *Trichoderma harzianum* M6

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In Korea, 315 fungal isolates causing green mold disease were collected from contaminated sawdust bags and artificial logs used in cultivating shiitake (*Lentinula edodes*). The fungal isolates were analyzed for the existence of double-stranded RNA(dsRNA). dsRNA-specific chromatography and dsRNA-specific Nuclease S1 digestion were used for purifying and verifying dsRNA, respectively. A total of 32 isolates were detected and the molecular taxonomy of dsRNA-infected isolates indicated that all isolates belonged to the *Trichoderma* spp.. The number and size of dsRNAs varied among isolates and the band patterns could be categorized into 15 groups. Although there were seven dsRNA groups observed in multiple isolates, eight groups were found to occur in single isolates. Northern blot analysis suggested that many different mycoviruses, which have not been identified yet, existed in *Trichoderma* spp.. *Trichoderma harzianum* M6 dsRNA, categorized under group III and having a single band of dsRNA, was selected for sequencing. For sequence analysis, dsRNA was purified from 1-week-old mycelia. A cDNA library of the dsRNA was then constructed using reverse transcriptase with an anchored random primer. At a result, we obtained a large segment (12,273 bp) and we carried out Rapid amplification of cDNA ends(RACE). Furthermore, we conducted phylogenetic analysis to find out which group was closest to this dsRNA.
H024
Korea Mushroom Resource Bank
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The Korea Mushroom Resource Bank (KMRB) was launched as a national research resource bank in 2015 by the Ministry of Science, ICT and Future Planning. The main goal of the KMRB is to secure important biological resources, mushroom-forming basidiomycota, significant sources of fundamental and novel substances and materials, as dried specimen, cultures, and genomic DNA. For wider application of fungal resources in education, medicinal and industrial uses, the KMRB will undertake following tasks: 1) Survey natural environments across Korea to catalogue mushroom diversity, 2) Establish resource management system based on accurate identification of mushroom, 3) Evaluate the usefulness of the discovered mushroom, 4) Create a secure preservation and loan system. With a global focus on utilizing natural resources, mushroom resources provide excellent opportunities for academic research, and discovering novel substances for use as medicine and energy.

H025
Effect of Different Feed Additives in the Gut Microbiota of Cyprinus carpio
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The feed additives for growth performance and immunity of Cyprinus carpio were evaluated however their effects on gut microbiota have not been analyzed. Thus, this study was conducted. One-year-old hatchery-raised C. carpio (weight: 62 ± 5 g; length: 16 ± 2 cm) were equally and randomly divided in 18 feeding tanks (68.5 × 48.5 × 41.5 cm) and fed diets of concentrated feed, with or without supplementation: Control (no supplementation), T1 (50 ppm oxytetracycline HCl, OTC), T2 (0.1% butyric acid), T3 (0.1% formic acid), T4 (0.1% gamma-aminobutyric acid, GABA), and T5 (0.05% isoflavone). Gut microbiome analysis in phylum level showed that Fusobacteria was the most abundant in treatment with 0.1% butyric acid (97.19%), but lowest in treatment with 0.1% formic acid. Cetobacterium was the predominant genus (97.19%) found in treatment with 0.1% butyric acid. Treatment with 0.1% formic acid showed higher percentage of Bacillus. Cetobacterium somerae predominated all the treatments wherein Marimicrobium arenosum was the next predominating species in treatments with 0.1% butyric acid, 0.1% GABA and control. Bacillus horikoshii also had high relative abundance next to C. somerae in treatments with 50 ppm OTC and 0.1% formic acid while Simkania negevensis did in treatment with 0.05% isoflavone. Overall, the gut microbiome of C. carpio altered depending on the feed additive supplemented.
[Supported by grants from Rural Development Administration (Project No. PJ013448012019).]
H026
Development of Human Monoclonal Antibody against Zika Virus Envelop Protein Using Phage Display Technology
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Zika virus (ZIKV) are a mosquito-borne flavivirus which caused epidemic outbreaks globally and poses a major threat to public health. Infection by ZIKV can be difficult to distinguish from infection by other flaviviruses due to high sequence similarity, antibody cross-reactivity, and virus co-circulation. ZIKV envelope protein (E) are an early surrogate marker of infection and can be used for the serological diagnosis of ZIKV infection. To develop ZIKV-E specific monoclonal antibody, the antibodies were selected through panning of the human synthetic Fab phage display library. Candidate antibodies were analyzed for affinity and stability against ZIKV, confirming the possibility of use as a diagnostic antibody. The ZIKV-E antibodies were performed using a human synthetic Fab phage display library. Screened antibodies measured affinity by soluble ELISA and analyzed thermal stability by protein thermal shift assay. After four rounds of panning, a panel of 12 ZIKV-specific Fabs with various binding affinities were identified. Three high-binding clones (Z31B9, Z31G7, and Z32H10) were selected for further identification and converted into a full-length human IgG1 format. Binding activity of three IgG with various ZIKV antigens was tested, it was confirmed that IgGZ32H10 had high affinity and no cross-reactivity. This anti-ZIKV IgG could be useful for the diagnosis of virus infection, discovery of vaccine candidates, and evaluating vaccine potency.

