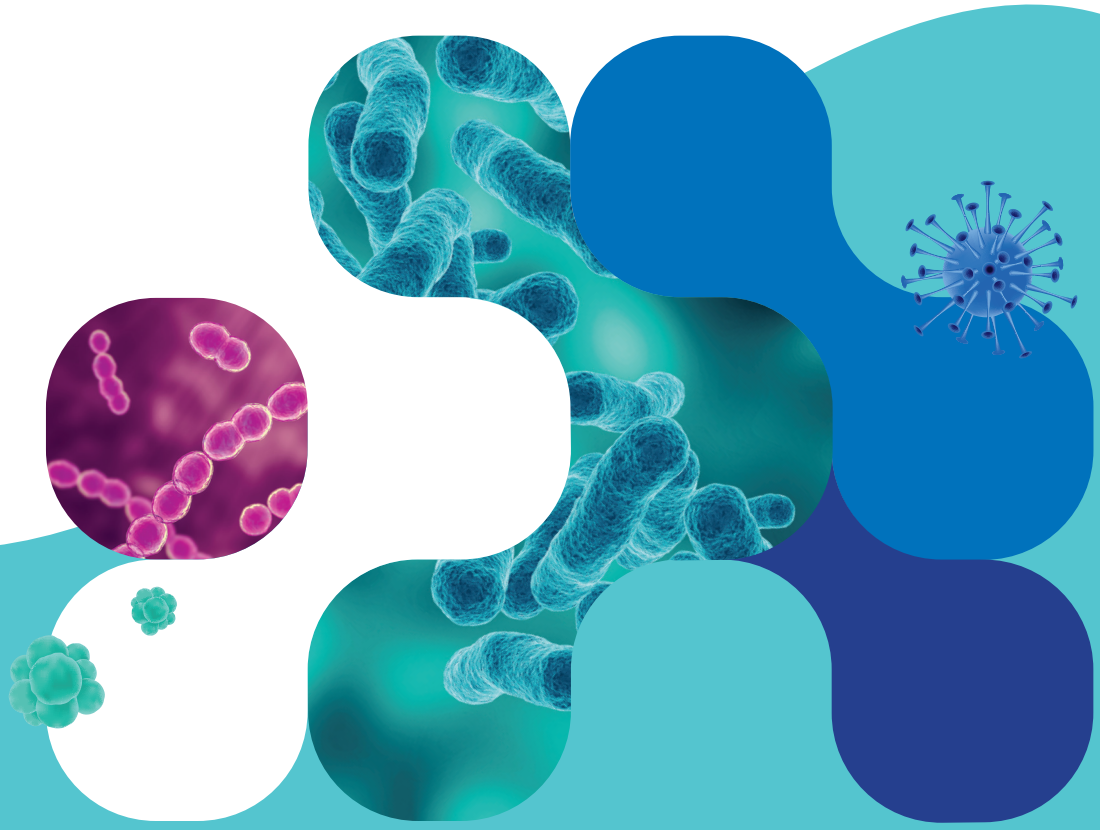
2025 KSM-KDCA-KIT Joint International Conference

148th Fall Conference of The Korean Society for Microbiology

10. 22.(WED)~24.(FRI)

Jeongsimhwa International Cultural Center



대한미생물학회 Korean Society for Microbiology

국립보건연구원 National Institute of Health

결핵연구원 THE KOREAN INSTITUTE OF TUBERCULOSIS

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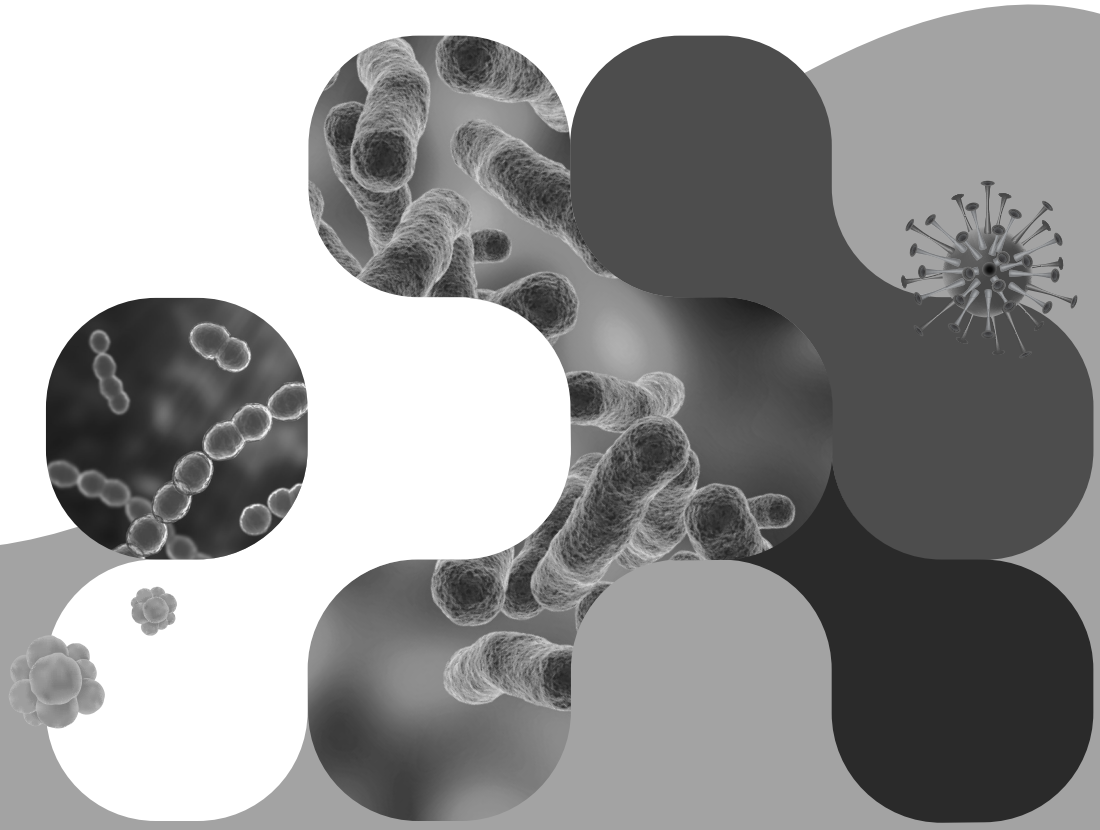

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Program

October 22 (Wed)

09:00~	**Registration**
09:15-09:30	**Opening remarks by President Hwa-Jung Kim and Congratulatory remarks by Chairman Wonyong Kim**

S1. Student and Early-Career Scientist Session

Chair : Jung Mogg Kim *Hanyang University*

09:30-09:45	S1-1	**Annotated gut microbes dataset for deep learning-based colony detection** Ayyaz Khan *Jeonbuk National University*	11
09:45-10:00	S1-2	**Fucosylated haptoglobin as a driver of inflammation via Mincle-mediated signaling in sepsis** Taylor Roh *Chungnam National University*	12
10:00-10:15	S1-3	**Mechanisms of Lymphopenia in Acute Scrub Typhus and Therapeutic Implications** Chaewon Kim *Seoul National University, College of Medicine, Seoul, South Korea*	13
10:15-10:30	S1-4	**First Detection of Korean Langya Virus and Evolutionary Characterization of *Parahenipavirus* in Shrews, Republic of Korea** Augustine Natasha *Hallym University*	14
10:30-10:45	S1-5	**Role of SaeS in controlling staphyloxanthin biosynthesis in *Staphylococcus aureus*** Bae, Eunhwan *Inha University*	15
10:45-11:00	S1-5	**The Potential of C-di-AMP as a Druggable Target for Reversing β-lactam Resistance in MRSA** Ji-Hoon Kim *Sungkyunkwan University*	16

11:00-11:15	**Coffee break**

S2. New Faculty Session

Chair : Seong-Tshool Hong *Jeonbuk National University*

11:15-11:40	S2-1	**SARS-CoV-2 viral characteristics and immune responses in normal and immunocompromised patients** Ji Yeun Kim *Hanyang University*	19
11:40-12:05	S2-2	**Translational Research for Immunomodulatory and Immunometabolic Therapies Targeting MRSA-Induced Septic Arthritis** Hyuk-Kwon Kwon *Gyeongsang National University*	20
12:05-12:30	S2-3	**Spatial transcriptomics research in COVID-19 Non-human primate model** Taehwan Oh *Dankook University*	21

12:30-13:30	**대한미생물학회 이사회의**
12:30-14:00	**Lunch**

S3. Plenary Lecture

Chair : Hwa-Jung Kim *Chungnam National University*

14:10-14:50	S3-PL	**From bacteria to cancer and Alzheimer's disease: A winding road journey with *Vibrio*** Joon Haeng Rhee Chonnam National University	25

14:50-15:00	**Coffee break**

S4. Advances in Mycobacterial Research and Clinical Practice

Chair : Jae-Seok Kim *Hallym University Kangdong Sacred Heart Hospital*

15:00-15:25	S4-1	**From Basic Research to Clinical Applications: Functions and In Vivo Relevance of *Mycobacterium tuberculosis* Proteins** Sohkichi MATSUMOTO *Niigata University Graduate School of Medical*	29

15:25-15:50 S4-2 **NTM-PD treatment dilemmas in real-world practice: what physicians struggle with** 30
Hyung-Jun Kim
Seoul National University Bundang Hospital

15:50-16:15 S4-3 **Tuberculosis Diagnostic Trends in Clinical Laboratory** 31
Namhee Kim
SMG-SNU Boramae Medical Center

16:15-16:40 S4-4 **Pan-lineage *Mycobacterium tuberculosis* reference genome for enhanced molecular diagnosis** 32
Jake Whang
Korea Institute of Tuberculosis

16:40-16:50 **Coffee break**

S5. Next-Generation Strategies in Infection Control and Therapeutics

Chair : Yong Woo Jung *Korea University*

16:50-17:15 S5-1 **Mechanistic Insights into MRSA β-lactam Sensitization: Role of LTA and RNA Polymerase Mutations** 35
Taeok Bae
Indiana University School of Medicine

17:15-17:40 S5-2 **Harnessing CRISPR Adaptation Systems for Directional Molecular Recording Technologies** 36
Sungchul Kim
POSTECH

17:40-18:05 S5-3 **Overcoming BCG Limitations: DC-Based Booster and Therapeutic Strategies Against TB** 37
Jong-Seok Kim
Konyang University

October 23 (Thu)

09:30-09:40 **Congratulatory remarks by Director Gyeong-In Lee**

S6. Innovative Vaccine Development using Cutting-Edge Technology

Chair : Joon Haeng Rhee *Chonnam National University*

09:40-10:05	S6-1	**A built-in adjuvanted ferritin nanocage mucosal vaccine against *Streptococcus pneumoniae*** Shee Eun Lee *Chonnam National University*	41
10:05-10:30	S6-2	**Kinetically-activating nanoadjuvant empowers broad and persistent antiviral immunity** Yong Taik Lim *Sungkyunkwan University*	42
10:30-10:55	S6-3	**Development of a Decentralized and Accelerated mRNA Vaccine Production System (DeCAFx) to Strengthen Pandemic Preparedness** Seo Sang Hwan *International Vaccine Institute*	43
10:55-11:20	S6-4	**$CD8^+$ T cell differentiation after COVID-19 mRNA vaccination** Eui-Cheol Shin *KAIST*	44

11:20-11:30 **Coffee break**

S7. Special Lecture

Chair : Eun-Kyeong Jo *Chungnam National University*

11:30-12:00	S7-1	**Metabolic perspectives on the Evolution of Multidrug Resistance in Mycobacteria** Hyungjin Eoh *University of Southern California*	47

12:00-12:30 **대한미생물학회 총회**

12:00-13:20 **Lunch**

13:20-14:00 **Poster Presentation**

S8. One Health Approach to Campylobacter Infections

Chair : Woo Kon Lee *Gyeongsang National University*

14:00-14:25	S8-1	***Campylobacter*: a major pathogen of foodborne enteritis** Seok Hoon Jeong *Gangnam Severance Hospital*	51
14:25-14:50	S8-2	**Campylobacteriosis: Pathogenesis and Control Strategy** Jang Won Yoon *Kangwon National University*	52
14:50-15:15	S8-3	**Development and application of a new isolation method for *Campylobacter* spp.** Jong-Hyun Kim *National Institute of Health*	53
15:15-15:40	S8-4	***Campylobacter jejuni* infection and Guillain-Barré syndrome in Korean patients** Byeol-A Yoon *Dong-A University*	54

15:40-16:05 **Coffee break**

S9. Journal of Bacteriology and Virology Academic Award JBV저널 학술상

Chair : So-Youn Woo *Ewha Womans University*

16:05-16:30	S9-1	**CHAP^{SAP26}-161, A Truncated Protein and Enzymatic Active Domain of Endolysin LysSAP26, as a Potential Therapeutic Agent to Combat *Clostridioides difficile* Infection** Yoon-Jung Choi *Kyungpook National University*	57
16:30-16:55	S9-2	**Lung Organoids from Human Embryonic Stem Cells to Investigate Pneumococcal Serotype 23F that does not Infect Mouse** Ho Seong Seo *Korea Atomic Energy Research Institute*	58
16:55-17:10	S9-3	**Transcription Profiling Signatures Distinguishing RSV Infection in Humans** Hye Jin Shin *Chungnam National University*	59

17:10–17:35	S9-4	**Contemporary Insights into Non-typhoidal *Salmonella*: Understanding the Pathogenicity, Infection Mechanisms, and Strategies for Prevention and Control** Minho Lee *Hallym University*	60

17:35	**시상식/경품추천**

October 24 (Fri)

S10. Medical Research Council meeting

10:00–12:00	**Medical Research Council meeting**

Poster Session

PB (Poster Bacteria) 63

PI (Poster Infection Immunology) 81

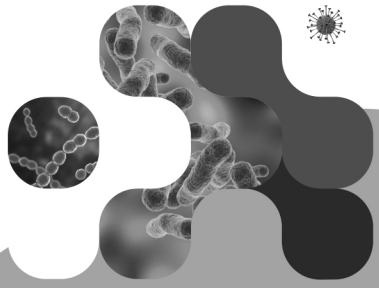
PVM (Poster Viruses and miscellanies) 105

MEMO

S1

Student and Early-Career Scientist Session

Chair Jung Mogg Kim
Hanyang University



MEMO

S1-1

Annotated gut microbes dataset for deep learning-based colony detection

Ayyaz Khan[1], Hee-Suk Chae [2,3], Seong-Tshool Hong[1]*

[1]*Department of Biomedical Sciences and Institute for Medical Science, Jeonbuk National University Medical School, Jeonju, 54907, South Korea*
[2]*Department of Obstetrics and Gynecology, Jeonbuk National University Medical School, Jeonju, Republic of Korea*
[3]*Research Institute of Clinical Medicine of Jeonbuk National University-Biomedical Research Institute of Jeonbuk National University Hospital*

Pure microbial cultures are essential for mechanistic microbiome research, but conventional isolation approaches are labor-intensive, low-throughput, and poorly integrate phenotypic and genotypic markers. Recent advances in computer vision have enabled automated colony detection, but robust colony-based species-level identification of human gut microbes remains limited. To address this gap, we developed a deep learning-based model that integrates multispectral imaging captured under five distinct lighting conditions with colony segmentation and classification pipelines. A gut microbial culture library was constructed on JM medium, comprising 763 bacterial and 37 fungal species, taxonomically assigned using 16S rRNA and ITS sequence identity thresholds. Colony images were captured with a FOBI in vivo imaging system, using a custom 3D-printed tube to minimize reflections and ensure uniform illumination. Image capture was standardized with NEOimage software. Colonies are first isolated with an instance-segmentation model, producing one mask per colony. The masked crops from all lighting conditions are then fused in a convolutional neural network architecture to classify each colony at the species level. For better visual separation of similar colonies, the pipeline augments learning with texture cues and uncertainty estimates during prediction. By using five different light condition images, the model outperforms single light images-based studies, yielding an efficient approach for high-throughput identification of live gut microbial colonies. Automated identification of gut microbial colonies can accelerate microbiome research and diagnostics by reducing the need for manual inspection.

S1-2

Fucosylated haptoglobin as a driver of inflammation via Mincle-mediated signaling in sepsis

Taylor Roh [1,2], Gyoungah Ryu [1,2], Young Jae Kim[1,2], Sang Min Jeon[1,2], Kyung Tae Kim[1,2], Soo In Kim[1,2], Bomi Lee[1,2], Geumseo Kim[1,2], Jinyoung Lee[1,2], Yuri Seo[1,2], Ji Woong Yu[1,2], So Young Park[3], Seung-Yeol Park[4], Eun-Kyeong Jo[1,2,5]

[1]*Department of Microbiology, College of Medicine, Chungnam National University, Daejeon, Republic of Korea*
[2]*Department of Medical Science, College of Medicine, Chungnam National University, Daejeon, Republic of Korea*
[3]*Division of Pulmonary, Allergy and Critical Care Medicine, Kangdong Sacred Heart Hospital, Hallym Medical Center, Seoul 05355, Republic of Korea*
[4]*Department of Life Sciences, Pohang University of Science and Technology, Pohang, 37673, Republic of Korea*
[5]*Biomedical Research Institute, Chungnam National University Hospital, Daejeon, Republic of Korea*

Sepsis remains a life-threatening condition in which profound immunoparalysis hampers effective treatment and contributes to poor outcomes. While haptoglobin (Hp) has long been associated with sepsis prognosis, the immunological consequences of its glycosylation remain unclear. Here, we identify fucosylated (Fu)-Hp as a proinflammatory driver in human sepsis. Plasma from sepsis patients exhibited elevated terminal fucosylation of Hp, especially at Asn207 and Asn211, which correlated with systemic cytokine levels. Functionally, Fu-Hp purified from patient plasma activated NF-κB/MAPK signaling and the NLRP3 inflammasome in human PBMCs and monocytes, inducing robust cytokine and chemokine production. Single-cell RNA sequencing revealed a distinct macrophage-like subpopulation enriched in inflammatory mediators, with marked upregulation of *FUT4*, *CLEC4E* (Mincle), and *IL1B*. Moreover, Fu-Hp bound directly to Mincle with high affinity, amplifying inflammatory responses; this effect was attenuated by defucosylation, Mincle blockade, or *Clec4e* deficiency. In vivo, Fu-Hp administration enhanced systemic inflammation in mice. Furthermore, macrophage-like clusters bearing Fu-Hp-Mincle signatures were enriched in survivors but absent in non-survivors, suggesting clinical relevance. Collectively, our findings define Fu-Hp as a glycoprotein signal that drives Mincle-mediated inflammation, and further suggest that this pathway may counteract sepsis-associated immunoparalysis and influence disease trajectory.

S1-3

Mechanisms of Lymphopenia in Acute Scrub Typhus and Therapeutic Implications

Chaewon Kim[1,2], Na-Young Ha[3], Yuri Kim[4], Yeon-Sook Kim[5], Nam-Hyuk Cho[1,2]*

[1]*Department of Microbiology and Immunology, Seoul National University College of Medicine, Seoul, Republic of Korea*
[2]*Department of Biomedical Sciences, Seoul National University College of Medicine, Seoul, Republic of Korea*
[3]*Biomedical Research Institute, Chungnam National University Hospital, Daejeon, Republic of Korea*
[4]*Department of Microbiology, SoonChun Hyang University College of Medicine, Cheonan, Chungcheongnam-do, Republic of Korea*
[5]*Division of Infectious Diseases, Department of Internal Medicine, Chungnam National University School of Medicine, Daejeon, Republic of Korea*

Scrub typhus, caused by *Orientia tsutsugamushi*, is characterized by profound lymphopenia during the acute phase, which is closely associated with impaired immune function and disease severity. However, the molecular mechanisms underlying lymphocyte loss remain unclear. This study aimed to elucidate the immunological mechanisms driving lymphopenia in acute scrub typhus and to identify potential therapeutic targets. Peripheral blood mononuclear cells (PBMCs) from patients were analyzed using single-cell RNA sequencing (scRNA-seq) and flow cytometry. Cell-cell interaction analysis based on CellChat was performed to infer apoptosis-related ligand-receptor signaling pathways. The analysis revealed a marked reduction of $CD4^+$ and $CD8^+$ T cells in the acute phase, accompanied by increased expression of TRAIL (TNFSF10) in monocytes and DR4/DR5 (TNFRSF10A/B) in T cells, indicating activation of the extrinsic apoptosis pathway. Furthermore, in a mouse infection model, blocking DR5 signaling with a neutralizing antibody suppressed T-cell apoptosis and significantly improved survival. These findings identify TRAIL-DR4/5-mediated apoptosis as a key mechanism driving lymphopenia in acute scrub typhus and suggest that targeting the extrinsic apoptosis pathway may serve as a promising therapeutic strategy to prevent immune collapse during infection.

S1-4

First Detection of Korean Langya Virus and Evolutionary Characterization of *Parahenipavirus* in Shrews, Republic of Korea

Augustine Natasha[1], Sarah E. Pye[2], Shivani Rajoriya[1], Haryo Seno Pangestu[1], Minsung Lee[1], Daehyun Kim[1], Intae Yang[1], Jieun Park[1], Sarah P. Prayitno,[1] Kyungmin Park[3,4], Jongwoo Kim[3,5], Yeonsu Oh[6], Carolina B. López[2], Jin-Won Song[3,5]*, Won-Keun Kim[1,7]*

[1]*Department of Microbiology, College of Medicine, Hallym University, Chuncheon 24252, Republic of Korea*
[2]*Department of Molecular Microbiology and Center for Women's Infectious Disease Research, Washington University School of Medicine in St. Louis, Missouri, United States of America.*
[3]*Department of Microbiology, Korea University College of Medicine, Seoul 02841, Republic of Korea*
[4]*Institute for Viral Diseases, Korea University College of Medicine, Seoul 02841, Republic of Korea*
[5]*BK21 Graduate Program, Biomedical Sciences, Korea University College of Medicine, Seoul 02841, the Republic of Korea*
[6]*College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, Chuncheon 24341, the Republic of Korea*
[7]*Institute of Medical Science, College of Medicine, Hallym University, Chuncheon 24252, Republic of Korea*

Background
In the Republic of Korea, presence of *Parahenipavirus* species is evidenced by the identification of Gamak virus and Daeryeong virus in shrews. Within the genus *Parahenipavirus*, the only species reported to be zoonotic is Langya virus (LayV). Since its discovery, no LayV detections have been reported outside of China. Surveillance of shrew populations was conducted to uncover other *Parahenipavirus* species.

Materials and Methods
Metagenomic raw reads from our 2017 study were reanalyzed. We then screened RNA extracted from kidney tissues of *Crocidura lasiura* collected during 2019-2024 for paramyxoviruses by PCR. PCR-positive samples underwent partial genome sequencing, and those showing low similarity to prototype *Parahenipavirus* strains were subjected to total-RNA metagenomic sequencing. Complete viral genomes reconstructed by de novo assembly and reference-guided mapping of the metagenomic data were used to design a LayV amplicon-based primer set. Suspected LayV-positive RNAs were amplified using tiled PCR and sequenced on an Oxford Nanopore Technologies platform. Amplicon reads were then mapped to the complete genome obtained from the prior metagenomic analysis. The resulting complete genomes were used to characterize evolutionary patterns via Bayesian phylogenetic inference and selection analyses.

Result
Analysis of the 2017 metagenomic data resulted in two complete paramyxovirus genomes, exhibiting approximately 80% and 95.5% homology at the nucleotide and amino acid levels, respectively, with LayV China. Paramyxovirus screening from 2019 to 2024 samples showed a 44.7% positivity rate, 23 out of 70 (32.8%) positives identified as LayV Korea. Phylogenetic analysis inferred the most recent common ancestor of *Parahenipavirus* at ~2400 years ago. LayV Korea and China inferred to diverge at ~200 years ago. Selection analysis showed predominance of negative selection process in the speciation of *Parahenipavirus*.

Conclusion:
This is the first report of LayV outside China, highlighting cross-border circulation and the recent emergence of *Parahenipavirus*.

S1-5

Role of SaeS in controlling staphyloxanthin biosynthesis in *Staphylococcus aureus*

Eunhwan Bae[1,2], Donggyu Kim[1,2], Minhye Shin[1,2]*

[1]*Department of Microbiology, College of Medicine, Inha University, Incheon, 22212, Republic of Korea*
[2]*Program in Biomedical Science and Engineering, Inha University, Incheon, 22212, Republic of Korea*

Staphylococcus aureus is a major human opportunistic pathogen that causes significant morbidity and mortality, particularly in immunocompromised individuals. SaeRS is a two-component system in *S. aureus* that regulates signal transduction related to virulence, including hemolysis and coagulation. Metal ions are essential for bacterial survival and virulence and are linked to regulatory systems, although the precise molecular mechanisms underlying these links remain unclear. Here, we investigated how SaeRS influences virulence, focusing on oxidative-stress resistance and staphyloxanthin (STX) production. *saeS* deletion reduced STX production via the SigB-CrtOPQMN pathway, increasing vulnerability to oxidative stress and susceptibility to host immune cells. Zinc supplementation suppressed STX-biosynthesis gene expression, thereby diminishing antioxidant capacity in vitro. In a murine bloodstream-infection model, SaeS was critical for *in vivo* bacterial survival; moreover, zinc reduced bacterial virulence and modulated host immune defenses. Collectively, our results reveal a previously unrecognized mechanistic link between SaeRS and staphyloxanthin (STX) biosynthesis and demonstrate that inhibiting SaeRS particularly when combined with zinc supplementation enhances innate immune killing of *S. aureus*.

S1-6

The Potential of C-di-AMP as a Druggable Target for Reversing β-lactam Resistance in MRSA

Ji-Hoon Kim[1], Yunmi Lee[2], Inseo Kim[1], JuOae Chang[1], Subin Hong[1], and Wonsik Lee*

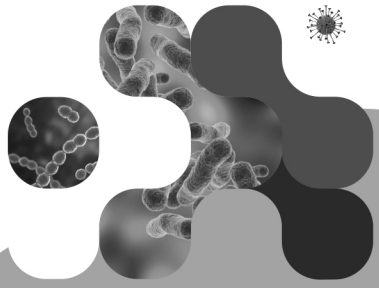
[1]*School of Pharmacy, Sungkyunkwan University*
[2]*Antibacterial Resistance Laboratory, Institut Pasteur Korea*

Cyclic-di-adenosine monophosphate (c-di-AMP) has been implicated in various bacterial physiologies, including osmoregulation and maintaining cell wall integrity. Particularly, the levels of c-di-AMP are known to be related to disruptions in bacterial cell wall homeostasis; however, the mechanisms are not fully understood. We identified a compound that effectively inhibited the growth of *S. aureus* USA300 only in the presence of methicillin, whereas neither the compound nor methicillin alone had observable effects. This synergistic effect was also confirmed in other MRSA strains, such as MW2 and clinical isolates. Furthermore, we showed that the synergistic is specific to β-lactam antibiotics, including cephalosporins, suggesting that the mechanism of action is related to the crosslinking of peptidoglycan (PG) biogenesis in MRSA. In our effort to elucidate the mechanism of action of the compound, we found mutations in the *gdpP* of the resistant mutants. The *gdpP* was inactivated in all the resistant mutants, which would lead to an increase in cellular c-di-AMP levels. Moreover, we demonstrated that the overexpression of *gdpP* led to a decrease in resistance to methicillin in MRSA. Overall, our results demonstrate that intracellular c-di-AMP is important for maintaining the crosslink of PG in *S. aureus*, highlighting c-di-AMP as a novel therapeutic target to overcome the resistance to β-lactams.

S2

New Faculty Session

Chair : Seong-Tshool Hong
Jeonbuk National University



MEMO

S2-1

SARS-CoV-2 viral characteristics and immune responses in normal and immunocompromised patients

Ji Yeun Kim

Hanyang University College of Medicine

The coronavirus disease 2019 (COVID-19) pandemic has become a worldwide crisis, with millions of confirmed cases and deaths. Despite the development of vaccines, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) continues to spread rapidly, making isolation essential to limit transmission and avoid overwhelming healthcare systems. This seminar introduces our investigations into the viral characteristics and immune responses of COVID-19, covering the following subtopics.

Diagnostic usefulness of subgenomic RNA detection

Comparison of viral characteristics between SARS-CoV2 wild type and their variants

Vaccine induced immune responses in accordance to vaccine types

Viral shedding and antibody responses in immunocompromised patients

S2-2

Translational Research for Immunomodulatory and Immunometabolic Therapies Targeting MRSA-Induced Septic Arthritis

Hyuk-Kwon Kwon[1,2], **Francis Y. Lee**[2]

[1]*Division of Applied Life Science, Gyeongsang National University, Jinju, 52828, Republic of Korea*
[2]*Department of Orthopaedics and Rehabilitation, Yale University, School of Medicine, New Haven, CT, 06510, USA*

Background: Septic arthritis represents a major clinical challenge, particularly in aging societies where the incidence of degenerative and infectious joint diseases continues to rise. Elderly individuals are especially susceptible due to immunosenescence, comorbidities, and impaired tissue repair, underscoring the urgent need for effective therapeutic strategies.
Methods and Results: We investigated dual-targeting approaches that address both bacterial persistence and host inflammation, the two major drivers of joint destruction. Local delivery of cell-penetrating antibiotics combined with inhibition of the NLRP3 inflammasome effectively eliminated intracellular *Staphylococcus aureus* while preserving articular cartilage. In parallel, glycolysis was identified as a convergent pathway fueling both methicillin-resistant *S. aureus* (MRSA) proliferation and host inflammatory cascades. Treatment with dimethyl fumarate (DMF), a glycolysis-targeting agent, exerted dual bacteriostatic and anti-inflammatory effects, and in combination with conventional antibiotics, markedly reduced bacterial burden, intra-articular inflammation, and cartilage damage.
Conclusion: These findings highlight a paradigm shift in the management of septic arthritis, emphasizing dual-targeting strategies that may improve outcomes in elderly populations at heightened risk of inflammatory and infectious joint diseases.

S2-3

Spatial Transcriptomics Researches in COVID-19 Non-human Primate Models

Taehwan Oh

Department of Microbiology, College of Medicine, Dankook University

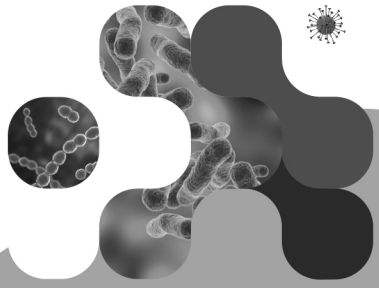
Characterizing the host response to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at the molecular level is necessary to understand viral pathogenesis and identify clinically relevant biomarkers. As the primary interface with the environment, the lungs require a robust local immune defense against pathogens. However, elucidating the molecular basis for pulmonary immune response alterations is challenging owing to the virus's heterogeneous distribution within complex tissue structure. In this study, we utilized Next-generation sequencing- and imaging-based spatial transcriptomics to delineate immune cell composition and tissue architecture formation in the lung and draining lymph nodes during primary infection, convalescence, and reinfection from COVID-19. We revealed the spatial transcriptomic profiles of pulmonary microstructures including inducible bronchus-associated lymphoid tissue(iBALT) at the SARS-CoV-2 infection site in the non-human primate models infected with the Delta and Omicron variants. These findings underscore the importance of identifying key drivers of disease progression and clinically applicable biomarkers by focusing on pulmonary microstructures appearing during emerging SARS-CoV-2 variants infection. This study may aid in understanding the pivotal role of local pulmonary immunity in preventing infection, which may facilitate optimization of vaccine strategies and the development of precise therapeutic interventions in the spatial context.

MEMO

S3

Plenary Lecture

Chair : Hwa-Jung Kim
Chungnam National University



MEMO

S3-PL

From bacteria to cancer and Alzheimer's disease: A winding road journey with *Vibrio*

Joon Haeng Rhee

Department of Microbiology and Combinatorial Tumor Immunotherapy MRC and Clinical Vaccine R&D Center, Chonnam National University Medical School, Hwasun, Korea

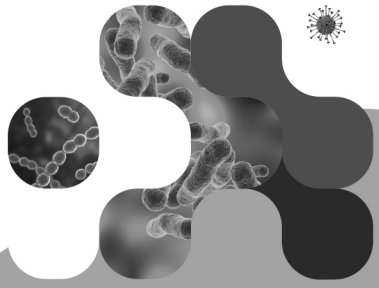
Modern vaccines became safer than old conventional vaccines by improving purity and regulating composition with defined constituents. Consequently, new vaccines confer lower immunogenicity because of the removal of built-in adjuvant components through more refined purification manufacture process. Hence, newly developed vaccines require coformulation with effective adjuvants. TLR ligands are considered attractive adjuvants for vaccines and immunotherapy. Flagellin is the cognate ligand for Toll-like receptor 5 (TLR5) of host cells. TLR stimulation leads to activation of innate immunity and subsequently modulates adaptive immune responses. While studying the host-pathogen interaction in Vibrio vulnificus infection, we came to know that flagellin serves an excellent vaccine antigen as well as potent immunostimulatory component. We later found that flagellin has an excellent adjuvanticity for mucosal vaccines. Mucosal co-administration of a *V. vulnificus* flagellin (FlaB) with microbial antigens induced significantly enhanced antigen-specific IgA responses in both mucosal and systemic compartments and IgG responses in the systemic compartment. Mucosally administered FlaB targets TLR5 expressing $CD11c^+$ DCs in draining lymph nodes and stimulate induction of antigen-specific T and B cell responses. Flagellin could be engineered as a component of built-in adjuvanted vaccines as a fusion partner of antigens or building blocks of multivalent nanoparticle formulations. The built-in adjuvanted vaccines could be further engineered to target antigen presenting cells and enhance cross-presentation resulting in stronger cellular immune responses, which could contribute to the development of potent therapeutic cancer vaccines. FlaB in combination of pathological Tau oligomers induced almost exclusive conformer-specific antibody responses enabling a dramatic inhibition of tauopathy progression, which should contribute to the development of efficacious vaccine against Alzheimer’s disease. We also improved clinical applicability by deimmunization of FlaB employing molecular dynamic analysis.

MEMO

S4

Advances in Mycobacterial Research and Clinical Practice

Chair : Hwa-Jung Kim
Chungnam National University



MEMO

S4-1

CNU P.R.I.D.E. 연구소
Platform for collaborative research between Regional, Industry, academy & research Institute

From Basic Research to Clinical Applications: Functions and In Vivo Relevance of *Mycobacterium tuberculosis* Proteins

Sohkichi Matsumoto[1,2,3,4]

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Mycobacterium tuberculosis (Mtb) is the lethal pathogen in human history, responsible for claiming an estimated one billion lives over the past two centuries. Tuberculosis (TB) remains the leading cause of death among infectious diseases, surpassing COVID-19 once again, with 1.3 million deaths reported in 2023. The global TB pandemic persists, as countless lives continue to be lost that would otherwise have been spared without Mtb infection.

One of the major obstacles in TB control is the phenomenon of bacterial dormancy. Mycobacteria, including Mtb, frequently enter dormant states, during which they acquire drug tolerance, necessitating long treatment regimens of six months to a year. Dormant bacilli can persist for extended periods, and it is estimated that one-quarter of the global population harbors asymptomatic latent Mtb infection. Reactivation of these bacilli is triggered by immune suppression associated with HIV infection, aging, or anti-inflammatory therapies, making this vast population of latently infected individuals a continuous reservoir for new TB cases.

Importantly, only patients with active TB who expel bacilli serve as sources of transmission. Therefore, identifying the risk and likelihood of progression from latent infection to active TB is of paramount clinical significance, as it would enable effective prevention of transmission. However, no reliable diagnostic methods for predicting disease progression currently exist. To achieve a fundamental solution, it is essential to elucidate the mechanisms underlying Mtb dormancy.

Our studies have focused on functional analyses of Mtb proteins expressed during proliferative and dormant phases. We have recently uncovered the potential to utilize these proteins as biomarkers to assess asymptomatic infection and predict disease progression risk. In this symposium, I will present our findings on the functions of Mtb proteins, their in vivo relevance, and the prospects for their clinical application.

S4-2

NTM-PD treatment dilemmas in real-world practice: what physicians struggle with

Hyung-Jun Kim

Seoul National University Bundang Hospital

Nontuberculous mycobacterial pulmonary disease (NTM-PD) is an increasingly recognized chronic lung infection caused by environmental mycobacteria. Although NTM-PD fulfills the criteria of an infectious disease, its clinical course and treatment paradigm diverge significantly from those of classical infections. Physicians often face considerable uncertainty when managing NTM-PD, due in part to the ambiguous distinction between colonization and true disease, the highly variable host susceptibility, and the complex microbiologic features that render the pathogens inherently resistant to many antibiotics.

This lecture will explore the real-world dilemmas clinicians encounter in the diagnosis and treatment of NTM-PD. Topics will include diagnostic challenges such as differentiating active disease from incidental isolation and deciding when to initiate or withhold therapy. Treatment-related struggles will be discussed in depth, including culture non-conversion, treatment failure, antibiotic-related toxicity, and the psychosocial burden of long-term therapy with uncertain benefit. The session will also underscore the limitations of current guidelines when applied to heterogeneous real-world populations and introduce emerging concepts in host-pathogen interaction that may redefine our understanding of NTM as a pathogen.

Understanding the complexity of NTM-PD requires a multidisciplinary perspective. By highlighting these clinical dilemmas, this talk aims to foster closer dialogue between microbiologists and clinicians, ultimately improving patient care through more biologically informed approaches.

S4-3

Tuberculosis Diagnostic Trends in Clinical Laboratories

Namhee Kim

SMG-SNU Boramae Medical Center, Department of Laboratory Medicine

Rapid and accurate identification of *Mycobacterium tuberculosis* (MTB) and early detection of drug resistance, particularly to rifampin, are the cornerstones of tuberculosis (TB) diagnostics in clinical laboratories. Globally, rapid nucleic acid amplification tests (NAATs) are now standard for simultaneous detection of MTB and rifampin resistance (and, in some assays, isoniazid resistance). More recently, next-generation sequencing (NGS) platforms, including targeted NGS (tNGS) and whole-genome sequencing (WGS), have emerged as complementary tools that can interrogate resistance-conferring variants across multiple anti-TB agents and determine the lineage in a single run.

Despite these advances, culture and conventional, culture-based phenotypic drug-susceptibility testing (pDST) remain indispensable. They are critical for definitive confirmation, interpretation of uncertain or novel mutations, assessment of certain drugs, verification of resistance to new agents, and resolving genotype–phenotype discordance.

Clinical laboratories in Korea generally follow this international paradigm. Molecular testing is prioritized at the outset to concurrently establish MTB detection and rifampin resistance. In parallel with clinical assessment and imaging, culture and pDST are pursued to confirm the diagnosis and to expand the resistance profile. Molecular assays do not replace the existing framework; therapeutic decisions are best made by integrating culture and pDST results with molecular findings.

In March 2024, the World Health Organization formally recommended clinical use of NGS and identified it as a priority for further development. Internationally, implementation includes both approved clinical in vitro diagnostic (IVD) solutions and diverse in-house panels. Sequencing capacity is concentrated in the United States, Western Europe, India, and China; some low-resource settings rely on out-of-country sequencing. These data are scalable and can substantially support clinical decision-making.

Within Korea, routine NGS is challenging to operationalize in general clinical laboratories. Adoption tends to be selective and concentrated in tertiary-care hospitals and reference laboratories. While some testing proceeds as research use only (RUO) or as adjunctive clinical testing, most specimens are transported to reference agencies, such as the Korea Disease Control and Prevention Agency (KDCA) and the Korea National Institute of Health (KNIH), primarily for surveillance and epidemiologic investigation. Unfortunately, limited bidirectional feedback and the absence of standardized clinical reporting constrain the use of these NGS results for individual patient management. To incorporate NGS into routine care, practical barriers—reimbursement, instrumentation, specialized personnel, quality management, and standardized reporting—must be addressed.

Session objectives. This lecture will (1) review TB diagnostic and drug-susceptibility testing workflows in Korean clinical laboratories, outlining the characteristics and operational considerations of each method; and (2) summarize current international developments in tNGS/WGS, share application cases and experience, and discuss key considerations for clinical implementation.