[Supported by grants from KRF]

H027
Antimicrobial and Air Quality Improvement Potentials of Hinoki Cypress Oil against Airborne Bacteria and Fungi
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This study was conducted to evaluate the active ingredient of 1.0% Hinoki Cypress oil as anti-air pollutants and antimicrobial. Four microbes were tested for antimicrobial activity of the active agent viz. Bacillus subtilis, Staphylococcus aureus, E. coli and Aspergillus oryzae. Total airborne bacteria and fungi were analyzed to assess indoor air quality. The bacteria and fungi were showed MIC after 100 hours of treatment compared to control. The S. aureus always showed MIC after 12 hours at a concentration of 0.3% or more. H₂S was reduced to 99.9% after 15 minutes of 1% cypress from the initial concentration 5575.4 ppb (p<0.05), and NH₃ decreased 46.07% (p<0.05) from the initial concentration of 18789.3 ppb to 10133.8 ppb after 30 min. HCHO gas concentration was not detected, and no decrease in the concentration of CO₂ was observed. CO was decreased by 96.0% (P<0.05) after 30 min of 1% scavenging activity at the initial concentration of 25 ppm. The airborne bacteria had a prevalence of 164.0 CFU/m³ to 28.0 CFU/m³ which decreased significantly from 235.7 CFU/m³ to 99.3 CFU/m³ after classroom instruction (P<0.05). Airborne fungi also decreased significantly from 33.7 CFU/m³ to 15.3 CFU/m³ before classroom instruction and from 191.3 CFU/m³ to 156.7 CFU/m³ after classroom instruction (P<0.05).

[This research was supported by the Cooperative Research Program for Jeonnam Technopark All right reserved, (Project No. PJ2017-0462), Republic of Korea.]
H028
Ornamental Fish, *Cyprinus carpio*, Fed with Fishmeal Replacement *Tenebrio molitor* and *Hermetia illucens*

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This study was conducted to determine the effect of black soldier fly (*Tenebrio molitor*; TM) and yellow mealworm (*Hermetia illucens*; HI) on the gut microbial diversity of *Cyprinus carpio* as an alternative fishmeal. A total of 240 hatchery-reared juvenile *C. carpio* L. (30 ± 5 g, 130 ± 5 mm) were equally and randomly divided in 12 rectangular tanks and then allowed to acclimatize seven days prior to 12-week feeding trial. Four experimental diets were formulated with insect replacements of black soldier fly and yellow mealworm with the following treatments:
- Control – Fish Meal (FM) 30%,
- Treatment 1 – FM 20% + TM and HI 10%,
- Treatment 2 – FM 10% + TM and HI 20%,
- Treatment 3 – TM and HI 30%.

Each treatment has three tanks (replicates) with each tank containing 20 fishes. Fishes were fed three times daily with a total feed of 1.5% fish body weight. Fusobacteria was the dominant phylum in *C. carpio* gut followed by Bacteroidetes, Firmicutes and Proteobacteria. *Cetobacterium somerae* was the dominant species in *C. carpio* gut and its relative abundance increased in treatments with 10% and 30% TM and HI. *Bacteroides massiliensis* relative abundance was highest in control and decreased in treatments with TM and HI. As a result, replacement of *T. molitor* and *H. illucens* as fishmeal replacement changed the gut microbiome of *C. carpio*.

[Supported by grants from the Cooperative Research Program for Ministry of Oceans and Fisheries (Project No. 2018-0201), Republic of Korea.]

H029
Effects of Adding Lactic Acid Bacteria on Fermentation Quality and *In Vitro* Rumen Fermentation of Total Mixed Ration

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This study was conducted to evaluate the effects of lactic acid bacteria (LAB) on the quality of total mixed ration (TMR) and *in vitro* ruminal fermentation. Three strains of LAB (*Lactobacillus plantarum* KACC 11451, *L. brevis* RNAL14, *L. mucosae* 521129) were used in this study. The fermented TMR feed with added LAB showed lower pH and higher concentrations of lactic acid, acetic acid and total organic acid compared to control, in which only water was added (P<0.05). In addition, the numbers of aerobic bacteria and LAB were higher, but *E. coli* were lower compared to the control (P<0.05). Notably, *L. brevis* treatment had the highest concentration of total organic acid and fungus was not detected. Total gas production, pH, ammonia-nitrogen was not differences according to incubation time. However, total VFA concentration was higher (P<0.05) in the LAB groups than the control at 48 h. Especially, total VFA concentration differed significantly among the treatments with the highest value observed in the *L. brevis* treatment. Overall, the use of *L. brevis* as a TMR fermentation agent, with its high production of propionic acid as well as total organic acids, inhibited fungi, promoted fermentation of the TMR feed, and enhanced ruminal fermentation by increasing the ruminal production of VFA.

[Supported by grants from the Cooperative Research Program for Institute of Planning and Evaluation for Technology (Project No. 319015-01), Republic of Korea.]
H030
Community Structure and Genomic Features of Undesirable White Colony-forming Yeasts on Fermented Vegetables
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White colony-forming yeasts (WCFYs) often appear in fermented foods, depending on the storage method. Despite the ongoing research on fermented foods, the community and genome features of WCFYs have not been well studied. In this study, the community structures of WCFYs on fermented vegetables (kimchi) prepared with various raw materials were investigated using deep sequencing. Only eight operational taxonomic units (OTUs) were detected, indicating that the community structure of WCFYs on kimchi is very simple. The five most abundant OTUs represented *Pichia kluyveri*, *Yarrowia lipolytica*, *Candida sake*, *Hanseniaspora uvarum*, and *Kazachstania servazzii*. Using a culture-dependent method, 41 strains representing the five major OTUs were isolated from the surface of the food samples. Whole genomes of the five major yeast strains were sequenced and annotated. This is the first study to report genome sequences of the two yeasts *Pichia kluyveri* and *Candida sake*. Genome analysis indicated that each yeast strain had core metabolic pathways such as oxidative phosphorylation; purine metabolism; glycolysis/gluconeogenesis; aminoacyl-tRNA biosynthesis; but strain specific pathways were also found. In addition, no toxin or antimicrobial resistance genes were identified. Our study provides genome information for five WCFY strains that may highlight their potential beneficial or harmful metabolic effects in fermented vegetables. [Supported by a grant from the WIKIM and NRF.]

H031
Changes in Microbial Community during Kimchi Fermentation Process by Carbon Dioxide Treatment
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Kimchi is a traditional fermented food in Korea. Kimchi is made from kimchi cabbage, which is a main ingredient, and various ingredients. Fermentation takes place by microorganisms in well-mixed ingredients, and the process is mainly carried out by lactic acid bacteria (LAB). The taste and flavor of kimchi is determined mainly by the result of fermentation metabolism of LAB. During fermentation, the microbial community of kimchi changes due to various causes such as temperature, ingredients, and salinity. Carbon dioxide (CO2) is one of the final products of heterolactic fermentation of LAB in kimchi. Here, we studied the effect of CO2 on the fermentation process of kimchi. The microbial communities and metabolites of kimchi with and without CO2 treatment were analyzed. Metatranscriptomic analysis was also performed at each stage of fermentation. Bacterial community analysis showed that the *Weissella koreensis* (heterofermentative LAB) was dominant in CO2 treated kimchi, while *Lactobacillus sakei* (homofermentative LAB) was the dominant species in kimchi without CO2 treatment. The concentrations of lactate and ethanol were also different, and the results of metatranscriptomic analysis using RNA sequencing also supported bacterial community analysis results. Collectively, our results highlight that the pre-treatment of CO2 in kimchi production is capable of affecting the microbial and metabolic profiles during the fermentation.
**H032**