S4-4

Pan-lineage *Mycobacterium tuberculosis* reference genome for enhanced molecular diagnosis

Kunhyung Bahk[1], Joohon Sung[1,2,3,4], Mitsuko Seki[5,6], Kyungjong Kim[7,8], Jina Kim[9], Hongjo Choi[10], Jake Whang[7], Satoshi Mitarai[11,12]

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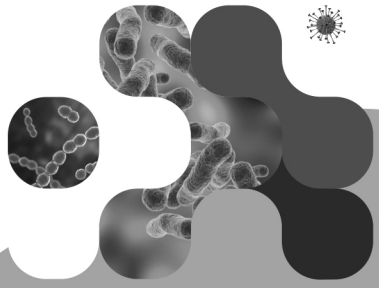
[8]*DNA Analysis Division, National Forensic Service, Ministry of the Interior and Safety, 139, Jiyang-ro, Seoul, 08036, Korea*
[9]*Departments of Urology and Computational Biomedicine, Cedars-Sinai Medical Center, 90048, Los Angeles, CA, USA*
[10]*Division of Health Policy and Management, Korea University, Seoul, 02841, Korea*
[11]*Department of Mycobacterium Reference and Research, Research Institute of Tuberculosis, Japan Anti-Tuberculosis Association, 3-1-24 Matsuyama, Kiyose, Tokyo, 204-8533Japan.*
[12]*Department of Basic Mycobacteriology, Graduate School of Biomedical Science, Nagasaki University, Nagasaki, 852-8523Japan*

In *Mycobacterium tuberculosis* (MTB) control, whole genome sequencing-based molecular drug susceptibility testing (molDST-WGS) has emerged as a pivotal tool. However, the current reliance on a single-strain reference limits molDST-WGS's true potential. To address this, we introduce a new pan-lineage reference genome, 'MtbRf'. We assembled 'unmapped' reads from 3,614 MTB genomes (751 L1; 881 L2; 1,700 L3; and 282 L4) into 35 shared, annotated contigs (54 coding sequences [CDSs]). We constructed MtbRf through: (1) searching for contig homologues among genome database that precipitate results uniquely within Mycobacteria genus; (2) comparing genomes with H37Rv ('lift-over') to define 18 insertions; and (3) filling gaps in H37Rv with insertions. MtbRf adds 1.18% sequences to H37rv, salvaging >60% of previously unmapped reads. Transcriptomics confirmed gene expression of new CDSs. The new variants provided a moderate DST predictive value (AUROC 0.60-0.75). MtbRf thus unveils previously hidden genomic information and lays the foundation for lineage-specific molDST-WGS.

S5

Next-Generation Strategies in Infection Control and Therapeutics

Chair : Yong Woo Jung
Korea University



MEMO

S5-1

충남대학교 CHUNGNAM NATIONAL UNIVERSITY 감염제어 리더연구단

Mechanistic Insights into MRSA β-lactam Sensitization: Role of LTA and RNA Polymerase Mutations

Taeok Bae

Indiana University School of Medicine-Northwest, Gary, Indiana, USA

Antibiotic resistance poses an escalating global health crisis. The development of new antibiotics is urgently needed but faces mounting scientific and economic challenges. An alternative and promising strategy is to restore the efficacy of existing antibiotics that have become ineffective against resistant pathogens.

Methicillin-resistant *Staphylococcus aureus* (MRSA) is among the most clinically significant resistant organisms, characterized by its near-universal resistance to β-lactam antibiotics. This resistance is primarily mediated by penicillin-binding protein 2a (PBP2a), whose active site is inaccessible to most β-lactams. However, recent studies reveal that additional bacterial factors, including lipoteichoic acid (LTA) and RNA polymerase mutations, profoundly influence β-lactam susceptibility. Disruption of LTA synthesis markedly sensitizes MRSA to β-lactams, while specific RNA polymerase mutations restore resistance in these LTA synthesis mutants. However, the molecular basis of this sensitization has remained unclear.

Recently, we found that LTA regulates both cell wall synthesis and degradation through direct binding to key enzymes and by modulating their transcription during active growth. Notably, LTA protects cell wall integrity by preventing premature localization of ScaH, an autolysin, to the cell wall. Furthermore, using suppressor mutation analysis, we show that RNA polymerase mutations restore resistance by reducing transcription of a mechanosensitive channel protein. This channel protein influences intracellular potassium levels, alters c-di-AMP signaling, and may regulate PBP4, a critical cell wall synthesis enzyme.

Together, these findings reveal novel pathways linking teichoic acid metabolism, ion homeostasis, and cell wall regulation to MRSA β-lactam resistance. By uncovering previously hidden vulnerabilities, this work provides a foundation for developing therapeutic strategies aimed at re-sensitizing MRSA to β-lactam antibiotics and reviving their clinical utility.

S5-2

Harnessing CRISPR Adaptation Systems for Directional Molecular Recording Technologies

Sungchul Kim

Department of Life Sciences, POSTECH, Pohang, Gyeongbuk, 37673 Republic of Korea

CRISPR-Cas adaptive immunity protects prokaryotes from foreign genetic elements, such as bacteriophages and plasmids, by employing the highly conserved Cas1-Cas2 complex to establish inheritable memory in the form of spacers. These spacers are acquired from cellular DNA fragments (prespacers) and integrated into the CRISPR array, enabling RNA-guided interference pathways for targeted immunity. While the mechanisms of prespacer acquisition and orientation-specific integration remain incompletely understood, recent advances utilizing single-molecule fluorescence imaging have revealed that Cas1-Cas2 captures prespacers in diverse forms, including single-stranded DNA and partial duplexes, through a selection process dependent on DNA length and protospacer adjacent motifs (PAMs). Additionally, DnaQ exonucleases have been identified as key enzymes that process Cas1-Cas2-bound precursor prespacers into integration-competent sizes. Cas1-Cas2 protects PAM sequences from exonuclease activity, ensuring the production of asymmetrically trimmed prespacers and their integration in the correct orientation. This kinetic coordination between prespacer selection and PAM trimming provides a mechanistic framework for understanding functional spacer integration. In some CRISPR-Cas systems, particularly RNA-targeting type III systems, Cas1 is fused with reverse transcriptase (RT), enabling the RT-Cas1-Cas2 complex to acquire RNA transcripts for spacer acquisition. This unique adaptation highlights the potential of RT-fused Cas1-Cas2 as a directional RNA-recording tool, expanding the scope of CRISPR-based applications. Current studies on the molecular structure and function of RT-Cas1-Cas2 integrase underscore its promise for innovative technologies, such as molecular recording and genome engineering. However, key questions remain regarding the mechanisms of RNA acquisition and integration by RT-Cas1-Cas2, as well as its broader applicability across diverse CRISPR-Cas subtypes. Future research into RT-fused Cas1-Cas2 systems and their RNA-recording capabilities will not only deepen our understanding of CRISPR adaptation but also unlock new possibilities for biotechnological and biomedical applications.

S5-3

Overcoming BCG Limitations: DC-Based Booster and Therapeutic Strategies Against TB

Jong-Seok Kim

Department of Cell Biology, Konyang University College of Medicine

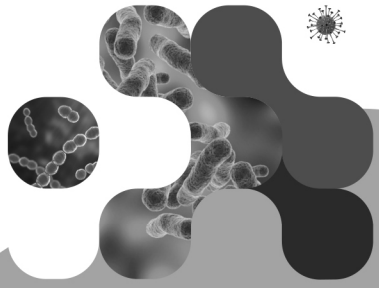
The limited efficacy of Bacillus Calmette-Guérin (BCG) vaccination and prolonged, costly tuberculosis (TB) treatment highlight the urgent need for improved strategies. We investigated whether dendritic cell (DC)-based vaccines pulsed with *Mycobacterium tuberculosis* (Mtb) culture filtrate antigens (CFA) could boost BCG-induced immunity and support chemotherapy. In BCG-vaccinated mice, adoptive transfer of CFA-pulsed DCs rapidly enhanced T cell recruitment into the lung parenchyma, reducing bacterial burden within 1 week post-infection. This response promoted tissue-resident memory formation and expansion of multifunctional $CD4^+$ T cells co-producing IFN-γ, IL-2, and TNF-α. The protective effect was sustained in both high- and low-dose Mtb infection models. Furthermore, CFA-DC administration during chemotherapy improved treatment efficacy while maintaining robust $CD4^+$ T cell responses. In latent TB models, this approach prevented reactivation of both drug-sensitive and multidrug-resistant strains. These findings suggest that DC-based prophylactic and therapeutic vaccines may overcome BCG limitations and enhance TB control when combined with standard treatments.

MEMO

S6

Innovative Vaccine Development using Cutting-Edge Technology

Chair : Joon Haeng Rhee
Chonnam National University



MEMO

S6-1

A built-in adjuvanted ferritin nanocage mucosal vaccine against *Streptococcus pneumoniae*

Tien Duc Nguyen[1], Giang Chau Dang[1], Yoonjoo Choi[1], Joon Haeng Rhee[1], Shee Eun Lee[2]

[1]*Chonnam National University Medical School*
[2]*School of Dentistry Chonnam National University*

Protein nanocages are multimeric structures that can be engineered to mimic the molecular conformation of microorganisms. Based on our previous finding that a mucosal FlaB-tPspA fusion vaccine (flagellin fused with truncated PspA antigen of *Streptococcus pneumoniae*) induces protective immune responses against *S. pneumoniae*, we developed a ferritin nanocage vaccine displaying both antigen and adjuvant multivalently on a nanocarrier via the SpyTag/SpyCatcher strategy. This 1:1 antigen/adjuvant nanocage was used as a mucosal vaccine capable of efficiently translocating to draining lymph nodes, showing superior delivery efficiency compared with the fusion vaccine. Intranasal immunization with the nanocage vaccine markedly enhanced mucosal immune responses, promoted efficient B-cell memory formation and antibody maturation, and induced more balanced Th1/Th2 responses with elevated IFN-γ and IL-17 production compared to the fusion vaccine. Mice immunized with the nanocage vaccine exhibited significantly enhanced protection against lethal pneumococcal infection compared to the FlaB-tPspA fusion group. Collectively, our study demonstrates the effectiveness of this all-in-one ferritin nanocage-based mucosal vaccine platform, which ensures enhanced protection and balanced immune responses.

S6-2

Kinetically-activating nanoadjuvant empowers broad and persistent antiviral immunity

Yong Taik Lim

Department of Nano Engineering, SKKU Advanced Institute of Nanotechnology (SAINT), School of Chemical Engineering, and Biomedical Institute for Convergence at SKKU, Sungkyunkwan University, Suwon, Republic of Korea

Rationally designed immunomodulatory materials can induce potent and persistent immune responses as well as minimize immune-related toxicities. Recently, taking cues from pathogen infection, our research group has developed a novel type of immunomodulatory system which integrated innate stimuli in the context of time, order, and duration. In this talk, I would like to present the representative immunological characteristics of the newly developed immunomodulatory system and discuss the prospects of it as a next-generation vaccine adjuvant system, which can provide design strategy for synchronous and dynamic tailoring of innate immunity. Based on newly developed timely-activating TLR7/8a, we suggest several engineered nanoadjuvant systems that can synergize innate stimuli as well as evoke germinal centre B cells and polyfunctional T cells via multiscale kinetic immunomodulation through clinically approved platform. Engineered nanoadjuvants demonstrate cross-protection against diverse influenza, SARS-CoV-2 variants, and SFTSV, demonstrating long-term and broad protective immunity against emerging pandemic and epidemic infectious viruses.

S6-3

Development of a Decentralized System for mRNA vaccine production (DeCAFx) to Strengthen Pandemic Preparedness.

Sang Hwan Seo

Director, Science Unit
International Vaccine Institute

The COVID-19 pandemic demonstrated the promise of mRNA vaccines as a rapid-response platform, while also revealing critical gaps in global manufacturing capacity, equitable access, and timely deployment. To address these challenges and enhance preparedness for future pandemics, the International Vaccine Institute (IVI) is leading the development of DeCAFx—a *Decentralized and Accelerated mRNA Vaccine Production System*. DeCAFx is designed to enable scalable, regionally distributed, and time-sensitive mRNA vaccine manufacturing through modular infrastructure, standardized technologies, and pre-established technical partnerships.

Aligned with global initiatives such as CEPI's 100 Days Mission, DeCAFx aims to ensure vaccine production and distribution within weeks of pathogen identification. As part of this effort, IVI is advancing mRNA vaccine R&D through a global network of collaborators. These include prototype vaccines against Lassa fever (with SK bioscience) and Rift Valley fever (with Afrigen), platform validation using self-amplifying mRNA (with Karolinska Institute), and novel delivery systems such as microneedle patches (with QuadMedicine). IVI is also validating UTR-modified mRNA constructs (with Seoul National University) and evaluating an mRNA COVID-19 vaccine developed by Green Cross under KDCA support.

Through DeCAFx, IVI aims to integrate technological innovation, regional manufacturing, and regulatory readiness to build a sustainable and equitable vaccine ecosystem capable of responding rapidly to future pandemic threats.

S6-4

$CD8^+$ T cell differentiation after COVID-19 mRNA vaccination

Eui-Cheol Shin

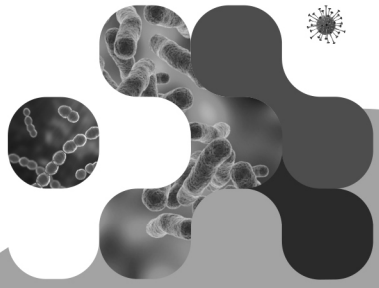
Graduate School of Medical Science and Engineering, KAIST, Daejeon, Republic of Korea

During the COVID-19 pandemic, mRNA-based SARS-CoV-2 vaccines were developed and clinically used at an unprecedented pace as an urgent response to the pandemic. Even though COVID-19 vaccination has been performed in large populations in many countries, new variants of concern (VOCs) and subvariants have been emerging continuously. Although antibodies elicited by vaccination exhibit significantly reduced neutralizing activities against new VOCs, vaccine-induced memory T cells substantially respond to VOCs (Jung MK et al. *Nat Microbiol* 7:909, 2022 and Noh JY et al. *Nat Rev Immunol* 21:687, 2021). During the pandemic, my lab demonstrated that SARS-CoV-2 infection or mRNA vaccination successfully generates $CD8^+$ stem cell-like memory T (T_{SCM}) cells which have the capacity for self-renewal and multipotency to repopulate the broad spectrum of memory and effector T cell subsets (Jung JH et al. *Nat Commun* 12:4043, 2021). Additionally, my lab also showed that mRNA vaccine-induced T_{SCM} cell generation significantly correlates with the longevity of $CD8^+$ memory T cell responses (Jung S et al. *Cell Rep* 40:111138, 2022). Furthermore, my lab examined effect of multiple mRNA vaccinations on $CD8^+$ T cell differentiation and found that memory $CD8^+$ T cells progressively gained a senescent-like T_{EMRA} cell phenotype after repeated mRNA vaccinations although the frequency and cytokine-producing effector functions of memory $CD8^+$ T cells were boosted. In this lecture, I will give a talk about $CD8^+$ T cell differentiation to T_{SCM} or T_{EMRA} and its clinical implication in the context of COVID-19 mRNA vaccinations.

S7

Special Lecture

Chair : Eun-Kyeong Jo
Chungnam National University



MEMO

S7-SP

Metabolic perspectives on the Evolution of Multidrug Resistance in Mycobacteria

Hyungjin Eoh

Department of Immunology and Immune Therapeutics (IIT), Keck School of Medicine, University of Southern California, Los Angeles, CA, USA

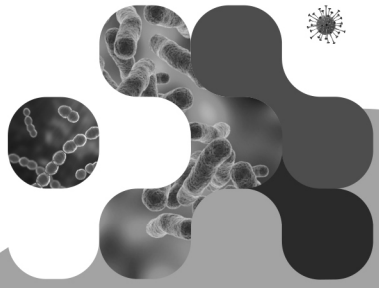
Multidrug-resistance (MDR) in bacteria often develops through the repetitive formation of drug- tolerant persisters, which survive antibiotics without genetic changes. Recent studies highlight changes in trehalose metabolism as crucial for persister formation and drug resistance in *Mycobacterium tuberculosis* (Mtb). In the present study, we observe that mutants lacking trehalose catalytic shift exhibited fewer MDR mutants due to decreased persisters. This catalytic shift enhances Mtb survival during antibiotic treatment by increasing metabolic heterogeneity and drug tolerance, facilitating MDR. Rifampicin (RIF) single-resistant bacilli display cross-resistance to other antibiotics linked to higher trehalose catalytic shift, explaining how MDR can follow RIF single-resistance. In particular, the lineage 2 clinical strain exhibits higher trehalose catalytic shift, increasing MDR risk. Both genetic and pharmacological inactivation of this shift reduces persister formation and MDR development, suggesting trehalose catalytic shift as a potential therapeutic target to combat MDR-TB.

MEMO

S8

One Health Approach to Campylobacter Infections

Chair : WOO KON Lee
Gyeongsang National University



MEMO

S8-1

Campylobacter: a major pathogen of foodborne enteritis

Seok Hoon Jeong

Department of Laboratory Medicine, Gangnam Severance Hospital, Yonsei University College of Medicine

Campylobacter is a genus of Gram-negative bacteria. It appears as curved or comma-shaped rods as its name means 'curved bacteria', and is able to move using unipolar or bipolar flagella. The best condition for its growth is between 37 and 42°C in a microaerophilic environment. *Campylobacter* is frequently found in raw food of animal (especially birds) origin and vegetables, and more than ten species of the genus have been implicated in human gastroenteritis. *C. jejuni* and *C. coli* have been identified as the most frequent pathogens for human among the species of the genus. And the genus has become one of the most common causes of gastroenteritis in South Korea with non-typhoidal *Salmonella*. This presentation will provide an overview of the current situation and countermeasures concerning *Campylobacter* enteritis in South Korea.

S8-2

Campylobacteriosis: Pathogenesis and Control Strategy

Jang Won Yoon

College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, Chuncheon, Gangwon State 24341, Republic of Korea

Campylobacter jejuni and the related species are the leading cause of enterocolitis in humans and animals. The clinical spectrum due to the disease ranges from a mild, non-inflammatory, and watery diarrhea in general to a severe inflammatory diarrhea. Among the species, *C. jejuni* and *C. coli* are most responsible for food-borne illnesses worldwide. Despite their importance in public health, our understanding how they cause the disease and interact with their hosts during the gastrointestinal tract (GIT) infection is limited due to the absence of appropriate infection models. In addition, there is no established virulence factors which were found in other enteric bacterial pathogens. In this presentation, the recent progress on the pathophysiology of *C. jejuni* and *C. coli* in the GIT will be summarized and discussed to improve our knowledge about how they survive and respond to against host defences. As an intervention strategy, one health approach will be introduced to control campylobacteriosis in humans and animals.

S8-3

Development and application of a new isolation method for *Campylobacter* spp.

Jonghyun Kim

Division of Zoonotic and Vector-borne Disease Research, Center for Infectious Diseases Research, National Institute of Health, Cheongju, South Korea

Campylobacter spp. are often the most common causative agent of gastroenteritis in developed countries, with an estimated 166 million people infected worldwide. *Campylobacter* infection has multiple potential sources; in particular, a high risk of infection occurs with handling raw poultry and eating undercooked chicken. *Campylobacter* are the second leading cause of known food poisoning due to bacterial pathogens in Korea. *Campylobacter* spp. identification from patient stool samples is difficult because of the specific media and culture conditions required. The isolation and cultivation of *Campylobacter* spp. are difficult because they require a microaerophilic environment and a specific medium; moreover, maintaining this pathogen in culture is more difficult compared to other gram-negative bacteria. The most problematic aspect is that the positive culture rate of *Campylobacter* spp. decreases in inverse proportion to the time the sample is exposed to oxygen. Therefore, this study is expected to improve confirmation of *C. jejuni* infection where diagnosis would previously fail with patient samples because of oxygen exposure, inappropriate diagnostic methods, and interference from other bacteria in the sample. In this study, we developed a rapid and sensitive isolation and detection method by combining *Campylobacter* (Campy)-IMS with PCR for the identification of live *Campylobacter jejuni* in human stool specimens

S8-4

Campylobacter jejuni and Guillain-Barré syndrome in Korean patients

Byeol-A Yoon, Jong Kuk Kim

Department of Neurology, Dong-A University College of Medicine

Introduction:
Guillain-Barré syndrome (GBS) is known to be triggered by preceding infections, particularly by *Campylobacter jejuni* (*C. jejuni*). However, real-world data on *C. jejuni* infections in Korean GBS patients remain unavailable. The aim of this study was to determine the prevalence of *C. jejuni*-associated GBS in Korea and to investigate the clinical significance of the patients.