**Molecular Surveillance of Tick-borne Pathogens in Dogs and Dog Ticks in Korea, 2017~2018**

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Many of the pathogenic agents transmitted by ticks, including *Ehrlichia* spp., *Anaplasma* spp., *Borrelia* spp. and *Babesia* spp. are known to be humans and animal pathogens. In this study, we are purposed to identify tick-borne pathogens in ticks and canine blood samples using molecular techniques and provide base line data in controlling of tick-borne diseases. Ticks and canine blood samples were taken from companion dogs in veterinary clinics, shelter dogs in abandoned animal shelter and military dogs. Ticks were identified as species by microscopic examination. DNA purified from ticks and blood samples was used for detection of 6 tick-borne pathogens (*A. phagocytophilum*, *A. platys*, *E. chaffeensis*, *E. canis*, *Borrelia* spp., *Babesia* spp.) using previously described PCR assays. A total of 2,215 dog blood samples and 2,294 ticks were collected from 2017 to 2018. Ticks were identified as 3 species (*2,261 Haemaphysalis longicornis*, *10 H. flava*, *22 Ixodes nipponensis*) and pooled according to collection date, site and species. As a result of PCR based on 16S rRNA gene, 35 samples were positive for *A. phagocytophilum*, 7 samples were *Borrelia* spp. and 2 samples were *Babesia gibsoni*. In this study, molecular surveillance of tick-borne diseases was conducted to investigate the infectious status in Korea. Furthermore, continuous monitoring is needed to prevent neglected tick-borne zoonoses having potential emerging diseases.

[Supported by grants from Animal and Plant Quarantine Agency]

**H033**

**The Neuroprotective Effect of Kaempferol-3-rhamnoside from *Ribes fasciculatum* Extract on Cognition and Memory Function in a Neurodegenerative Mouse Model**

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Neurodegenerative disorders are characterized by a decline of cognitive function and progressive loss of memory. The dysfunction of cholinergic system, which are reduced synthesis of acetylcholine, and impairments of brain-derived neurotrophic factor and cAMP response element binding protein (BDNF-CREB) play a major role in pathogenesis of neurodegenerative disorders. In this study, we investigated the neuroprotective effect of kaempferol-3-rhamnoside (KR) from *Ribes fasciculatum* extract on scopolamine-induced learning and memory impairment in mice. The KR was administered to C57BL/6 mice by intracerebroventricular (i.c.v) injection for 28 day, and cognitive impairment was induced by intraperitoneal (i.p) injection of scopolamine (1 mg/kg). Administration of KR ameliorated impairment of memory and cognition induced by scopolamine in the novel object recognition test, Y-maze test, and passive avoidance test and restored cholinergic system. Additionally, KR up-regulated the protein expression of BDNF-CREB pathway, which are involved in synaptic plasticity and memory performance, in both cortex and hippocampus. These findings suggest that KR could be a potent neuropharmacological drug against neurodegenerative disorders, and its mechanism might be modulation of cholinergic activity via BDNF-CREB pathway.
H034
Evaluation of Recombinant Baculoviral DNA Vaccine against Middle East Respiratory Syndrome Coronavirus in Mice
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Middle East respiratory syndrome coronavirus (MERS-CoV) is a novel betacoronavirus that has been emerging infectious disease in human. In 2015, the MERS-CoV outbreak occurred with 186 cases in the Republic of Korea. To aid preventive strategies and control of MERS-CoV outbreak in future, we have developed a MERS-CoV DNA Vaccine using the baculoviral delivery system. For enhancing cellular delivery, we constructed a non-replicating recombinant baculovirus coated with human endogenous retrovirus envelope (AcHERV). First, we constructed a recombinant baculovirus encoding each of S, S1, RBD genes under the control of the AcHERV system, and confirmed MERS-CoV S, S1 and RBD genes expression levels by western blot in Huh7 cell. To investigate the efficacy of the vaccine, recombinant baculoviruses were immunized in Balb/c mice. All three recombinant baculoviruses delivering each of MERS-CoV S, S1 and RBD genes elicited a high level of IgG, neutralizing antibody, and IFN-γ. Especially S1 showed the highest humoral and cellular immune response. The immunized mice were intranasally infected with MERS-CoV 5 days after inoculation with Ad5 expressing hDPP4. The results of the MERS-CoV challenge test matched the neutralized antibody results for each test mouse. In conclusions, AcHERV baculovirus could be a potential prophylactic vaccine against MERS-CoV.