Methods:
We prospectively recruited GBS patients from 11 referral centers in Korea from September 2023. Acute-phase serum samples were tested for IgG, IgA, and IgM antibodies against *C. jejuni* lipooligosaccharides (LOS) and IgG and IgM antibodies against 11 types of gangliosides. The results were then compared with patients' clinical and laboratory findings.

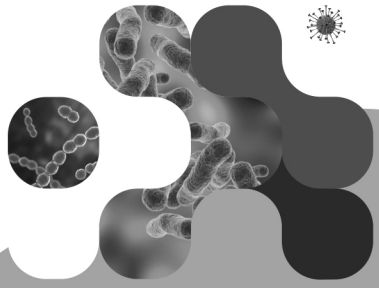
Results:
A total 111 GBS patients were enrolled, of whom 61 were male (55%). The median age of the patients was 62.5 years (range 21-90). Among patients with available data, 81 (78%) had a history of previous infection. Upper respiratory infection (46%) was most common, followed by gastrointestinal infection (43%). Patients with prior vaccination or COVID-19 infection were also included in the analysis. A total 61 patients (55%) tested positive for at least one of IgG, IgA, or IgM antibodies against *C. jejuni* LOS (here after, anti-*C. jejuni* antibody), and 64 patients (58%) were positive for anti-ganglioside antibodies. The MRC sum socre at the nadir was significantly lower in patients positive for anti-*C. jejuni* antibody, indicating more severe initial symptoms. Nevertheless, there was no significant differences between the groups at 3 and 6 months after onset.

Conclusions:
In conclusion, Korean GBS patients exhibited a higher prevalence of gastrointestinal infection history and frequently detected *anti-C. jejuni* antibodies and anti-ganglioside antibodies, compared to other international studies. These findings could explain the reason why Korean GBS patients have various subtypes. Patients with *C. jejuni*-associated GBS presented with more severe symptoms, but their long-term outcomes did not differ from those of other patients.

S9

Journal of Bacteriology and Virology Academic Award
JBV저널 학술상

Chair : So-Youn Woo
Ewha Womans University



MEMO

S9-1

CHAP^{SAP26}-161, A Truncated Protein and Enzymatic Active Domain of Endolysin LysSAP26, as a Potential Therapeutic Agent to Combat *Clostridioides difficile* Infection

Ram Hari Dahal†, Yoon-Jung Choi†, Shukho Kim, Jungmin Kim*

Department of Microbiology, School of Medicine, Kyungpook National University, Daegu 41944, Republic of Korea
†These authors have contributed equally to this work and are co-first authors

Clostridioides difficile is a spore-forming enteric pathogen that causes life-threatening diarrhea and colitis. Notably, *C. difficile* infection (CDI) is a major healthcare-associated infection with increasing incidence and morbidity rates. Antibiotic-induced microbial disruption has been linked to susceptibility to CDI transmission and relapse. Therefore, alternative therapeutic approaches that effectively prevent *C. difficile* growth and spore germination are urgently needed. Bacteriophage-derived en- dolysins and their derivatives have recently shown potential as novel antibacterial agents. Hence, this study aimed to investigate the efficacy of a novel truncated cysteine-histidine-dependent amidohydrolase/peptidase (CHAP) modular endolysin, CHAP^{SAP26}-161, in combating CDI. *In vitro* studies demonstrated its potent bacte- ricidal activity against several clinically relevant *C. difficile* strains, including toxin A- and toxin B-producing and nontoxigenic strains. CHAP^{SAP26}-161 exhibited rapid and specific killing activity, thereby significantly reducing *C. difficile* colony-forming units. Furthermore, in a murine CDI model, CHAP^{SAP26}-161 treatment remarkably reduced *C. difficile* burden and clinical symptoms, such as diarrhea and weight loss. In histopathological analysis, colonic inflammation and tissue damage decreased in CHAP^{SAP26}-161-treated mice compared with that in the control group. More- over, no cytotoxic effects were observed on the A549 cell line, indicating that CHAP^{SAP26}-161 is safe as a therapeutic agent. These findings highlight that CHAP^{SAP26}-161 is a promising treatment option for CDI. Importantly, preclinical and clinical studies are warranted to fully evaluate the therapeutic potential of CHAP^{SAP26}-161 and its possible implementation in clinical practice.

S9-2

Lung Organoids from Human Embryonic Stem Cells to Investigate Pneumococcal Serotype 23F that does not Infect Mouse

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Streptococcus pneumoniae (*S. pneumoniae*, Pneumococcus) is a predominant patho- gen in community-acquired pneumonia. Infection animal models using certain pneu- mococcal serotypes are well established, but some serotypes, such as ST14 and ST23F, exhibit low or negligible infectivity in mouse models, posing challenges for the development of comprehensive pneumococcal vaccines. In this study, we developed human lung organoids (hLOs) derived from human embryonic stem cells (hESCs) to model pneumococcal infection. hLOs were microinjected with serotype ST23F to assess its infective potential compared with ST4. Our results demonstrate that ST23F successfully colonizes and invades the epithelial cells of hLOs, triggering significant inflammatory responses. This response was quanti- tatively comparable to that induced by the highly virulent serotype ST4 in mouse models. This organoid-based infection model provides a viable and effective platform for studying pneumococcal serotypes that are inadequately represented in traditional mouse models. Furthermore, it underscores the potential utility of hLOs in the preclinical evaluation of novel multivalent pneumococcal conjugate vaccines, addressing serotypes with historically low virulence in animal models.

S9-3

Transcription Profiling Signatures Distinguishing RSV Infection in Humans

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Respiratory syncytial virus (RSV) is a major global health threat, causing severe respiratory illness in young children, the elderly, and individuals with chronic lung conditions. Despite its high morbidity and mortality, effective treatments remain lacking. RSV infection initiates in the respiratory tract, primarily targeting airway epithelial cells (AECs), which act as the first line of defense against pathogens. Upon entering the nasal passages, the virus spreads to the lower respiratory tract, where it replicates, leading to inflammation and epithelial damage, including cell shedding, mucus overproduction, and impaired ciliary function. RSV replication in both upper and lower airway epithelial cells exacerbates disease severity. A better understanding of AECs' role during viral infection is crucial for advancing RSV research, especially given their function as a barrier to severe disease progression. Studies using upper and lower airway epithelial cell systems have revealed key insights into antiviral mechanisms. Moreover, systems biology approaches, such as transcriptional profiling, provide valuable insights into virus-specific molecular pathways and immune responses to RSV infection. In particular, the transcrip- tional analysis of age-specific patient samples is increasingly recognized as essen- tial for understanding the pathogenesis of RSV, as gene expression and signaling responses can differ across age groups. Here, we present a comprehensive summary of the current state of knowledge regarding the available publicly accessible data from transcriptional profiling studies related to RSV infection, aiming to better understand the transcriptional changes and cellular responses triggered by RSV infection.

S9-4

Contemporary insights into non-typhoidal *Salmonella*: Understanding the pathogenicity, infection mechanisms, and strategies for prevention and control

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Salmonella is a foodborne zoonotic pathogen that causes diarrheal disease in humans through the consumption of contaminated water, animal products, or plant-based foods. This bacterium infects a diverse range of hosts, including birds, reptiles, and mammals (including humans) and ranks as the third leading cause of death from diarrheal diseases globally. Salmonellosis, caused by *Salmonella*, remains a serious public health concern, requiring integrated interventions to control its spread. Despite extensive research on the pathogenicity and mechanisms of infection of *Salmonella*, salmonellosis outbreaks remain a global threat. This study provides an overview of *Salmonella* pathogenicity, infection mechanisms, and prevention and control strategies.

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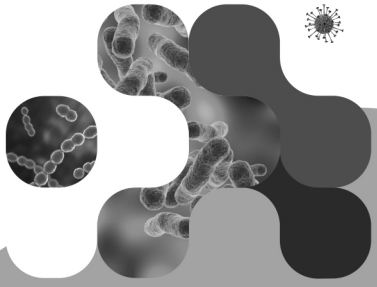
Poster Session

PB (Poster Bacteria)
PI (Poster Infection Immunology)
PVM (Poster Viruses and miscellanies)



MEMO

PB-2

Association between gut microbiome and atopic dermatitis

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Accumulating evidence implicates a pivotal "gut-skin axis" in atopic dermatitis (AD). Cross-sectional and longitudinal studies consistently associate AD with reduced early-life microbial diversity, an altered Bacteroidetes/Firmicutes ratio, and depletion of butyrate-producing taxa. These compositional shifts coincide with lower short-chain fatty acids (SCFAs), impaired tight-junction integrity, and mucosal immune skewing toward Th2/Th17 with diminished Treg function. Disruption of tryptophan-derived aryl hydrocarbon receptor (AHR) ligands and secondary bile acids further modulates epidermal inflammation and barrier repair. Interventional studies indicate that selected probiotics, synbiotics, and postbiotics may reduce AD risk or improve EASI scores and pruritus in subsets of patients; however, heterogeneity in strains, dosing, timing, and endpoints limits generalizability. Early signals from fecal microbiota transplantation and targeted metabolite supplementation suggest feasibility but require rigorous validation. Overall, AD is robustly linked to gut dysbiosis through barrier, metabolic, and immune pathways. Priorities for future randomized trials include standardized outcomes, mechanism-guided strain or metabolite selection, and patient stratification by age, endotype, and baseline microbiome to enable reproducible, personalized microbiome-based therapeutics for AD.

PB-3

Comparison of REA protein and DNA vaccine-induced protection against *Mycobacterium tuberculosis*

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Mycobacterium tuberculosis (Mtb) remains a major global health concern, causing over 1.3 million deaths in 2022. The only licensed vaccine, BCG, provides limited protection against pulmonary TB. To develop a more effective vaccine, we designed an REA-based construct composed of three Mtb antigens.
A thiolated DNA fragment encoding REA was generated by PCR and conjugated to gold nanoparticles (AuNPs) to create the NES-DNA-REA-Vx formulation. Immunofluorescence confirmed successful intracellular transcription of the DNA in macrophages, accompanied by immune activation.
Mice immunized three times at two-week intervals with REA-protein or REA-DNA vaccines were challenged intratracheally with Mtb and analyzed at 6 and 16 weeks post-infection. Both vaccines elicited strong Th1-biased responses and reduced bacterial burdens in lungs and spleens. Notably, the DNA vaccine induced higher IgG2a/IgG2b titers and maintained stronger long-term protection.
These findings highlight the REA-DNA vaccine as a promising next-generation candidate for enhanced protection against tuberculosis.

PB-4

Unveiling Genomic Insights from the Gut: Whole Genome Sequencing of Three Novel Fecal Bacterial Isolates

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The human gut microbiome harbors immense microbial diversity, with many members remaining uncultured and taxonomically unclassified. In this study, we employed anaerobic culturing to isolate three novel bacterial strains from fecal samples and performed whole-genome sequencing (WGS) for comprehensive characterization. Initial 16S rRNA gene analysis suggested these isolates were previously unclassified, showing sequence identities below the species-level threshold. Subsequent phylogenomic and comparative genomic analyses confirmed their novelty, revealing distinct genomic signatures and no matches in established MLST databases. Genomic screening with RefSeqMasher and the Comprehensive Antibiotic Resistance Database (CARD) identified antimicrobial resistance -associated loci, while virulence potential was assessed using the Bacannot pipeline and the Virulence Factor Database (VFDB). Two isolates lacked virulence determinants, whereas one harbored homologs of known virulence proteins. Analysis of mobile genetic elements further highlighted the dynamic genomic architecture of these strains. Collectively, our findings demonstrate the utility of WGS for characterizing unclassified gut microbes, providing insights into their functional potential, resistance profiles, and evolutionary relationships. These results expand our understanding of gut microbial diversity and offer new opportunities for microbiome-based diagnostics and therapeutics.

PB-5

Antibiotic-Induced Growth Rate Suppression as Prognostic Marker in NTM Pulmonary Disease

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Background: Nontuberculous mycobacterial pulmonary disease (NTM-PD) represents a major therapeutic challenge due to the need for prolonged antibiotic regimens, high relapse rates, and the lack of reliable prognostic biomarkers. In *Mycobacterium tuberculosis*, antibiotic exposure has been shown to trigger metabolic slowdown, an early event in the development of drug resistance. We hypothesized that a similar mechanism occurs in NTM-PD and investigated the relationship between antibiotic-induced changes in growth rate and clinical outcomes.
Methods: Clinical isolates from the multicenter NTM-KOREA cohort were analyzed before and after antibiotic exposure. Growth dynamics were evaluated by measuring optical density (OD) at days 7, 14, and 21, and validated using the Mycobacteria Growth Indicator Tube (MGIT) system. Patients were categorized into treatment success, failure, and recurrence groups, and growth rate differences were compared statistically.
Results: Isolates from the treatment failure group exhibited significant OD reductions after antibiotic exposure at all time points (day 7, $p < 0.0001$; day 14, $p < 0.01$; day 21, $p < 0.05$), indicating marked metabolic suppression. In contrast, isolates from the success and recurrence groups showed no significant growth reduction. MGIT-based analyses confirmed these findings, demonstrating consistent growth inhibition in failure cases. These results suggest that reduced growth rates following antibiotic exposure are strongly associated with treatment failure and may serve as an early indicator of emerging resistance.
Conclusion: Antibiotic-induced growth suppression in NTM clinical isolates is closely linked to unfavorable treatment outcomes, underscoring its potential as a prognostic biomarker. Growth rate analysis could serve as a practical diagnostic tool for predicting treatment failure and guiding personalized therapeutic strategies in NTM-PD.

PB-6

Therapeutic Targeting of *Pseudomonas aeruginosa* Virulence Factors in Bacterial Scleritis Using a Novel Hagfish-Derived Antibody Platform

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Recently, ocular infections due to indiscriminate use of steroid eye drops and neglect of contact lens management are on the rise. The infectious diseases cause a high probability of blindness during treatment and clinically poor prognosis. As *Pseudomonas aeruginosa* is a major pathogen of infectious eye disease among Gram-negative bacteria, a study is essential on the virulence factors of *P. aeruginosa* affecting ocular infection. This study aimed to characterize clinically relevant virulence factors of *P. aeruginosa* isolated from ocular infections and to identify and therapeutically target them using an eel-derived antibody platform. By integrating the characteristics of the ocular infection-causing bacteria and the clinical symptoms of these patients, we finally attempted to determine the virulence factors of *P. aeruginosa* that contribute to ocular infections. In the present study, *P. aeruginosa* was isolated from patients at Gyeongsang National University Hospital over the past 5 years and was divided into two groups: ocular (15 strains) and other (13 strains, including 1 reference strain) infections. Bacterial genotypes were confirmed using a multiplex PCR method for the major genes encoding toxins, pigments, motility, and enzymes. Most of these genes were present, or there was no difference in prevalence rate between the groups. Motility and enzymatic activity were measured in size of diameter and area on agar plates. The *P. aeruginosa* derived from ocular infection showed higher motility (swimming and twitching) and enzymatic activity (protease and lecithinase) than other infections. Among clinical signs of scleritis, the size of the scleral necrosis area showed a moderate correlation with twitching, lecithinase activity, and invasiveness. Furthermore, the presence of multifocal scleral abscesses was associated with a strong negative correlation with protease activity. We focused on twitching, which showed the most significant difference among bacterial traits in the ocular infection group compared to others. Since twitching motility occurs through the extension and retraction of type IV pili, an antibody (ccombody) was produced targeting PilA, a core pili structure, using a hagfish-derived antibody platform. This ccombody inhibited twitching in *P. aeruginosa* but didn't show significant differences in cell invasiveness and cytotoxicity. This study confirmed the potential of ccombody as a therapeutic agent, and further cell-based validation is planned by producing ccombodies with different epitopes.

PB-7

Computerized Region of Interests Detection for Single-Bacterial Metabolic Analysis Using Intracellular Dynamics-Resolved Rayleigh Scattering

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Understanding the physiological status of bacterial cells is crucial for microbiology and antibiotic research. Conventional approaches require labeled probes or targeted staining, which can perturb metabolism or limit long-term observation. Intracellular Dynamics-Resolved Rayleigh Scattering (IDRS) offers a label-free alternative, enabling real-time characterization of bacterial metabolic states. However, standard analyses rely on manual Region of Interest (ROI) selection, which is time-consuming, subjective, and prone to inconsistency.
To address this, we developed an automated algorithm for quantitative monitoring of single-cell metabolic activity in IDRS images. Individual scattering signals were identified as blobs, and blob-level ROIs were automatically detected. Multiple blobs from the same cell were combined into clusters representing single bacteria.
Validation on bacterial time-lapse videos demonstrated that the algorithm outperforms manual ROI selection in speed, consistency, and accuracy. It reliably detects multiple ROIs per cell, separates closely adjacent bacteria, and supports real-time processing across large datasets. Resulting labeled data can be used to train deep learning models, facilitating automated analysis of bacterial metabolism and antibiotic susceptibility.
This framework provides a robust, scalable solution for label-free single-bacterial metabolic analysis, minimizing subjective bias and enabling high-throughput studies across multiple bacterial species.

PB-8

Swine Erysipelas in Korea: Domestic Occurrence and Biochemical Characteristics of Porcine Isolates

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Erysipelothrix rhusiopathiae is the causative agent of swine erysipelas, which leads to septicemia, skin lesions, endocarditis, and arthritis, as well as economic losses in pig farming. It is also a zoonotic pathogen that can cause erysipeloid, meningitis, and endocarditis in humans. In Korea, sporadic outbreaks of swine erysipelas have been reported in provinces such as Chungnam, Jeju, and Gyeonggi over the past five years, and a total of four human cases have been documented since 1986. This study confirmed the biochemical characteristics of five *E. rhusiopathiae* isolates from pigs in Korea and presented them in relation to domestic outbreaks and human infection cases. The domestic occurrence of swine erysipelas over the past five years (2020-2024) was investigated using data from the Korea Animal Health Integrated System (KAHIS), and human infections with *E. rhusiopathiae* over the past 20 years (2000-2020) were reviewed from published case reports. Five isolates of *E. rhusiopathiae* (three from blood in 2008, and two from liver and spleen in 2019) were examined. Biochemical tests included catalase, esculin hydrolysis, gelatin liquefaction, and triple sugar iron (TSI) agar reaction. Between 2020 and 2024, a total of 33 outbreaks of swine erysipelas involving 56 pigs were reported in Korea, with the highest number of cases occurring in Chungnam Province (15 outbreaks). Four human cases were reported, presenting with diverse clinical manifestations such as endocarditis, septicemia, meningitis, and peritonitis; all recovered after treatment with β-lactam antibiotics. Biochemical assays of the five porcine isolates showed negative results for catalase, esculin hydrolysis, and gelatin liquefaction, while TSI agar demonstrated positive H2S production. Swine erysipelas in Korea continues to occur sporadically and can be transmitted to humans as a zoonotic disease. The five isolates analyzed in this study exhibited typical biochemical characteristics of *E. rhusiopathiae*. Theses findings highlight the need for continuous surveillance of swine erysipelas outbreaks and monitoring of human infection cases.

PB-9

The differential effect of plasma-activated water on oral pathogenic bacteria and on beneficial bacteria

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Background Plasma-activated water (PAW) produced by exposing atmospheric pressure plasma shows antibacterial effects; however, the oral applicability of PAW as an oral disinfectant has not been well studied.
Objectives We aimed to investigate the antibacterial effects of PAW on oral pathogens and beneficial bacteria, as well as its safety in human oral cell lines.
Methods We generated PAW using a microwave plasma system. The viability of the post-treated bacteria with PAW was evaluated by monitoring their growth in the broth and by counting their colonies on agar plates. The cytotoxic effects of PAW were assessed in oral squamous carcinoma cell lines (HSC-2, Ca9-22, and YD-10B) using MTT assay and propidium iodide labeling assay.
Results The antibacterial effect of PAW was examined on oral pathogens (*Streptococcus mutans, Porphyromonas gingivalis, Fusobacterium nucleatum,* and *Enterococcus faecalis*) and beneficial bacteria (*Streptococcus salivarius* and *Lactobacillus acidophilus*). At pH 3, PAW significantly reduced the viability of *S. mutans* and *E. faecalis* ($P < 0.01$), while demonstrating its potential to spare beneficial species such as *S. salivarius* and *L. acidophilus*. Although PAW resulted in the death of HSC-2, Ca9-22, and YD-10B cells, its cytotoxicity was lower than that of chlorhexidine, the oral disinfectant currently used.
Conclusion These findings suggest the potential of PAW as an effective and safe oral disinfectant. They also highlight the need for further study to investigate the effects of PAW on the broad range of oral bacteria and biofilm, as well as its safety in the primary cells that line the oral cavity.

PB-10

Genomic Characterization and Antimicrobial Resistance Patterns of Clinical *Salmonella* spp. isolated in Korea

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Objectives: One of the major zoonotic pathogens causing acute diarrhea in South Korea is *Salmonella* spp. *Salmonella* spp. is a zoonotic pathogen that significantly contributes to acute diarrhea in Korea. Both the patient number and the rate of human isolate resistance are steadily rising. As a result, it is necessary to investigate the current human-driven antibiotic resistance status as well as other molecular characteristics. Additionally, utilizing genome-based antibiotic-resistant bacteria data, it is required to examine the mechanism of human-derived resistance.

Methods: In this study, 437 clinical isolates of *Salmonella* spp. were obtained from patients with acute diarrhea from 106 medical institutions of six provinces. Following a sensititer panel investigation of their antibiotic resistance, we used multilocus sequence typing (MLST) analysis to identify prevalent clonal patterns. Furthermore, we examined into the presence of mcr genes in 11 clinical isolates that were resistant to colistin and utilized whole-genome sequencing to investigate the mechanism of resistance.

Results: Antimicrobial susceptibility testing of 437 *Salmonella* clinical isolates revealed high resistance rates to nalidixic acid (30.4%), ampicillin (30.2%), tetracycline (24.9%), and cefotaxime (14.2%). Notably, colistin resistance was detected in 13.7% (60/437) of isolates, confirming a multidrug-resistant (MDR) phenotype in the majority of strains. Eleven colistin-resistant isolates were selected for further study. The presence of mcrgenes was checked, and Whole-Genome Sequencing (WGS) was performed. All 11 isolates were negative for mcr genes, suggesting a chromosome-mediated resistance mechanism. Comparative genomic analysis revealed multiple non-synonymous mutationsin genes related to LPS modification and outer membrane proteins, which are postulated to play a crucial role in conferring colistin resistance.

Conclusion: Most colistin-resistant *Salmonella* isolates were *S*. Enteritidis (mainly ST203 and ST11). Whole-genome analysis revealed variations in in LPS-related genes, O-antigen synthesis genes, and membrane-associated systems. These findings provide a genomic foundation for future functional analyses to clarify resistance mechanisms in *Salmonella s*pp.

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PB-11

Analysis of Foodborne illness Outbreaks in Busan, 2022-2024

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Foodborne illness is an important indicator of public health hygiene. This study analyzed foodborne illness cases reported to the Busan Metropolitan City Institute of Health and Environment from 2022 to 2024, aiming to provide baseline data for improving community-level food hygiene.

A total of 166 cases were reported: 49 cases in 2022, 63 cases in 2023, and 54 cases in 2024. Among these, 119 cases (71.7 %) occurred in general restaurants, 43 cases (25.9 %) in food service institutions, and 4 cases (2.4 %) in others. Foodborne illnesses due to bacterial pathogens were most frequent from July to September, with July showing the highest number of cases (24). In food samples, pathogens were isolated in 27 cases: *Salmonella* spp. (12), *Bacillus cereus* (6), *Staphylococcus aureus* (3), *Vibrio parahaemolyticus* (5), Pathogenic *E. coli* (1).

To prevent foodborne illness, it is essential to enforce strict personal hygiene, maintain appropriate storage temperatures for food and ingredients, and provide comprehensive sanitary training for food service staff. Furthermore, in the event of an outbreak, accurate epidemiological investigation in coordination with relevant agencies is crucial to identify the causative agent.

PB-12

Genetic characteristics and antibiotic resistance of Enterohemorrhagic *Escherichia coli* strains isolated in Gyeongbuk

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Enterohemorrhagic *Escherichia coli* (EHEC) is a major foodborne pathogen responsible for diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome, with *stx2*-positive strains showing strong association with severe outcomes. This study investigated the genetic characteristics and virulence gene profiles of EHEC strains isolated from diarrheic patients and cattle in Gyeongbuk Province between 2019 and 2023. A total of 54 isolates were analyzed by PCR for major virulence genes (*saa, eae, ehxA, tir, espA, espB, espD, espP*), antibiotic susceptibility testing (VITEK 2), and whole genome sequencing (WGS) for genomic characterization. Among the isolates, 22 carried *stx1*, 25 carried *stx2*, and 7 carried both genes. Patient-derived isolates showed significantly higher prevalence of *eae, tir, espB, espD*, and *espP* compared with cattle-derived isolates, which harbored only limited virulence factors. Notably, *stx2*-positive isolates from patients increased after 2021, suggesting enhanced clinical relevance. WGS analysis further revealed antimicrobial resistance genes and serotype diversity, indicating genetic variability and potential horizontal gene transfer events. These findings highlight distinct differences between human- and cattle-derived EHEC isolates and provide baseline data for understanding the pathogenic mechanisms and guiding future strategies for EHEC infection control in Korea.

PB-13

The Development of CPP-PNA Conjugates Targeting *carA* in *Acinetobacter baumannii*

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Acinetobacter baumannii is a major opportunistic pathogen that causes serious clinical problems due to its multidrug resistance, particularly in hospital-acquired infections. In this study, we explored an alternative antibacterial strategy using antisense peptide nucleic acids (PNAs) conjugated with cell-penetrating peptides (CPPs), focusing on the essential gene *carA*. To maximize antibacterial activity, we systematically adjusted the PNA length, binding site, and chemical modifications. The synthesized CPP-PNA conjugates were evaluated against *A. baumannii* ATCC 17978 by determining minimum inhibitory concentrations (MICs) and minimum bactericidal concentrations (MBCs). Their effects on gene and protein expression were further examined using qRT-PCR and Western blotting, while cytotoxicity was assessed in A549 and HEp-2 cell lines. Among the tested constructs, KFFK$(FFK)_2$-PNA exhibited the most pronounced antibacterial effect, whereas excessive addition of positively charged residues diminished activity. Notably, a 10mer α-modified PNA targeting the ribosomal binding site of *carA* achieved the lowest MIC value (6.25 μM) and induced approximately 70% reduction in *carA* transcript levels, along with clear suppression of protein expression. In contrast, CPP-PNAs directed against other essential genes (*acpP, ftsZ, rne*) displayed weaker inhibitory effects. Cytotoxicity was evident at higher concentrations ($\geq$12.5 μM), but negligible at lower levels. Overall, the optimized CPP- PNA targeting *carA* represents a promising candidate for suppressing *A. baumannii* growth, and this work highlights a distinct approach centered on structural optimization of PNAs rather than CPP discovery.

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PB-14

Evaluation of the Antimicrobial Activity of a Novel Peptide, Hirunipin 2, Against Multidrug-Resistant *Klebsiella pneumoniae* Including CRE Strain

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The increasing prevalence of multidrug-resistant (MDR) *Klebsiella pneumoniae* poses a significant challenge to current antimicrobial therapy. In this study, we evaluated the antimicrobial activity of a novel antimicrobial peptide (AMP), hirunipin 2, against MDR *K. pneumoniae* clinical isolates. First, patient-derived MDR strains were collected and subjected to *in vitro* susceptibility testing. The minimum inhibitory concentrations (MICs) of hirunipin 2 were determined using the broth microdilution assay. Time-kill assays were performed to investigate the bactericidal activity of hirunipin 2. A checkerboard assay was performed to assess the potential synergistic effects of the combination of conventional antibiotics. Hirunipin 2 exhibited potent antimicrobial activity, as demonstrated by its low MIC values, rapid bactericidal kinetics, and synergistic interactions with selected antibiotics. These findings suggest that hirunipin 2 has strong *in vitro* potential and may serve as a promising candidate for developing novel antimicrobial agents targeting MDR *K. pneumoniae*.

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PB-15

Capsular types, virulence genes, and antimicrobial susceptibility of *Pasteurella multocida* isolated from pneumonic swine lungs

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Background

Pasteurella multocida (P. multocida) is widely recognized as a bacterial pathogen involved in the porcine respiratory disease complex (PRDC). It often acts as a secondary invader following viral infections such as PRRS and PCV2. Most cases depend on antimicrobials to treat the pathogens. This study aimed to examine the association of *P. multocida* with pulmonary lesions, capsular types, virulence genes, and antimicrobial susceptibility to support effective therapeutic strategies.

Methods

A total of 65 isolates of *P. multocida* were isolated from 794 pneumonic lungs from 2020 to 2024. Pneumonia was classified into fibrinous/pleuritic, interstitial, bronchopneumonia, and suppurative bronchopneumonia based on clinical and histopathological findings. Capsular typing (A, B, C, D, E, and F) was performed using the kmt1 gene amplifications. Virulence-associated genes related to adhesion, hyaluronidase, iron metabolism, and toxins were also determined by PCR assays. Antimicrobial susceptibility was performed by disc diffusion according to CLSI and EUCAST guidelines.

Results

A total of 65 isolates were identified as capsular type A (n=38), D (n=23), and F (n=4). *P. multocida c*apsular type A isolates were primarily associated with fibrinous and suppurative pneumonia, However, capsular type D was likely to be associated with interstitial pneumonia. Virulence genes such as *fimA, hsf, ptfA, nan*B/*nan*H*, exb*B - *ton*B*, fur*, and *hgb*A were identified in all capsular types. In contrast, *pm*HAS and *hgb*B were more frequent in type D than type A. Antimicrobial susceptibility testing demonstrated high susceptibility to β-lactams, tetracyclines, and colistin across all capsular types. Enrofloxacin susceptibility was higher in type A isolates but low in type D isolates.

Conclusion

Differences among capsular types were likely to be associated with lesions and antimicrobial susceptibility. These findings suggest thatcapsular type may influence lesion association and antimicrobial response. The data could be informative to understand the association between antimicrobial susceptibility and pneumonic lesions.

PB-16

Vitamin B6 metabolism pathway in *Acinetobacter baumannii* as a target for peptide nucleic acids

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Acinetobacter baumannii is an opportunistic pathogen recognized by the World Health Organization (WHO) as a critical-priority antibiotic-resistant bacterium. Multidrug-resistant (MDR) *A. baumannii* is a serious clinical threat because it resists many different antibiotics, including carbapenems. Consequently, the development of novel antibacterial agents with alternative mechanisms of action is urgently required. Peptide nucleic acids (PNAs) are being investigated as potential antisense therapeutics that bind to complementary mRNA sequences, leading to inhibition of essential bacterial gene expression. In this study, we synthesized a cell-penetrating peptide (CPP)-PNA conjugate targeting *pdxA*, an essential gene involved in vitamin B6 biosynthesis. The conjugate significantly inhibited *A. baumannii* growth by impairing vitamin B6 production. Notably, the antisense construct $(KFF)_3K$-*pdxA* (PNA-pdxA6) exhibited potent activity, achieving complete growth inhibition at 1.56 μM. Minimal or negligible inhibitory activity was observed against other Gram-negative species and Gram-positive bacteria, underscoring its target specificity. Although RT-qPCR analysis did not demonstrate marked suppression of *pdxA* mRNA, ELISA quantification revealed an approximately 80% reduction in vitamin B6 levels, consistent with previous findings that PNAs inhibit protein synthesis by blocking ribosomal binding rather than inducing transcript degradation. Furthermore, $(KFF)_3K$-pdxA PNA exhibited no detectable cytotoxicity in human cells even at relatively high concentrations, supporting its potential as a novel antibiotic alternative with a distinct mode of action. Although further studies are required for clinical application, the present findings suggest that CPP-PNA targeting *pdxA* represents a potential new therapeutic option against MDR *A. baumannii*.

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PB-17

Characteristics of *Salmonella* spp. Isolated from Human and Sewage in Daegu

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[Background] *Salmonella* spp., a Gram-negative bacterium belonging to the Enterobacteriaceae family, is a major causative agent of water- and foodborne infectious diseases, causing gastroenteritis or septicemia in both humans and animals. Transmission primarily occurs through contaminated food or water, and it can affect humans via contact with infected animal feces, sewage, and the environment. Given that *Salmonella* infection is a significant global public health concern and cases are continuously reported in South Korea, continuous monitoring and analysis of the infection sources are crucial. Therefore, this study aimed to analyze the characteristics of *Salmonella* strains isolated from human clinical specimens submitted by medical institutions and those from wastewater collected from a local wastewater treatment plant in the Daegu area in 2024, utilizing the findings as fundamental epidemiological data for community infection management.

[Methods] This study targeted *Salmonella* strains isolated from suspected *Salmonella* Typhi and Paratyphi cases submitted by medical institutions in Daegu and strains isolated from wastewater samples collected concurrently from the Sincheon Wastewater Treatment Plant in the same region in 2024. All isolates were serotyped according to the Kauffmann-White scheme based on O and H antigens using slide and tube agglutination tests. The presence of nine virulence genes (*invA*, *tolC*, *orgA*, *spaN*, *prgH*, *sipB*, *sopB*, *sitC*, and *cdtB*) was confirmed using PCR. Antimicrobial susceptibility testing was performed against 16 antimicrobial agents using the Vitek 2 AST-N415 card to analyze antimicrobial resistance patterns.

[Results and Discussion] The analysis showed that the human and wastewater-derived strains were classified into 14 different serotypes, respectively. While some serotypes were shared between the two groups, overall direct association was not observed. Analysis of the nine virulence genes revealed that eight genes were detected in most serotypes, but the *cdtB* gene, associated with typhoid toxin, was detected in 4 out of 41 human isolates and 2 out of 53 wastewater isolates. Antimicrobial susceptibility testing indicated that 58.5% of the human isolates were susceptible to all tested antimicrobials, which was the highest proportion. Resistance to Ampicillin was the most common (31.7%), with resistance to Ciprofloxacin, Cefazolin, and Trimethoprim/Sulfamethoxazole also partially observed. In wastewater isolates, the overall resistance rate was lower than in human isolates, with Ampicillin resistance being the highest (11.3%), similar to the human isolates.

[Conclusion] Consequently, a clear association in serotypes, virulence genes, and antimicrobial resistance patterns between the *Salmonella* strains isolated from human and wastewater samples in the Daegu area was not identified, likely due to the small sample size and short investigation period. However, considering the overlapping detection of some serotypes in a hospital located in Daegu Buk-gu and the Sincheon Wastewater Treatment Plant during the same period, pathogen surveillance via wastewater monitoring may aid in the early identification of the infection status in the local population and predict disease trends. Further research is anticipated to establish the wastewater surveillance system as a critical tool for managing *Salmonella* infections within the community.

PB-18

Population Genomic Analysis of the Distribution Characteristics of Antibiotic Resistant Bacteria and Resistance Genes in Wastewater

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Sewage treatment plants are major reservoirs of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs) within communities, serving as important research targets for understanding the dissemination of antibiotic resistance markers. In this study, we conducted metagenomic and genomic analyzes of 64 sewage influent samples (32 each collected in March and July 2025) from 8 sewage treatment plants in Gyeongsangbuk-do (Yeongcheon; YC, Gimcheon; GC, Gumi; GM, Gyeongju; GY, Pohang; PH, Andong; AD, Mungyeong; MG, and Gyeongsan; GS) to compare the seasonal and regional distribution characteristics of ARB and ARGs. We analysis identified a total of 62 ARB species and 265 ARGs. Regional comparison of the top 15 antibiotic-resistant bacteria revealed *Citrobacter freundii complex*, *Bifidobacterium breve*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterococcus faecium* as dominant species, with notable differences in their relative abundance across sewage treatment plants. Regarding ARG profiles, sul1, sul2, tetW, and AAC-Ib4 were identified as the major resistance determinants, and their abundance varied according to season. α-Diversity index analysis revealed that bacterial communities were mainly influenced by seasonal factors, whereas AMR diversity was significantly shaped by both seasonal and regional factors. Principal coordinates analysis (PCoA) revealed distinct separation of community structures across certain regions and seasons. Heatmap analysis based on Spearman correlation coefficients demonstrated strong associations between specific bacterial species and ARGs. In particular, *K. pneumoniae*, *E. faecium*, and *E. coli* showed close correlations with β-lactam- and tetracycline-related genes. Overall, this study not only characterized the seasonal and regional distributions of ARB and ARGs in wastewater treatment plants but also highlighted the close associations between clinically important strains (*K. pneumoniae*, *E. coli*, and *E. faecium*) and resistance genes. These findings provide valuable baseline data for developing wastewater-based antibiotic resistance markers monitoring systems and for advancing the understanding of resistance dissemination mechanisms.

PI-1

Methyl jasmonate an autophagy activator boosts antimicrobial response during mycobacterial infection

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Methyl jamonates (MeJA) are the conjugates of jasmonates which are the potential plant growth regulators. and played a role in the plant defense against insect and pathogens. However, its role in antimicrobial responses in mammalian cells and *in vivo* has not been widely defined. In this study, we investigated the antimicrobial effects of MeJA against *Mycobacterium tuberculosis* (Mtb) and NTM infections to assess its usefulness for host-directed therapy. We found that MeJA did not exert direct antimycobacterial effects; however, it showed suppression on intracellular bacterial growth and reduction of lung bacterial growth during infection with Mtb- and *Mycobacteroides abscessus* (Mabc). In addition, it markedly reduced the expression of pro-inflammatory cytokines and chemokines in macrophages during infections. Notably, we found that MeJA considerably inhibited the activation of ERK1/2 in infected macrophages. Additionally, MeJA robustly induced autophagosome formation, promoted the nuclear translocation of transcription factor EB (TFEB), and upregulated its downstream genes enhancing antimicrobial responses. Together, this study provides the potential of MeJA in the development of novel, plant-derived strategies for combating mycobacterial infections, emphasizing its role in strengthening host defenses.

PI-2

Inhibiting lipid droplet biogenesis enhances host protection against hypervirulent *Klebsiella pneumoniae* infections

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Hypervirulent *Klebsiella pneumoniae* (hvKp) has emerged as a serious global pathogen causing life-threatening infections even in healthy individuals. However, the mechanisms by which hvKp modulates host metabolic responses remain poorly understood. In this study, we demonstrated that clinical hvKp strains promote triacylglycerol synthesis and lipid droplet (LD) formation in murine macrophages through activation of the mammalian target of rapamycin (mTOR) signaling pathway. Pharmacological inhibition of mTOR by rapamycin, or blockade of lipogenesis using diacylglycerol O-acyltransferase 1 (DGAT1) and cytosolic phospholipase 2 (cPLA2) inhibitors (A922500 and CAY10650), significantly reduced lipid droplet formation, lipogenic gene expression, and intracellular bacterial survival. Inhibition of LD biogenesis also suppressed proinflammatory cytokine production, including TNF-α and IL-6, at both mRNA and protein levels. Furthermore, siRNA-mediated knockdown of DGAT1 or cPLA2 decreased hvKp survival in macrophages. In a murine infection model, administration of A922500 improved survival, reduced bacterial burdens in the lung, liver, and spleen, and alleviated tissue inflammation. These findings suggest that LD biogenesis links lipid metabolism to host immune responses during hvKp infection and that pharmacological inhibition of LD formation represents a promising strategy to enhance host defense against hvKp.

PI-3

Establishment of a Fluorescent Reporter *Mycobacterium tuberculosis* Platform for Evaluating Anti-Tuberculosis Drug Candidates

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The persistence of *Mycobacterium tuberculosis* (Mtb) within host macrophages, involving transitions between active and latent states, poses a major challenge for tuberculosis (TB) drug development. Conventional evaluation methods mainly rely on growth inhibition assays and fail to capture the dynamics of bacterial dormancy and intracellular adaptation.

To establish a more comprehensive evaluation system, we constructed fluorescent reporter plasmids driven by the smyc promoter (active-state marker) and the hspX promoter (latent-state marker). These plasmids are being introduced into the Mtb H37Rv strain to generate a dual-reporter strain capable of monitoring active-to-latent transitions in macrophages. This reporter-based platform is intended to provide real-time assessment of candidate compounds not only against bacterial growth but also against dormancy-associated phenotypes.