H035
Characterization of Bacillus sp. Having Potential Probiotics Activity Isolated from Traditional Fermented Soybean Pastes and Application of Manufacturing Fermented Foods
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The purpose of this study was to improve the quality and to given potential probiotics properties of traditional fermented soybean product by selected Bacillus strain. We isolated Bacillus-like bacteria from traditional fermented soybean pastes, and confirmed the probiotic properties including safety of bio-resource properties that did not contain of B. cereus toxin gene and harmful molecules. Selected strains were able to survive in acidic and bile conditions, and had high extra-cellular enzyme activities, broad-spectrum against pathogenic bacteria, adherence to CCD-18Co cells. Final selected strain, SRCM 101439 was identified as B. amyloliquefaciens by 16S rRNA sequence analysis. We are manufacturing the cheonggukjang with SRCM 101439 and confirmed about B. cereus concentration, amino nitrogen and free amino acid contents as well as extra-cellular enzyme activities. SRCM 101439 cheonggukjang was not detected B. cereus, had a high protease, amylase, cellulase activity. These results suggest that the B. amyloliquefaciens SRCM 101439 have a high potential property as probiotics resource for commercial application such as soybean fermented products and synbiotic materials.

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H036
Screening of Biogenic Amine Non-producing Saccharomyces cerevisiae and Its Characterization for Manufacturing Berries Wine
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Biogenic amines (BAs) are produced primarily by microorganisms found in fermented foods and are often implicated seriously poisoning in the body of humans. And then, tyramine and histamine can evoke unwanted symptoms such as nausea, vomiting, migraine, hypertension, and headache. BAs are thus considered a risk for human health and their toxicity has led to the universal concept that they should not be allowed to accumulate in food and beverages. Therefore, we isolated BBA31 as biogenic amine non-producing strain for manufacturing wine, and then investigated the potential properties such as alcohol fermenting ability, and resistance of alcohol, glucose and sulfur dioxide. BBA31 was confirmed Saccharomyces cerevisiae using 18S rRNA sequencing. BBA31 was produced alcohol of 11.10% in YPD24 media. Thought the manufacturing berries wine using BBA31, we investigated ethanol content in wine. Finally, BBA31 strain was confirmed to be the useful yeast as probiotic materials which can be used for the manufacturing the berries wine.

[This research was supported by the Ministry of Agriculture, Food and Rural Affairs (MAFRA), through the 2019 Healthy Local Food Branding Project of the Rural Resources Complex Industrialization Support Program].

H037
Quality Characteristics of Doenjang Prepared with Different Types of Salt
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In this study, doenjang samples were prepared with different types of salts: Meju preparation: The yellow soybean (Glycine max Merrill) was washed, soaked in water for 3 h at room temperature (RT), and cooked 30 min at 100°C. After cooling, the cooked soybean was inoculated with Aspergillus oryzae (0.2%, w/w) and incubated for 19 h at 33°C. After that the soybean was dried 12 h at RT. Deonjang preparation: The prepared grain type meju, water, and salt were mixed at the ratio of 2.5:5:1.1 (wt: wt: wt), placed in a jar (onggi), and fermented at 28°C for 4 weeks and 16 weeks. Seven types (PS : purified salt, CS: conventionally manufactured solar salt, DS : dehydrated solar salt, WDS: washed and dehydrated solar salt, WDDS: washed, dehydrated, and dried solar salt 3YS: 3 years aged solar, BS : bamboo salt (9X) salt) of Deonjang were manufactured and analyzed. There were significant differences between experimental groups in terms of DPPH, Protease activity and a-amylase activity. All Deonjang samples showed increased moisture contents and pH as well as increased acidity and amino-type nitrogen during fermentation.
H038
Efficacy of Oral Administration of Live Probiotics against Influenza Infection in Mice
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Probiotics are defined as nonpathogenic living microorganisms that have beneficial effects on host health and disease prevention. Some probiotics is known to increase the secretion of cytokines in response to early influenza infections, thereby increasing the survival rate of mice infected with influenza.

In this study, we received two kinds of probiotics from CJ. To evaluate their immunological activity as a functional food, anti-influenza efficacy of oral administration of probiotics was tested in mice. Probiotics were administered twice a day from one week before the influenza infection, and oseltamivir and red ginseng extract used as a control group.

As a result, the administration of probiotics showed an equivalent level of survival rate improvement for influenza virus infection. Also, we identified the reduction of virus titer due to probiotics in lungs and BALF. These results were found to be due to changes in the amount of influenza-specific IgG in the blood, or an increase in the amount of influenza-specific IgA in the lung and BALF, or an increase in the activity of NK cells in the spleen.

In conclusion, the two kinds of probiotics used in this experiment seem to have enough potential as a supplement to stimulate immune strength against influenza infection. We will perform further studying to evaluate their optimal dosage and duration of administration.

[This study supported by grants from Beneficial Microorganisms center of CJ.]

H039
Survey and Quality Control of Commercial Probiotics for Livestock in South Korea
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The purpose of this study was to survey and evaluate the product information of commercial probiotics for livestock in South Korea. The products were randomly collected and evaluated for the indicated strains, the number of microorganisms, the date of manufacture, the expiration date, and the quality of the actual product. The microorganisms indicated in the product were 34 species of lactic acid bacteria, 33 species of Bacillus sp., 25 species of yeast, and 22 other species. The product with the number of viable cells matched to the indicated strain was 57.78%, the product with the indicated strain was 37.78%, number of viable cells and indicated strain matched was 22.22%. The information on the microbial strains of the product was different with the actual microbes’ amount and species identified. Saccharomyces cerevisiae, Bacillus amyloliquefaciens, Bacillus licheniformis, and Enterococcus faecium were the major microorganisms analyzed in the actual product. Probiotic products were compared within 2 months and over 3 months. The value of all products within 2 months was 9.45% to 4.38% higher than over 3 month products. In order to restore the reliability of probiotics products and to verify their effectiveness, it is necessary to strengthen regulations of management institutions and improve quality control of producers.

[This work was supported by a grant from the Next-Generation BioGreen21 Program Rural Development Administration (PJ01322302).]
H040
Flavoring Properties of Bacterial and Yeast Strains Isolated from Korean Fermented Soybean Foods (Doenjang and Ganjang)
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To investigate the flavoring properties of microorganisms during fermentation of Korean soybean foods, 60 bacterial (each 10 of *Bacillus*, *Staphylococcus*, and *Tetragenococcus*) and yeast strains (each 10 of *Debaryomyces*, *Wickerhamomyces*, and *Millerozyma*) were isolated from Korean fermented soybean foods, doenjang and ganjang, and their flavoring properties were evaluated in commercial culture media and simulated soybean foods through a SPME-GC/MS analysis. Heat-map and hierarchical clustering analyses of flavoring compounds in commercial culture media showed that flavoring compound profiles of the strains were clearly differentiated according to their genus. In particular, a principle component analysis showed that *Tetragenococcus* and *Wickerhamomyces* strains had flavoring compound profiles more distinctive from other genus strains. The analyses of flavoring compounds in simulated soybean foods also showed that the flavoring compound profiles were differentiated according to the genera of the strains. A statistical analysis showed that *Wickerhamomyces*, *Debaryomyces*, and *Tetragenococcus* were majorly responsible for the production of 2-phenylethanol, ethyl cinnamate, and acid compounds in simulated soybean foods, respectively. Our analysis also showed that the flavoring compound profiles were differentiated depending on bacterial and yeast strains. This study will provide a better understating of the flavoring properties of Korean fermented soybean foods during fermentation.