As preliminary validation, we screened ~30 natural products as one class of anti-TB drug candidates. Using wild-type H37Rv, three compounds showed significant activity in MIC assays and macrophage CFU assays. These findings demonstrate the feasibility of applying this platform for candidate evaluation once the fluorescent reporter strain is fully established.

In conclusion, this study aims to develop a fluorescent reporter Mtb system as a novel platform for evaluating anti-TB drug candidates. By integrating both active and latent states of Mtb into the assessment, this approach will broaden the scope of anti-TB drug discovery beyond conventional growth inhibition assays.

PI-4

Synergistic Anti-mycobacterial Mechanisms of IFN-γ/IL-17 via Coronin-1A Regulation and Tryptophan Metabolic Pathway Modulation.

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Background: Tuberculosis (TB), caused by infection with *Mycobacterium tuberculosis* (Mtb), remains one of the most devastating infectious diseases worldwide. According to the 2024 WHO report, over 8.2 million new TB cases were reported in 2023, the highest incidence since global monitoring began. The prolonged duration of chemotherapy, frequent treatment failure, and the emergence of drug-resistant TB underscore the urgent need for innovative therapeutic strategies beyond conventional pathogen-directed therapies.
Methods and Results: Here, we demonstrate that IFN-γ and IL-17 elicit synergistic anti-mycobacterial responses by modulating a key immunometabolic pathway. Co-stimulation with low concentrations of IFN-γ and IL-17 enhanced bactericidal activity compared with IFN-γ alone in Mtb-infected macrophages. This synergy reduced coronin-1A retention on Mtb-containing phagosomes, upregulated LRG47 expression, and suppressed STAT3 phosphorylation, thereby promoting phagolysosomal fusion and Mtb killing. In murine models, adjunctive treatment with IFN-γ/IL-17 in combination with first-line anti-TB drugs accelerated bacterial clearance and reduced relapse compared with chemotherapy or IFN-γ alone. Importantly, immunofluorescence staining of Mtb-infected mouse lung tissues confirmed the regulation of the STAT-1-LRG47-coronin-1A axis *in vivo*. Moreover, gene expression and enzymatic analyses revealed that IFN-γ/IL-17 co-stimulation downregulated *ido1*, indoleamine 2,3-dioxygenase 1, the enzyme catalyzing the conversion of tryptophan to kynurenine, and reduced tryptophan-to-kynurenine conversion, suggesting that co-stimulation may alleviate Mtb infection-induced immunosuppressive metabolic reprograming.
Conclusion: These findings uncover a dual mechanism by which IFN-γ/IL-17 act synergistically —by disrupting coronin-1A-mediated phagosomal retention and by attenuating IDO1-driven tryptophan metabolism— thereby enhancing host anti-mycobacterial immunity. Our study highlights the potential of IFN-γ/IL-17-based adjunctive immunotherapy as a promising strategy against TB.

PI-5

Induction of Th17 and Memory T Cells and Suppression of *M. avium* Infection by the MRT301

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Mycobacterial infections, including tuberculosis and nontuberculous mycobacteria (NTM), remain a global health challenge due to antibiotic resistance and limitations of existing vaccines. This study aimed to develop and evaluate a novel subunit vaccine candidate, MRT301, composed of a fusion of multiple *M. tuberculosis* antigens ($Rv2299c_{D2D3}$-ESAT6-$Rv3463_{D2}$-$Rv2005_{D3}$-$RpfE_{D1}$) formulated with Alum-M-CWGL adjuvant. Mice were infected intranasally with 1×10^6 CFU of *M. avium*, followed by comparison of immune responses and bacterial burden between groups treated with azithromycin and those immunized with MRT301 at two-week intervals for two doses. Immunization with MRT301 induced a marked increase in Th17 responses, as demonstrated by elevated IL-17 production in ELISA and intracellular cytokine staining of $CD4^+$ T cells. Furthermore, memory T cell populations were substantially expanded in MRT301-immunized mice. Most notably, the bacterial load of *M. avium* in lung tissues was significantly reduced in the MRT301-immunized group compared to the antibiotic-treated group. These findings indicate that MRT301 elicits robust Th17 and memory T cell immunity, leading to superior control of *M. avium* infection. This strategy holds promise as an integrative immunotherapeutic platform for the management of tuberculosis and NTM infections.

PI-6

Synergistic Impact of Gram-Negative Bacteria on the Pathogenesis of *Mycobacterium avium* Complex Pulmonary Disease

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Mycobacterium avium complex pulmonary disease (MAC-PD) is divided into fibro cavitary and nodular bronchiectasis types, the latter occurring without underlying disease and highly associated with chronic *Pseudomonas aeruginosa* (PA) infection. While MAC is introduced into macrophages by phagocytosis and retained in the cells, co-infected PAs can impact MAC-infected host cells.
To mimic gram-negative bacterial co-infection, including PA, we conducted in vitro and in vivo experiments. In vitro, we established an LPS co-stimulation model using mouse bone marrow-derived macrophages (BMDMs) from TLR4-competent C3H/HeN and TLR4-deficient C3H/HeJ mice. In vivo, we performed a parallel infection model in C3H/HeN and C3H/HeJ mice. Both models evaluated cytokine responses, macrophage polarization, bacterial burden, and pulmonary pathology
In vitro, LPS triggered an early pro-inflammatory response (M1-dominant) in HeN BMDMs but led to late tolerance (increased M2 and IL-10), promoting bacterial persistence. In HeJ BMDMs, the response was muted, with limited cytokine induction and macrophage switching. In vivo, LPS exacerbated MAC infection in HeN mice, resulting in higher bacterial burdens, more severe pneumonia, and macrophage phenotype switching that promoted persistent infection. In contrast, HeJ mice showed relative resistance, with lower bacterial burdens and milder pathology, underscoring TLR4 as a central mechanism in the pathogenesis of gram-negative bacterial co-infection with MAC.
Conclusion: Co-infection with gram-negative bacteria enhances IL-10-mediated immune modulation during MAC infection, promoting macrophage phenotype switching and bacterial persistence. This immunological interaction may underline the exacerbation of clinical manifestations in MAC-PD patients with gram-negative co-infections.

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PI-7

Immunologic responses to an extracellular vesicle-based vaccine expressing the full suite of SARS-CoV2 structural proteins

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In an attempt to develop a novel extracellular vesicles (EVs)-based vaccine against COVID-19, we designed EVs harboring a full set of SARS-CoV-2 structural proteins. Thus, the receptor-binding domain (RBD) of spike protein (S) of SARS-CoV-2 variant BA.2 or BA.4/5 with the stabilized wild type spike protein backbone, nucleocapsid protein (N) C-terminally fused with CD63, membrane (M), and envelope (E) proteins were stably expressed in 293T cells. Then, cell death-associated EVs were collected from the cells and evaluated for the expression of SARS-CoV-2 structural proteins. As a result, it was confirmed that trimers of spike fusion protein, N, M, and E were successfully loaded in the EVs. In an intramuscular injection model of mice, the inoculation of 50 μg EVs resulted in significant IgG antibody responses to S after the booster injection and neutralized the entry of S-pseudotyped VSVs. Anti-nucleocapsid antibodies were efficiently increased in mice primarily injected with 25 or 50 μg EVs, showing further increased values after booster dosages. Memory $CD4^+$ T_{H1} cells and $CD8^+$ T_C cells against S and N proteins was generated in mice that received a booster-immunization with all dosages (10, 25, or 50 μg) of EVs. Additionally, T cells responses against M and E peptides were increased in booster-immunized mice that received 50 μg of EVs. Taken together, this work proved feasibility of EVs expressing SARS-CoV-2 proteins as a universal vaccine candidate, potentially offering protection against emerging SARS-CoV-2 variants and future pandemics.

PI-8

The Bioactive Potential of the Rarely Investigated Red Macroalga AN01: Chemical Profile, Antioxidant, and Anti-inflammatory effects

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The widely distributed species AN01 is considered to have a limited or no reports on their biomedical applications. This study aims to investigate the chemical composition of this alga and its protective effect against oxidative stress and inflammation. The total phenolic content was estimated in the 80% methanol extract of the species. The chemical composition of the extract was analyzed using High-performance liquid chromatography (HPLC) and gas chromatography-mass spectrometry (GC-MS). The cytotoxicity of the extract was measured in Vero cell line using the MTT assay bone marrow-derived dendritic cells (BMDC). The protective effect of the extract against AAPH- or H_2O_2-induced oxidative stress was estimated in Vero cell line using the MTT assay. For anti-inflammatory activity, the nitric oxide (NO) production was estimated in LPS-stimulated RAW264.7 cells using the Griess assay. Furthermore, the inhibition of cytokine production was estimated in LPS-stimulated BMDC using the enzyme linked immunosorbent assay. The species showed a significant amount of phenolic content. The HPLC exhibited the presence of 11 phenolic compound, dominated with catechin (20.33 μg/g). GC-MS profile gave rise to 20 compounds of fatty acids and derivatives. The tested cells for cytotoxicity showed a good adaptation towards the extract with a slight decrease in Vero cell viability % at the high concentration. The extract showed protective effects against oxidative stress. Moreover, the extract was able to inhibit the production of NO and cytokines in a dose-dependent manner. The findings indicate the potential therapeutic effect of the species against oxidative stress and inflammation, suggesting its nutraceutical and pharmaceutical applications.

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PI-9

Chromosomal co-carriage of *bla*$_{OXA-23}$ and *bla*$_{OXA-500}$ in a carbapenem-resistant *Acinetobacter pittii* isolate

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Carbapenem resistance in non-*baumannii Acinetobacter* has been increasingly reported worldwide. This study investigated the genetic basis of carbapenem resistance in *Acinetobacter pittii* isolate KBN12P06770 carrying *bla*$_{OXA-23}$ and *bla*$_{OXA-500}$ using whole-genome sequencing. Two carbapenemase genes were located on the chromosome. Two copies of *bla*$_{OXA-23}$ located on Tn*2006* were identified. Additional chromosomally encoded antimicrobial resistance genes, including *bla*$_{ADC-18}$ and *ant(3")-IIc*, as well as efflux pump genes (*adeIJK*, *adeFGH*, *abeM*, and *abaQ*), were identified, with the exception of plasmid-borne *ant(2")-Ia*. qPCR analysis revealed that the *bla*$_{OXA-23}$ was more highly expressed than *bla*$_{OXA-500}$. Notably, *bla*$_{OXA-23}$ featured a novel Ser225Pro substitution, which may enhance β-lactamase activity based on structural modeling. Furthermore, multilocus sequence typing (MLST) assigned KBN12P06770 to ST1611 within clonal complex 63 (CC63), with close clustering to ST2737 indicating recent divergence. The comprehensive genomic analysis of *A. pittii* isolate KBN12P06770 highlights the complex genetic architecture underlying carbapenem resistance.

PI-10

Overcoming Oral Bioavailability Limitations of Ciprofloxacin Through a Novel Nanoformulation Drug Delivery System

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Streptococcus pneumoniae remains a leading cause of pneumonia, meningitis, and bacteremia worldwide, contributing to significant morbidity and mortality. The rapid emergence of antibiotic-resistant *S. pneumoniae* strains has diminished the efficacy of many standard therapeutic options. Ciprofloxacin (CIP), a widely prescribed fluoroquinolone antibiotic, exhibits potent activity against a broad spectrum of bacterial pathogens, including *S. pneumoniae*. However, its clinical utility via oral administration is restricted by poor solubility and limited bioavailability, resulting in suboptimal systemic drug levels. To address these limitations, we developed CIP-nano, a novel nanoformulation consisting of ciprofloxacin and tauroursodeoxycholic acid (TUDCA), prepared through a simple nanoprecipitation technique. The optimized nanoparticles displayed an average size of approximately 135 nm, favoring enhanced gastrointestinal uptake. Pharmacokinetic profiling in Sprague-Dawley rats demonstrated that CIP-nano markedly improved plasma drug exposure and sustained systemic concentrations compared to unformulated CIP. Furthermore, oral administration of CIP-nano in C57BL/6J mice resulted in superior therapeutic outcomes, including faster recovery rates and improved clinical parameters, without inducing detectable toxicity or adverse effects on body weight, feeding behavior, or general health. These findings highlight the potential of CIP-nano as a safe, orally deliverable nanotherapeutic strategy to enhance the effectiveness of ciprofloxacin against antibiotic-resistant *S. pneumoniae* infections.

PI-11

Protective Efficacy of the REA Fusion Protein Vaccine against *Mycobacterium tuberculosis* in a Guinea Pig Model

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Tuberculosis (TB) is an infectious disease caused by the intracellular pathogen *Mycobacterium tuberculosis* (Mtb), which primarily affects the lungs. Currently, bacillus Calmette-Guérin (BCG) remains the only licensed vaccine against TB. Although preclinical evaluation of tuberculosis vaccine candidates is commonly conducted in mice, studies utilizing guinea pig models remain limited. Guinea pigs are a reliable model for testing TB vaccines due to their ability to develop human-like disease, providing a stringent assessment of vaccine efficacy. Previous studies have demonstrated that Rv2299cD2D3-ESAT-6-Ag85B (REA) fusion protein is a promising primary preventive vaccine candidate against tuberculosis in mice; however, its evaluation in other animal models has not yet been conducted. This study aimed to determine whether the protective effects of REA fusion protein observed in mice can be replicated in guinea pigs. Guinea pigs were immunized with the REA fusion protein three times at three-week intervals, starting 12 weeks prior to challenge with Mtb. Six weeks after infection, the animals were sacrificed, and bacterial loads in the lungs and spleen were assessed. As a result, REA fusion protein exhibited a preventive effect against TB, although its efficacy was slightly lower than that of BCG. These findings indicate its potential as an alternative TB vaccine candidate to complement BCG.

PI-12

Characteristics of pulmonary CD4$^+$ and CD8$^+$ T cell subsets in BCG-immunized mice against *Mycobacterium avium* infection

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Although the prevalence of *Mycobacterium avium* complex pulmonary disease (MAC-PD) is increasing, data on host vulnerability to MAC infection remain limited. Understanding the pathobiology of MAC-host immune interactions requires detailed characterization of pulmonary T cell phenotypes and functions in MAC-PD. We previously established an infection-susceptible murine model by immunizing with BCG prior to MAC challenge. Lungs from the BCG-immunized group were harvested at 5- and 11- weeks post-infection for histopathological examination, bacterial colony counts, and flow cytometric analysis of T cell phenotypes. Histological examination revealed significantly increased pulmonary inflammation in BCG-immunized mice compared with non-immunized mice (at 5 weeks, $P = 0.0006$), and bacterial loads were also consistently higher in the BCG group (at 5 weeks, $P = 0.0030$; at 11 weeks, $P = 0.0279$). In line with this phenotype, We observed that effector T cells, gated on CD4$^+$ CD44$^+$ and CD8$^+$CD44$^+$ subsets, exhibit reduced proliferative capacity, as indicated by decreased Ki67 expression, along with increased expression of exhaustion markers including PD-1 and KLRG1, at 5 and 11 weeks post-infection. In conclusion, these findings highlight that disease severity of MAC-PD is closely associated with T cell dysfunction. Further studies are required to elucidate the mechanisms by which T cell exhaustion contributes to the exacerbation of MAC-PD. This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (RS-2023-00210371 and RS-2022-00164735).

PI-13

Sirtuin 3 plays a crucial role in controlling host defense against nontuberculous mycobacterial infections

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Sirtuin 3 (SIRT3), a mitochondrial deacetylase, plays a critical role in regulating cellular metabolism, oxidative stress, and immune responses. Recent studies have highlighted its involvement in the immune response to nontuberculous mycobacterial (NTM) infections, a group of emerging pathogens that cause chronic pulmonary diseases, especially in immunocompromised individuals. SIRT3 modulates mitochondrial function and reactive oxygen species (ROS) production, which are crucial in the host defense against NTM. Specifically, SIRT3 has been shown to enhance the antimicrobial activity of macrophages by promoting autophagy and regulating the production of pro-inflammatory cytokines. Additionally, SIRT3 influences the balance between pro- and anti-inflammatory responses, which is essential in controlling NTM infection and preventing excessive tissue damage. Dysregulation of SIRT3 expression or activity may contribute to impaired immune responses and increased susceptibility to NTM infections. Therefore, understanding the role of SIRT3 in NTM pathogenesis could open new avenues for therapeutic interventions aimed at enhancing host defense mechanisms and improving clinical outcomes in patients with NTM infections.

PI-14

Myeloid mitofusin 2 orchestrates antimycobacterial defense through hypoxia-inducible factor 1A-dependent xenophagy and inflammatory responses

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Mycobacterium tuberculosis (Mtb) is the causative pathogen of human tuberculosis, a major global health concern. Intracellular infection with Mtb can significantly alter mitochondrial homeostasis and dynamics. While mitofusin 2 (MFN2) is known to regulate mitochondrial fusion and dynamics, its specific contribution to host defense mechanisms against intracellular bacterial pathogens remains incompletely understood. Using myeloid-specific *Mfn2* conditional knockout (*Mfn2* CKO) mice, we investigated the role of MFN2 in myeloid cells during mycobacterial infections. Our findings revealed that MFN2-deficient macrophages showed compromised antimicrobial responses, resulting in enhanced intracellular bacterial survival. Accordingly, *Mfn2* CKO mice demonstrated increased susceptibility to both Mtb and *M. bovis* Bacillus Calmette-Guérin infection *in vivo*. Mechanistically, we discovered that MFN2 functions as a critical regulator of xenophagy, facilitating the autophagic clearance of intracellular mycobacteria. MFN2 was essential for efficient targeting of mycobacteria to autophagosomes and lysosomes, maintaining proper autophagic flux. This process was found to be dependent on hypoxia-inducible factor (HIF)1A signaling, which was activated through MFN2-mediated mitochondrial reactive oxygen species production. Furthermore, we identified a novel interaction between MFN2 and the small GTPase RAB7, which proved crucial for xenophagy activation during mycobacterial infection. These findings establish MFN2 as a central coordinator of antimycobacterial defense, linking mitochondrial dynamics to innate immune responses through the regulation of HIF1A-dependent pathways.

PI-15

Development of Broad-spectrum Antiviral Tabamide A Derivative against Human Rhinovirus and Multiple Zoonotic Viruses, Using AI-based Docking analysis and Lung Organoid

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Human rhinovirus (HRV), a common cause of the common cold, was first isolated in 1956. HRV causes mild symptoms, but also causes severe respiratory disease such as asthma, chronic obstructive pulmonary disease (COPD) and pneumonia. However, there are no FDA-approved anti-viral or anti-inflammation drugs against for HRV. TA25 is a phenolic amide isolated from the leaves of *Nicotiana tabacum*. In this study, the antiviral and anti-inflammatory activities of TA25 were evaluated against HRV-B14. The inhibition of replication by TA25 treatment was confirmed using virus genome strand-specific RT-qPCR. Moreover, interaction of TA25 with HRV 2B protein that promote virus replication examined by AI-driven structure-based analysis. TA25 showed the broad-spectrum antiviral activity against multiple viruses, including HRV-1A, Zika virus, Dengue virus, Influenza B virus, and Vaccinia virus. In addition, embryonic stem cells derived lung organoids (LOs) were developed with expression of alveolar genes. Additionally, optimal condition of HRV-B14 infection was confirmed in LOs. In conclusion, TA25 demonstrated antiviral and anti-inflammation activities against HRV. This study provides insights into a potential candidate of TA25 for antiviral therapeutics against human rhinovirus as well as zoonotic viruses.

PI-16

BCG and β-glucan induce susceptibility to *Mycobacterium avium* infection by reprogramming myeloid cells

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Bacille Calmette-Guérin (BCG) and β-glucan are potent inducers of epigenetic and functional reprogramming of innate immune cells, a process called trained immunity, resulting in an enhanced host response against secondary infections. In this study, we investigated whether BCG- and β-glucan-induced trained immunity could protect against *Mycobacterium avium* (MAV) infection. After mice were treated with BCG and β-glucan, the frequency of hematopoietic progenitors (LKS; Lineage$^-$c-Kit$^+$Sca-1$^+$) and myeloid-biased multipotent progenitors (MPP3; Flt$^-$CD48$^+$CD150$^-$LKS) was increased in the bone marrow (BM), and mice in both treatment groups showed a significant increase in lung inflammation and bacterial loads upon MAV infection. In addition, bone marrow-derived macrophages (BMDMs) primed with β-glucan displayed a proinflammatory phenotype by secreting high levels of IL-6 and TNF in response to lipopolysaccharide (LPS) stimulation and MAV infection. Moreover, β-glucan-primed BMDMs failed to restrict intracellular growth of MAV. Notably, treatment with epigenetic modulators reversed this phenotype in response to LPS stimulation and MAV infection. These findings suggest that BCG- and β-glucan-induced reprogramming of myeloid cells may not confer protective effects in MAV-infected mice. We are currently investigating how acquired proinflammatory phenotypes in myeloid cells cause a shift toward disease exacerbation in MAV complex pulmonary disease (MAC-PD).