H041
The Effects of Paticulate Matter on Respiratory System Disease and Possibility of Virus Transmission
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Airborne microorganisms (AM), which are important components of the particulate matters (PM), are widely distributed in the atmosphere. Some AM are pathogenic and can cause a wide range of diseases in human and other organisms. Among the various risk factors of PM pollutants, PM$_{2.5}$ and PM$_{10}$ microorganisms seem to be responsible for the spread of various allergies and respiratory diseases. This study was conducted to evaluate the characterization of airborne pathogens in PM of Busan. A total of 554 PM samples were investigated. PM samples were screened for the presence of targeted viruses [adenovirus (ADV), bocavirus (BoV), rhinovirus (RV), respiratory syncytial virus (RSV), metapneumovirus (MPV), influenza virus (IFV), classical swine fever virus (CSFV) and foot and mouth disease virus (FMDV)] using multiplex real-time (reverse transcription) polymerase chain reaction method. No viruses were identified in the PM samples. although no virus was found in this study, negative aspects of PM, such as immune dysfunction and various respiratory diseases, are constantly being reported so continuous research is needed to determine safe exposure level or manage air quality. Also in this paper, we utilized the public data of medical history information and analyzed the relation of fine dust with respiratory disease using Pearson correlation coefficient. As a result Increased fine dust concentrations were found to be statistically related to hospitalization and outpatient respiratory disease.
H042
Effects of Lactobacillus sp., Galacto-oligosaccharide and Synbiotics on Swine Intestinal Microflora and In Vitro Fermentation
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In the present study we aimed to evaluate the role of Lactobacillus sp. (L. amylovorus and L. plantarum), galacto-oligosaccharides (GO) and their synbiotics on the in vitro fermentation characteristics, microbial ecology and odor gas emission using fecal inoculum which mimicked the small intestinal physiological conditions. Results showed a significant reduction in pH with corresponding increase in total gas production in the GO, L. amylovorus plus GO, and L. plantarum plus GO after 12 h and 24 h of in vitro fermentation. The major VFA produced after 24 h were acetate, butyrate and propionate. These individual VFA and the bacterial phylotype showed a more distinct increase in the fermentation culture of GO, L. amylovorus plus GO, and L. plantarum plus GO in the time points. All the treatments revealed a significant reduction in the concentration of hydrogen sulfide, methyl mercaptan and ammonia odor compounds throughout the fermentation period except a drastic increase in ammonia after 24 h of fermentation in L. amylovorus plus GO. Our findings suggest that the prebiotic contributed most to the fermentation characteristics, with consequent enhancement of the effects of the synbiotics on modulation of the bacterial phylogeny population, increase in the concentration of acetate and butyrate and significant reduction in the odor compounds.

[This work was supported by a grant from the Next-Generation BioGreen21 Program Rural Development Administration (PJ01322302).]

H043
A Methods of Bacterial Genome and Microbiome Analysis Using EzBioCloud System on the iSeq 100 Platform
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Over the last decade, next-generation sequencing (NGS) technology has been widely applied in most microbiome and genome research. Among them, analyses of the 16S rRNA-based microbiome and bacterial genome have been used as common methods to understand the microbiome function and taxonomic profiling. Here we present the experiment method of the 16S rRNA microbiome and bacterial whole genome using EzBioCloud systems on the Illumina iSeq 100 platform. This experiment will be guiding for 16S rRNA microbiome and bacterial genome analysis on iSeq 100 platform.
H044
Identification of Bacteria Responsible for Producing Biogenic Amines during Ganjang Fermentation through a Metagenomic and Metatranscriptomic Approach
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To identify bacteria responsible for producing biogenic amines during ganjang (a Korean traditional soy sauce) fermentation, a metagenomic and metatranscriptomic approach was applied to ganjang which was confirmed to produce histamine, putrescine, cadaverine, and tyramine during fermentation through 1H-NMR. A BLASTN analysis based on decarboxylase genes associated with the biogenic amine production was performed against ganjang metagenome and one histidine decarboxylase gene, one ornithine decarboxylase gene, one lysine decarboxylase gene and five tyrosine decarboxylase genes were identified. Phylogenetic analyses of the identified decarboxylases genes showed that *Tetragenococcus* sp. (histidine and tyrosine decarboxylases), *Lactobacillus* sp. (ornithine, lysine, and tyrosine decarboxylases), *Enterococcus* sp. (tyrosine decarboxylase), and *Virgibacillus* sp. (tyrosine decarboxylase) might be biogenic amine producing bacteria during ganjang fermentation. A metatranscriptome analysis of the biogenic amine production genes showed that *Lactobacillus* sp. (putrescine and cadaverine) and *Tetragenococcus* sp. (histamine and tyramine) were probably responsible for the production of biogenic amines especially during the middle of fermentation time. The analysis also showed that *Enterococcus* sp. and *Virgibacillus* sp. were probably responsible for the tyramine production during the early fermentation time. These results were well consistent with the biogenic amine profiles.