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PI-17

Roles of CNU-42, a Naphthoquinone Derivative, in inhibiting *Mycobacteroides abscessus* Complex-induced excessive inflammation within murine macrophages

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Pulmonary disease caused by nontuberculous mycobacterial species, including *Mycobacteroides abscessus* (Mabc) and *Mycobacteroides bolletii* (Mboll), is gradually prevalent worldwide. Despite the low cure rate and high relapse occurrence, the severity of nontuberculous mycobacteria-caused pulmonary disease is poorly understood. Naphthoquinone has been known to possess antibacterial as well as many other activities. Due to its cell cytotoxicity, numerous studies have attempted to develop its derivatives with reduced toxicity; however, studies regarding antimycobacterial activity are limited. Here, we investigated CNU-42, a derivative of the natural compound naphthoquinone, for its antimicrobial activity against *Mycobacteroides abscessus* and *Mycobacteroides bolletii*. CNU-42 exhibited the direct inhibition of mycobacterial growth. Enhancing this result, the number of intracellular Mabc and Mboll, phagocytosed within murine macrophages, decreased dose-dependently under CNU-42 treatment. Moreover, Mabc- or Mboll-induced excessive inflammation was diminished in murine macrophages with CNU-42 treatment. Furthermore, the treatment of Mabc- or Mboll-infected murine macrophages with CNU-42 suppressed the activation of extracellular signal-regulated kinase. Collectively, these data demonstrate CNU-42 may be a bidirectional drug candidate to inhibit both Mabc- and Mboll-derived pulmonary diseases, via direct growth suppression and host-directed therapeutic ways.

PI-18

S100 Calcium-Binding Proteins A8/A9 Play a Crucial Role in Controlling Antimicrobial Responses against *Mycobacterium tuberculosis*

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Mycobacterium tuberculosis (Mtb) still remains as a considerable challenge in prevalence and mortality worldwide. A deeper understanding upon host-pathogen interaction during Mtb infection is critically involved in developing effective therapeutics against Mtb. This study aimed to investigate the role of paquinimod (Pq), an inhibitor of S100 calcium-binding proteins A8/A9 (S100A8/A9), in the intracellular survival of Mtb and the regulation of inflammatory responses. In peripheral immune cells from patients with pulmonary tuberculosis and tuberculous lymphadenitis, the expression of S100A8/A9 and chemokines was significantly upregulated. Treatment with Pq significantly increased the growth of Mtb within macrophages and substantially enhanced granulomatous lesions in the lungs of Mtb-infected mice. Additionally, Pq did not suppress Mtb-induced production of pro-inflammatory cytokines and chemokines in macrophages. Moreover, Pq increased the mRNA expression levels of inflammatory cytokines and chemokines in the lung tissues from mice infected with Mtb, compared with untreated controls. Ongoing studies are being conducted to elucidate the mechanisms by which Pq contributes to the suppression of antimicrobial responses. Collectively, these findings suggest that S100A8/A9 play a critical role in limiting intracellular mycobacterial survival and modulating inflammatory responses during infection.

PI-19

Berberine inhibits intracellular growth of hypervirulent *Klebsiella pneumoniae* via regulation of lipid metabolism and inflammatory signaling

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Hypervirulent *Klebsiella pneumoniae* (hvKp) is a highly pathogenic strain capable of causing severe, invasive infections even in healthy individuals. During intracellular infection, host macrophages attempt to restrict bacterial replication, but hvKp circumvents these defenses by modulating lipid metabolism and inflammatory signaling. In this study, we examined the effect of berberine on hvKp-infected macrophages. Berberine markedly suppressed intracellular bacterial proliferation, accompanied by alterations in lipid metabolism. Specifically, berberine reduced the phosphorylation of mechanistic target of rapamycin, a central regulator of lipid biosynthesis, as confirmed by Western blot analysis. Consistently, RT-qPCR demonstrated decreased expression of lipid droplet-associated genes (*Fasn*, *Scd1*, and *Acaca*), along with reduced intracellular triglyceride levels. Moreover, berberine attenuated the phosphorylation of ERK and JNK, thereby modulating inflammatory responses. Collectively, these findings suggest that berberine restricts hvKp replication and dampens macrophage inflammation, at least in part by targeting lipid metabolic pathways and MAPK signaling.

PI-20

Ceramide Chain Length Determines Host Immune Responses to Mycobacteria

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Mycobacterium tuberculosis (MTB) and *Mycobacterium abscessus* (*M. abscessus*) are the major causative agents of tuberculosis and nontuberculous mycobacterial pulmonary diseases, respectively, with the ability to survive long-term in the host. Both pathogens possess lipid-rich cell walls and modulate host lipid metabolism to evade immune responses. Ceramides, lipid metabolites composed of sphingosine and a fatty acid, not only serve as essential components of cellular membranes but also play critical roles in immune processes such as apoptosis and inflammation. Ceramides are classified into numerous subspecies depending on the length and saturation of their fatty acid chains, with distinct tissue-specific patterns determined by ceramide synthases (CerS1-6). Recent studies have shown that MTB infection alters ceramide metabolism, while sphingosine, a ceramide metabolite, contributes to host defense against *M. abscessus*. In this study, we investigated the effects of ceramide subspecies on immune responses to MTB and *M. abscessus* infection. Bone marrow-derived macrophages and peripheral blood mononuclear cells were infected with MTB or *M. abscessus* and treated with ceramides of varying chain lengths (C16:0, C24:0). We then assessed intracellular bacterial growth and cytokine expression profiles. Treatment with C16:0 ceramide showed a trend toward inhibiting bacterial growth and was associated with an increase in pro-inflammatory cytokine expression. In contrast, treatment with C24:0 or C2:0 ceramide significantly enhanced bacterial growth and also increased pro-inflammatory cytokine expression, while decreasing anti-inflammatory cytokine expression. These findings demonstrate that fatty acid chain length-specific ceramides differentially modulate host immune responses against MTB and *M. abscessus*. Our results suggest that particular ceramide subspecies could serve as potential targets for host-directed therapy against both tuberculosis and NTM infections.

PI-21

Comparison of qPCR assay sensitivity for scrub typhus and Q fever in blood samples by DNA extraction method

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Background: Scrub typhus (ST) and Q-fever are vector-borne zoonotic diseases caused by intracellular bacteria, *Orientia tsutsugamushi* and *Coxiella burnetii,* often presenting with nonspecific symptoms that complicate clinical diagnosis. Delayed recognition can result in severe complications and increased mortality. Real-time PCR is a rapid and sensitive diagnostic tool; however, its accuracy depends on efficient DNA extraction from clinical specimens. In this study, we compared the detection sensitivity of qPCR assays for of Scrub typhus and Q fever in blood samples according to the DNA extraction method.

Methods: Plasma samples from patients suspected of ST or Q-fever were processed using both magnetic bead-based and silica column-based DNA extraction methods. Extracted DNA was analyzed by pathogen-specific real-time PCR using a QuantStudio5 system to determine cycle threshold (CT) values and detection rates.

Results: Magnetic bead-based extraction showed lower CT values and higher detection rates compared with the silica column method. For scrub typhus, positivity was 41.7% (5/12) with beads versus 8% (2/25) with columns. For Q fever, detection was 16.7% (3/18) with beads versus 5.4% (2/37) with columns. Notably, several samples negative by the silica column method were identified as positive using the magnetic bead method.

Conclusion: Magnetic bead-based DNA extraction enhances the sensitivity of qPCR for detecting low concentrations of pathogen DNA in blood. Our results provide supporting evidence that efficient extraction improves pathogen detection.

PI-22

ATG7 in innate immune cells mediates host protection against pulmonary NTM infections

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Nontuberculous mycobacterial pulmonary diseases (NTM-PD) are increasingly prevalent, with rising antibiotic resistance posing a significant clinical challenge. Despite this, the factor(s) governing host defense against NTM-PD remain poorly understood. Autophagy, a fundamental intracellular degradation pathway relying on lysosomal processes, is crucial for maintaining organelle integrity and quality control under various stresses, including infections. In our study, patients with NTM-PD exhibited reduced autophagy-related gene (*ATG*)*7* expression in blood mononuclear cells and necrotic lesions at disease sites. Furthermore, patients with NTM-PD exhibited significantly decreased *ATG7* levels, inversely correlated with proinflammatory cytokines/chemokines in peripheral blood mononuclear cells (PBMCs). Here, using innate immune cell-specific deletion of *Atg7* in mice, we identified that ATG7 innate immune cells is essential for effective *in vivo* antimicrobial responses against various NTM species. Spatial and bulk RNA sequencing, combined with biological assays, revealed increased bacterial burden, excessive inflammation, mitochondrial damage, and a combination of cell death pathways (pyroptosis, necrosis, and apoptosis), in the lungs of mice with *Atg7* deficiency in innate immune cells (*Atg7* cKO). Furthermore, single-cell RNA sequencing analysis demonstrated that infiltrating neutrophils in *Atg7* cKO lungs primarily drive exacerbated inflammation and cell death, which precede NTM overgrowth. *In vitro*, *Atg7*-deficient macrophages exhibited impaired antimicrobial responses and reduced phagolysosomal fusion, although they showed only marginal differences in inflammation and cell death. These findings highlight a critical role of ATG7 in innate immune cells, particularly in or25chestrating protective *in vivo* responses against NTM-PD by alleviating neutrophil-driven pathological inflammation and cell death.

PI-23

Detection of Pathogen-Specific Memory CD8$^+$ T Cell Using Lens-free Shadow Imaging

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Evaluation of virus-specific CD8$^+$ T cell responses is essential for assessing vaccine efficacy, particularly in the context of rapidly mutating viruses such as SARS-CoV-2. Conventional methods for measuring virus-specific T cell responses remain expensive and technically demanding due to the polymorphism of MHC molecules. To overcome these challenges, we investigated a label-free approach using the Lens-Free Shadow Imaging Technique (LSIT), which captures the morphological and structural features of individual cells, aiming to detect activation-induced morphological changes in memory CD8$^+$ T cells. To test this, splenocytes from memory chimeric mice were stimulated with their cognate peptide for either 6 or 18 hours, followed by CD8$^+$ T cell enrichment. LSIT analysis revealed an increase in shadow image parameters after 18 hours of stimulation compared to 6 hours. Based on this observation, we aimed to determine whether the LSIT parameters of activated Ag-specific memory CD8$^+$ T cells are clearly distinguishable from those of other CD8$^+$ T cells, and to evaluate whether this approach is suitable for detecting activated Ag-specific memory CD8$^+$ T cells. To demonstrate this approach, we stimulated splenocytes for 15 hours and sorted peptide-specific memory CD8$^+$ T cells by FACS. These activated memory CD8+ T cells increased cell shadow parameters compared to non-specific CD8$^+$ T cells. Additionally, measurement of activated memory CD8$^+$ T cells following 15 hours of peptide stimulation by flow cytometry confirmed an increase in FSC and SSC values., supporting that the morphological changes detected by LSIT reflect T cell activation. Altogether, these results suggest that LSIT enables the quantification of cell size and morphological alterations to detect antigen-specific memory CD8$^+$ T cell activation without labeling, providing a rapid and cost-effective platform for evaluating vaccine-induced T cell responses.

PI-24

Genome-wide identification of clade-specific sequences in *Candida auris* and development of a multiplex qPCR assay for differential detection

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Since its first recognition in Japan in 2009, *Candida auris* has become a major concern due to multidrug resistance, nosocomial spread, persistence on skin and surfaces, and frequent misidentification in routine laboratories. Whole-genome studies define six clades(I to VI), with distinct geographic origins. They differ signficantlyl differences in resistance, environmental persistence, transmissibility, and virulence, making clade-level identification clinically important. *C. auris* Clade II was the predominant lineage until the emergence of Clade I in 2022, which subsequently triggered a hospital outbreak in South Korea. Clade I exhibited higher virulence, enhanced skin colonization and environmental survival, and broader antifungal drug resistance, all of which raise the risk of transmission and treatment failure. However, the diagnostic tools currently used in clinical laboratories such as MALDI-TOF MS and commercial PCRs, provide only species-level identification. Clade assignment requires the application of additionally resource-intensive whole-genome sequencing (WGS) or multilocus sequence typing (MLST). In the study, we developed a multiplex qPCR method that can identify *Candida auris* and differentiate Clades I and II with high sensitivity and specificity. Genome alignment identified a 211 bp Clade I-specific locus and an 820 bp Clade II-specific locus. We designed an optimized multiplex qPCR that targets these specific regions, achieving limits of detection of 10fg/μL with no cross-reactivity. This multiplex qPCR was applied to 15 clinical isolates, all results were fully concordant with those obtained MLST (100%, 15/15). The newly developed multiplex qPCR method is expected to be more rapid and cost-effective than current clade-typing methods and will make it a more efficient tool for Candida surveillance and management, thereby improving infection control.

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PVM-1

The crucial role of HTRA1 protein in the progression of CADASIL

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Currently, how to treat CADASIL is a crucial issue. Studies have shown that the absence of HTRA1 can alter the Notch and TGF-β pathways, leading to abnormal development/stasis of VSMCs, which may mediate the pathogenic process of CADASIL. HTRA1 is a key member of the HtrA family and belongs to a type of heat shock protein. HTRA1 has been proven to have the function of inhibiting the migration and differentiation of trophoblast cells. The C-terminal of HTRA1 is a PDZ domain, which plays an important role in regulating protein self-catalysis, regulating protease activity, and substrate entry.
In this experiment, a recombinant HTRA1 plasmid was constructed to induce the recombinant HTRA1 protein. The recombinant HTRA1 protein was then used to treat CADASIL-afflicted mice, and the behavioral changes of the diseased mice were observed. The role of the HTRA1 protein in the CADASIL disease process was investigated. The results showed that HTRA1 could effectively alleviate the symptoms of CADASIL mice and make the behavioral patterns of the diseased mice return to normal. This proved that HTRA1 plays an important role in the pathogenesis of CADASIL.

PVM-2

The Specific Thrombolytic Activity of HtrA1 Without Plasmin Activation for the Treatment of Ischemic Stroke

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Stroke remains one of the leading causes of death and disability worldwide, with ischemic stroke (IS) accounting for approximately 62.4% of all cases and an estimated 7.8 million new cases annually. IS imposes a substantial health and economic burden. Although thrombolytic therapy can be life-saving during the acute phase, its application is severely limited by a narrow therapeutic window and the risk of hemorrhagic transformation. Currently used thrombolytic agents—such as streptokinase, urokinase, and tissue plasminogen activator (tPA)—act by converting circulating plasminogen into plasmin, a serine protease that dissolves fibrin clots. However, plasmin is a potent non-specific protease that not only degrades fibrin but also damages proteins essential for tissue repair and wound healing, including fibrinogen, a key factor in coagulation. As a result, tPA and similar plasmin-dependent agents are clinically indicated only for a small subset of acute IS patients and are effective only within 4.5 hours of symptom onset, rendering approximately 90% of patients ineligible for thrombolysis. The limitations of current plasmin-dependent agents highlight the urgent need for novel thrombolytics that function independently of plasmin activation. Recently, we identified high-temperature requirement A1 (HtrA1) as a potential plasmin-independent thrombolytic enzyme. However, its mechanism of action remained unclear. In this study, we demonstrate for the first time that HtrA1 functions as a clot-selective thrombolytic agent, effectively targeting thrombi without compromising the integrity of hemostatic clots involved in wound healing. These findings provide a promising new direction for the safe and effective treatment of ischemic stroke.

PVM-3

KSHV infected tumor cells induce immune tolerance in trained macrophages

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Kaposi's sarcoma-associated herpesvirus (KSHV) is the causative agent of tumors like primary effusion lymphoma (PEL) and Kaposi's sarcoma (KS) in immunocompromised individuals. Given the lack of effective treatments and trained immune cells emerging as candidate cellular therapies, we investigated a therapeutic potential in KSHV-related malignancies. To test this, we examined interaction between KSHV-infected tumor cells (BCBL) and trained macrophages. In co-culture experiments, we observed that KSHV mRNA expression was elevated in the BCBL cells, while pro-inflammatory cytokine mRNA expression was suppressed in the trained macrophages, suggesting that KSHV may dampen inflammatory signaling to sustain its persistence. Conversely, when BCBL cells were treated with conditioned media from trained macrophages, KSHV mRNA expression was decreased. This led us to hypothesize that pro-inflammatory cytokines could suppress KSHV replication. To verify this, BCBL cells were treated with key pro-inflammatory cytokine mixture derived from trained macrophages, which activated NF-κB and STAT3 pathways and resulted in significant reductions in KSHV mRNA, viral protein level, and episome copy number. Collectively, our study reveals a new mechanism in which KSHV-infected cells exploit the innate immune system by inducing immune tolerance in macrophages to evade antiviral signals, providing important insights for future therapeutic strategies.

PVM-4

In Silico Investigation of β1-Adrenergic Receptor Interactions with L-Glutamine and α-δ-N-Acetyl-Glutamine: Implications for GPCR Signaling Pathways

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The β1-adrenergic receptor (β1-AR), a prototypical G protein-coupled receptor (GPCR), integrates extracellular signals with intracellular pathways that regulate metabolism, mitochondrial function, and stress responses—key determinants of aging. Here, we performed an in-silico investigation of L-glutamine and its derivative α-δ-N-acetyl-glutamine to explore their interactions with β1-AR. Molecular docking revealed stable binding through hydrogen bonds and hydrophobic contacts, while molecular dynamics simulations demonstrated conformational stabilization of the receptor–ligand complexes. Mechanistically, L-glutamine and its derivative-mediated modulation of β1-AR may influence nutrient-sensing and longevity-related pathways, including PI3K/Akt/mTOR signaling, which controls mitochondrial bioenergetics, proteostasis, and cellular stress resilience. These findings suggest a novel link between L-glutamine and its derivative α-δ-N-acetyl-glutamine and GPCR signaling, providing a potential strategy for anti-aging interventions.

PVM-5

Design and Immunogenicity Evaluation of Recombinant Subunit Vaccine Candidates Against Henipaviruses

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Nipah virus (NiV) is a highly pathogenic member of the *Paramyxoviridae* family that causes severe neurological and respiratory diseases and has led to outbreaks in Southeast Asia. Human infection with NiV results in a high case fatality rate of 40-75%, yet no approved vaccines or therapeutics are currently available. The major protective antigens that elicit immune defense against NiV are the fusion (F) and attachment (G) glycoproteins, which mediate membrane fusion and host receptor binding during viral entry. This study focuses on evaluating NiV vaccine antigen design options based on these key glycoproteins.
NiV consists of two major strains, Malaysia (NiV-M) and Bangladesh (NiV-B), which share high sequence similarity in the F and G proteins responsible for virus-host cell attachment. Therefore, consensus sequences of the NiV-M and NiV-B were synthesized to develop recombinant subunit vaccine candidates, which were subsequently evaluated for immunogenicity in BALB/c mice and Syrian golden hamsters using various antigen-adjuvant combinations. Among these, the G(ct) antigen induced neutralizing antibody titers comparable to those elicited by G2 (NiV-M + NiV-B), previously identified as the most effective vaccine candidate. Strong humoral immune responses were observed across all candidates, and notably, G(ct) alone was sufficient to induce robust immunity. In addition, binding antibodies against the Hendra virus antigen—known to cross-react with Nipah virus—were also detected. Furthermore, G(ct) formulated with AddaS03, a water-in-oil nanoemulsion adjuvant, elicited stronger neutralizing antibody responses than those induced with other adjuvants.
Collectively, these findings demonstrate that consensus G protein-based subunit vaccine candidate represent promising candidates for the prevention of both Nipah and Hendra virus infections. This study highlights the rational design of NiV vaccines as a key step toward strengthening preparedness and response strategies against future outbreaks of these biosafety level 4 pathogens and emphasizes the need for further validation using NiV challenge models.