H045
Isoflavone Content and Physicochemical Properties of Soybean Leaves According to Extraction Conditions
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Soybean leaves are rich in isoflavones when compared to other plant leaves and are known to have a large antioxidant activity. Extraction efficiency and physicochemical properties of these soybean leaves were investigated in order to utilize them as high-value food raw materials. Isoflavone content by time and temperature, DPPH(1,1-diphenyl-2-picrylhydrazyl) radical-scavenging activity, tannin content and total polyphenol content were investigated. Isoflavone content was the highest at 59.74 ± 4.54 mg/ml when extracted at 90°C for 12 hrs, and there was no significant difference between 12 hrs and 24 hrs. The soybean leaves extracted at 90°C showed relatively high DPPH radical-scavenging activity compared with the soybean leaves extracted at 50°C and 70°C. DPPH(1,1-diphenyl-2-picrylhydrazyl) radical-scavenging activity and total polyphenol contents reached maximum levels of 67.26 ± 3.67% and 1,688.68 ± 97.37 μg/ml chlorogenic acid equivalent, respectively. Therefore, considering the content of isoflavone and polyphenol and antioxidant activity, hot water extraction of soybean leaves is optimal condition at 90°C for 12 hrs.

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H046
Effect of Growth Medium for Enrichment of Specific Bacteria Groups in the Pig Feces
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There are several media for isolation and identification of specific bacterial groups have been described; however, little is known about the effect of changes in the bacterial community after cultivation. Understanding the change of bacterial groups according to the medium is greatly advantageous for detecting a target strain, for example a novel beneficial *Lactobacillus* strain. Thus, we used four different types of sugars that are commonly used in a commercial product as prebiotics for enrichment of *Lactobacillus* group. Using three healthy pigs mixed feces, we observed changes in pigs’ fecal microbiota according to sugar component. Additionally, two different pH condition (pH 6~7 and pH 5) was tested because of *Lactobacilli* survive in an acidic environment. To assess the bacteria composition and bacterial communities in each medium, the 16S rRNA region was sequenced and analyzed using Quantitative Insights Into Microbial Ecology (QIIME). The cultivated fecal microbiota in each different conditions, were separated into clusters by sugar type and pH condition. The relative abundance of several phyla and genera were significantly different between each condition. The genus *Lactobacillus* was a dominant group in all the conditions (composition of 64.7 ~ 99.8%), especially in the low pH conditions (98.0 ~ 99.8%). In addition, we predicted the functions of the cultivated fecal microbiota were significantly different between each medium condition. Sugar type and pH condition of medium contribute changes of fecal microbiota, pH condition is much more critical factor for enrichment of the *Lactobacillus* group than sugar type. These findings contribute an initial description changes of microbial ecology after cultivation using different sugar type and pH of medium, and the results demonstrate capable with obvious applications in industry and research.

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H047
Identification and Characterization of *Oryctes rhinoceros* Nudivirus from *Allomyrina dichotoma* in Korea
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An *Oryctes rhinoceros* Nudivirus (OrNV) was isolated from diseased larvae of the Korean horn beetle, *Allomyrina dichotoma*, collected from local farms rearing larvae related to insect industry throughout Korea. Transmission electron microscopic observations confirmed that OrNV isolated from *A. dichotoma* in Korea was an enveloped rod-shaped virion. The morphological size of the enveloped particle was about 260 x 40 nm on TEM. The genome size of OrNV from *A. dichotoma* in Korea was estimated to be 127,615 bp and potentially contains 139 predicted protein-coding open reading frames (ORFs) by Next Generation Sequencing (NGS). According to the Lee’s article (2015), the peroral virus infection rated for third instar larvae of *A. dichotoma* was determined as about 80% positive. Most of the OrNV infected larvae died and only 21.1% of larvae went through metamorphosis (Lee et al., 2015).