PVM-6

Immunogenicity Evaluation of a Gn-Based mRNA Vaccine Candidate Against the Tick-Borne RNA Virus SFTSV

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Severe Fever with Thrombocytopenia Syndrome (SFTS) is a fatal tick-borne disease caused by SFTS virus (SFTSV), with mortality rates approaching 40%. It is characterized by high fever, gastrointestinal symptoms, thrombocytopenia, and leukopenia. Despite its severity, no licensed vaccines or therapeutics are currently available, underscoring the urgent need for effective preventive strategies. We developed an mRNA vaccine candidate encoding a modified Gn glycoprotein subunit, a major antigenic component of SFTSV. Mutations introduced into the signal peptide and transmembrane regions enhanced glycoprotein secretion, and the engineered mRNA formulated with a nanoparticle delivery system showed efficient expression. In both in vitro and in vivo studies, the vaccine candidate elicited promising immunogenicity, supporting its ability to induce protective immune responses. These findings demonstrate that the Gn-based mRNA vaccine candidate represents a feasible approach for SFTS prevention and highlight the broader potential of the mRNA platform as a countermeasure against emerging viral infections.

PVM-7

Small Interfering RNA Screen Identifies Human Host Factors Critical for Dabie Bandavirus Infection

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Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne viral disease characterized by high case-fatality rates and the absence of approved vaccines or antiviral therapies. To investigate host-virus interactions and identify potential antiviral targets, we performed siRNA screening of host factors previously identified through high-throughput protein chip microarray technology as binding partners of the Dabie Bandavirus (SFTSV) nucleoprotein (NP) or nonstructural protein (NSs). Several host genes were identified as significant regulators of viral replication, acting either to promote or restrict SFTSV growth. These findings provide new insights into host dependencies of SFTSV and highlight promising candidates for therapeutic intervention. However, further studies are needed to validate the molecular functions of these host factors and elucidate their mechanisms during infection. Our study advances understanding of SFTSV replication and supports the development of novel antiviral strategies.

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PVM-8

Development of a Gut Microbe-Based Pan-Coronavirus Vaccine via Activation of Host-Directed IL-2 and IFN-γ Immunity

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The rapid evolution and continual emergence of pathogenic coronaviruses have exposed the limitations of strain-specific vaccines and emphasize the urgent need for broadly protective prophylactics. Despite intense global efforts, no countermeasure has yet provided cross-protective efficacy across the Coronaviridae family. Here, we report that a pair of human commensal gut microbes (GMP), *Oribacterium* sp. GMB0313 and *Ruminococcus* sp. GMB0270, confers complete protection against SARS-CoV-2, its Omicron variant, and MERS-CoV in multiple preclinical models. Colonization of GMP activated a host-intrinsic immune pathway, selectively expanding IL-2- and IFN-γ-producing CD8+ T cells through dendritic cell-mediated cross-presentation of microbial antigens. The GMP-mediated response provided superior prophylactic efficacy compared with current mRNA vaccines, characterized by enhanced cellular immunity, restrained inflammation, and rapid induction of antigen-specific antibodies. These findings establish a proof-of-concept for a host-directed, microbiota-based vaccine and suggest that rational use of defined commensal microbes may enable development of a universal coronavirus vaccine.

PVM-9

Establishment of an mRNA Vaccine Platform for Chikungunya Virus

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Chikungunya virus (CHIKV) is a mosquito-borne RNA virus of the Alphavirus genus that has expanded globally since its first recognition in Tanzania in 1952. Recurrent outbreaks across tropical and subtropical regions have raised major public health concerns due to prolonged joint pain and socioeconomic impact. To address the urgent need for vaccination, we previously developed a recombinant protein-based CHIKV vaccine that showed strong immunogenicity in mice. Building on these findings, we are developing an mRNA-based vaccine platform to enable rapid and scalable vaccine production. The mRNA candidate, encoding CHIKV structural proteins, was designed with optimized coding and regulatory sequences for efficient expression and formulated with lipid nanoparticles (LNPs) for enhanced delivery. Production of the vaccine candidate is currently in progress, and preclinical efficacy studies will be conducted to evaluate humoral and cellular immune responses. This study establishes the foundation for an mRNA-based CHIKV vaccine platform and provides a framework for extending mRNA vaccine development to other emerging arboviral diseases.

PVM-10

α, δ-N-acetyl-glutamine suppresses neutrophilic airway inflammation by activating the GPCR/MKP-1 pathway

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L-glutamine (Gln) suppresses inflammation via upregulation of mitogen-activated protein kinase (MAPK) phosphatase (MKP)-1; however, high dosages required may cause serious side effects. Here, we developed a glutaminase-resistant less-hydrolyzable Gln derivative, α, δ-N-acetyl-glutamine (α, δ-NAG). Oral administration of α, δ-NAG and Gln to ovalbumin-induced asthma model mice suppressed asthmatic parameters at 0.2 and 2 g/kg body weight, respectively. α, δ-NAG upregulated MKP-1 in an extracellular signal-regulated kinase (ERK) MAPK-dependent manner. MKP-1 siRNA abrogated the beneficial effects of α, δ-NAG. α, δ-NAG transiently increased intracellular calcium ([Ca^{2+}]i), resulting in increased Ras activity. Inhibition of Gαq, a G-protein subfamily, abrogated the effects of α, δ-NAG on [Ca^{2+}]i and Ras activity. Inhibition of Gαq, Ca^{2+}, and Ras abrogated the α, δ-NAG effects, such as ERK phosphorylation and MKP-1 upregulation and neutrophilia/Th1 responses in asthmatic mice. Overall, α, δ-NAG exhibited ~10,000-fold stronger anti-inflammatory activity than Gln, likely attributable to its upregulation of MKP-1 by activating the G protein-coupled receptor (GPCR)/Gα q/Ca^{2+}/Ras/ERK cascade.

PVM-11

Establishment of Immunogenicity Assay Platforms for Lassa Virus Vaccine Candidates Using a Guinea Pig Model

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Background

Lassa virus (LASV) is an arenavirus that causes Lassa hemorrhagic fever in humans and other primates. The virus is endemic in West African countries, with an estimated 300,000 to 500,000 infections and approximately 5,000 deaths annually. While the overall mortality rate is around 1%, it exceeds 15% among hospitalized patients with severe symptoms. Currently, there is no approved human vaccine for Lassa fever. Organizations such as CEPI have designated Lassa fever as a priority infectious disease and are actively supporting vaccine development efforts. Several domestic companies are also developing Lassa vaccines, and therefore, our institution—which operates a Biosafety Level 4 (BSL-4) facility—is working to establish evaluation methods to support these private sector initiatives.

Methodology and Results

We first selected LASV prefusion glycoprotein complex (GPC) antigens and IFN-γ antibody pairs to optimize antigen-specific IgG ELISA and IFN-γ ELISpot assays in a guinea pig model. Subsequently, we optimized antigen and antibody concentrations to establish protocols suitable for supporting private-sector vaccine development. Our experimental methods demonstrated high repeatability and precision, showing consistent and reproducible results throughout.

Model Selection and Future Applications

Although various animal models—including mice, guinea pigs, and non-human primates—are used in LASV research, non-human primates are expensive and logistically challenging to use, while mouse models are limited to immunodeficient strains (e.g., STAT1-/-). For this reason, we selected a fully immunocompetent guinea pig model, which develops clinical symptoms similar to those observed in humans after LASV infection. We are currently documenting these procedures as standard operating protocols (SOPs) and aim to utilize our optimized ELISA and ELISpot methods for the future evaluation of LASV vaccine candidates submitted by companies.

PVM-12

Development of Monoclonal Antibodies Targeting the Nipah Virus G glycoprotein

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Nipah virus (NiV) is a zoonotic pathogen belonging to the Paramyxoviridae family and the Henipavirus genus, first identified during a 1998 outbreak in Malaysia. It is primarily endemic to Southeast Asia and India, causing a severe infectious disease with a case fatality rate of up to 75%. The Nipah virus glycoprotein G (NiV-G) is a surface attachment protein essential for viral entry. NiV-G binds to host cell receptors ephrin-B2 and ephrin-B3, and monoclonal antibodies(mAbs) targeting this glycoprotein can effectively suppress viral spread during the early stages of infection. However, no approved therapeutics are currently available for Nipah virus infection. In this study, we developed mAbs against the NiV-G and evaluated their binding affinity and neutralizing efficacy. BALB/c mice were immunized with a formulation containing the NiV-G antigen and an adjuvant, and antibody titers were monitored by enzyme-linked immunosorbent assay (ELISA). B cells were isolated from the spleen, fused with myeloma cells to generate hybridomas, and antigen-specific mAbs-producing clones were selected. Subsequently, the mAbs were produced in mouse ascitic fluid and purified by Protein G affinity chromatography. Both SPR and ELISA analysis confirmed that all purified antibodies exhibited high affinity and specific binding to the NiV-G. Finally, three antibodies demonstrated neutralizing activity in evaluation using Vesicular stomatitis virus (VSV)-based pseudovirus assay. Taken together, the developed neutralizing antibodies could potentially be considered as candidates for the development of Nipah virus therapeutics.

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PVM-13

2025 Infectious Disease Monitoring in the Wastewater-Based Infectious Disease Surveillance System in Chungcheongnam-do

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Wastewater-based surveillance allows monitoring of infectious disease trends in communities by detecting pathogens excreted before clinical symptoms appear. In Korea, after a pilot project during 2021-2022, the national wastewater-based infectious disease surveillance program has been implemented in collaboration with 18 regional Institutes of Health and Environment Research since April 2023.

From January to September 2025, weekly influent wastewater samples were collected from eight public wastewater treatment facilities in Chungcheongnam-do. A total of 4,344 samples were analyzed for 14 pathogens, including SARS-CoV-2, Norovirus G I /G II, Influenza virus A/B, and other viruses. Samples underwent large-volume concentration and nucleic acid extraction, followed by real-time PCR and digital PCR. SARS-CoV-2 concentrations were compared with weekly confirmed COVID-19 case from the Korea Sentinel Surveillance(K-SenS).

A total of 13 viral pathogens were detected, with 2,099 of 4,344 samples testing positive (48.3%). Detection rates were highest for SARS-CoV-2 and Norovirus (100%). Among respiratory viruses, Human bocavirus (69.9%), Influenza virus A/B (52.2%), and Human adenovirus (51.8%) were most frequently observed. For enteric viruses, Astrovirus (94.2%), Enteric adenovirus (90.1%) predominated, followed by Rotavirus (44.9%). SARS-CoV-2 concentration in wastewater showed a relatively high correlation with Korea sentinel surveillance data on confirmed COVID-19 cases ($r = 0.80$).

Wastewater-based surveillance effectively detects multiple viral pathogens and reflects community-level infection trends. These findings support its integration into public health surveillance frameworks to enhance preparedness and response to emerging infectious diseases.

PVM-14

Efficacy Evaluation of hzVSF-v13, an Antiviral Candidate for RNA Virus Infection

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Finding an effective treatment against coronavirus disease-2019 (COVID-19) is urgently needed. COVID-19 can disrupt the regulation of the innate host immune system, leading to hypercoagulation, hyperinflammatory. The lungs are the main affected organ in severe COVID-19. Humanized virus suppressing factor-variant 13 (hzVSF-v13) is a monoclonal IgG4 against vimentin, which is expressed on the surface of virus-infected cells. Therapeutic efficacy of a hzVSF-v13 was evaluated with the SARS-CoV-2 infected Roborovski hamster. The SARS-CoV-2-infected hamster rapidly fell into hypothermia after a high fever and showed a typical COVID-19 infection pattern entering the terminal stage equivalent to death at 4 dpi (days post infection). But the hamster injected with hzVSF-v13 had a slight increase in body temperature and gradually began to recover to normal from 2 dpi. The hzVSF-v13 was effective in treating severe COVID-19 by inhibiting the growth of viruses and inflammation. The hzVSF-v13 is significant currently when there is no suitable COVID-19 treatment.

PVM-15

Antioxidant and Antithrombotic Activities of Hempseed Protein Isolate

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Hempseed (*Cannabis sativa L.*) is the seed of industrial hemp, which contains negligible levels of the psychoactive compound Δ^9-tetrahydrocannabinol (THC). Recently, hempseed has attracted considerable attention as a functional food ingredient due to its richness in proteins, essential fatty acids, dietary fiber, vitamins, and minerals. In particular, hempseed cake (HSC), a by-product obtained after oil extraction, has been investigated for product development. HSC contains concentrated proteins and dietary fiber, making it valuable for use in animal feed, protein supplements, and food processing materials. However, HSC has several limitations, including susceptibility to microbial and insect contamination, an oil content exceeding 10% that leads to rancidity during long-term storage, and the presence of crushed seed residues that lower sensory quality. In this study, hempseed protein isolate (HPI) was prepared by hot water extraction of HSC to evaluate the feasibility of producing a protein powder with superior functionality, sensory quality, and storage stability. Under high-temperature aqueous extraction conditions, the yield of HPI was 25-30%, with a protein content exceeding 80%. Compared with HSC, HPI exhibited increased levels of valine, isoleucine, serine, arginine, tyrosine, and phenylalanine. In addition, HPI contained higher amounts of total sugars and total polyphenols. Serial Amicon fractionation and Sephadex G-150 column chromatography of HPI ultimately identified a 45.8 kDa protein fraction, which demonstrated potent antioxidant and antithrombotic activities. These findings suggest that HSC can be utilized to produce hempseed protein isolates with enhanced antioxidant and antithrombotic activities, offering potential as a high-value functional protein ingredient.

PVM-16

Anti-coagulant, antioxidant and antifungal activities of different parts of *Larix kaempferi*

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Larix kaempferi (Japanese larch), a conifer belonging to the Pinaceae family, is both a deciduous and needle-leaf tree. Its name originates from its resemblance to pine trees, with the distinction of shedding its needles annually. In this study, 70% ethanol extracts were obtained from the leaf and branch of *Larix kaempferi* to evaluate their bioactive properties. The total polyphenol content, antioxidant activities (DPPH and ABTS radical scavenging, nitrite scavenging, and reducing power), anti-coagulant activities (assessed by thrombin time [TT], prothrombin time [PT], and activated partial thromboplastin time [aPTT]), and antifungal activities (using the disk diffusion method) were analyzed. The total polyphenol content of the leaf extract was 176.2 mg/g, while the branch extract was slightly higher at 299.3 mg/g. branch extracts exhibited superior antioxidant activities, whereas leaf extracts demonstrated more effective nitrite scavenging abilities. Both extracts showed over 15-fold stronger anti-coagulant activities compared to aspirin at a concentration of 5.0 mg/mL. Notably, the branch extract enhanced TT and aPTT by more than 15-fold even at 2.5 mg/mL and exhibited 2.14-fold prothrombin inhibition activity, surpassing aspirin (1.40-fold) at 1.5 mg/mL. Additionally, the leaf extract displayed antifungal activity against *Candida albicans* CCARM 14016 and 14020, which are resistant to the antibiotic miconazole. These findings suggest that the leaf and branch of *Larix kaempferi* possess significant bioactive properties, highlighting their potential as functional food ingredients.

PVM-17

Anti-coagulant and antioxidant activities of different parts of *Amelanchier asiatica*

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Amelanchier asiatica (commonly known as Dogyo tree) belongs to the Rosaceae family and is widely distributed across temperate regions of the Northern Hemisphere, including Korea, China, and Japan, as well as parts of the United States. Previous studies have reported its antioxidant, anti-gout, antihypertensive, anti-wrinkle, and anti-inflammatory properties. In this study, the physiological activities of 70% ethanol extracts from the leaves and fruits of *A. asiatica* were evaluated. The total polyphenol content in the leaf extract (240.0 mg/g) was higher than that in the fruit extract (3.8 mg/g). Antioxidant activity assays revealed that the leaf extract exhibited superior radical scavenging activity against DPPH and ABTS radicals, nitrite scavenging activity, and reducing power compared to the fruit extract. Anticoagulant activity was assessed by measuring prothrombin time (PT), activated partial thromboplastin time (aPTT), and thrombin time (TT). At a concentration of 5.0 mg/ml, the fruit extract showed no significant activity, with TT, PT, and aPTT values of 0.92-fold, 0.92-fold, and 0.99-fold, respectively, relative to the control. In contrast, the leaf extract demonstrated over 15-fold prolongation in TT, PT, and aPTT at the same concentration, indicating significant anticoagulant effects. Neither extract exhibited hemolytic activity.In conclusion, the leaf extract of *A. asiatica* exhibited strong antioxidant and anticoagulant activities, suggesting its potential as a functional food ingredient.

PVM-18

Anti-coagulant, antioxidant and anti-diabetic activities of different parts of *Sorbus alnifolia*

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Sorbus alnifolia, a species in the Rosaceae family, is distributed across Korea, Japan, and China. Its fruits have been traditionally used to treat anemia and weakness. This study evaluated the bioactive properties of 70% ethanol extracts from the fruits and leaves of *S. alnifolia*. The total polyphenol content was higher in the leaf extract (221.8 mg/g) than in the fruit extract (64.2 mg/g). Antioxidant assays revealed that the leaf extract exhibited superior DPPH and ABTS radical scavenging activity, while the fruit extract showed higher nitrite scavenging and reducing power. Anticoagulant activity was assessed by measuring prothrombin time (PT), activated partial thromboplastin time (aPTT), and thrombin time (TT). At 5.0 mg/ml, the fruit extract showed 15-fold increases in TT and PT and a 1.64-fold increase in aPTT compared to the control. The leaf extract also exhibited over 15-fold increases in all three tests, indicating strong anticoagulant potential. No hemolytic effects were observed in either extract. Antidiabetic activity was evaluated through α-glucosidase and α-amylase inhibition. The fruit and leaf extracts inhibited α-glucosidase by 10.7% and 12.6%, respectively, at 0.5 mg/ml. α-Amylase inhibition was observed only in the leaf extract, which showed significant activity. In conclusion, the fruit and leaf extracts of *S. alnifolia* demonstrated notable antioxidant, anticoagulant, and antidiabetic activities, suggesting their potential as functional food resources.

PVM-19

Anti-coagulant, antioxidant and anti-diabetic activities of different parts of *Litsea japonica*

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Litsea japonica, commonly planted as a roadside tree in coastal areas such as Jeju Island, has been studied for its potential in cancer prevention, diabetic complication mitigation, anti-inflammatory properties, and inhibition of bone metabolism-related factors. This study evaluated the physiological activities of ethanol and hot water extracts from the leaves and fruits of *Litsea japonica*. The total polyphenol content was highest in the ethanol extract of the leaves (98.3 mg/g), whereas the fruits exhibited higher polyphenol content in the hot water extract (39.3 mg/g) than in the ethanol extract. Antioxidant assessments showed that the ethanol extract of the leaves demonstrated superior DPPH radical and nitrite scavenging activities, while the hot water extract of the fruits exhibited strong ABTS radical scavenging and reducing power. Anti-coagulant activity was analyzed based on prothrombin time (PT), activated partial thromboplastin time (aPTT), and thrombin time (TT). At 5.0 mg/ml, the hot water extract of the leaves showed 15-fold and 1.02-fold higher activity in TT, aPTT, and PT, respectively. Similarly, the ethanol extract of the leaves exhibited 2.12-fold, 2.14-fold, and 0.99-fold higher activity in TT, aPTT, and PT. In contrast, the fruit extracts displayed little to no anti-coagulant activity. Neither extract induced hemolytic reactions. For anti-diabetic activity, at 0.5 mg/ml, the ethanol extracts of the leaves and fruits exhibited 21.8% and 22.9% α-glucosidase inhibitory activity, respectively. In conclusion, the leaf extracts of *Litsea japonica* demonstrated excellent antioxidant, anti-coagulant, and anti-diabetic activities, suggesting their potential as valuable resources for functional foods.

PVM-20

Distinct host antiviral responses to EGFR inhibition during RSV infection

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Respiratory syncytial virus (RSV) is a leading cause of severe lower respiratory tract disease in infants, older adults, and immunocompromised individuals, yet effective therapeutic interventions remain limited. Although supportive care and nucleoside analogs such as ribavirin offer limited clinical benefit, no broadly effective antiviral therapy is currently available. Increasing evidence implicates epidermal growth factor receptor (EGFR) signaling in RSV pathogenesis, but the intracellular functions of EGFR during infection remain poorly understood. Here, we show that inhibition of EGFR signaling markedly suppresses RSV replication in a dose- and time-dependent manner, establishing EGFR as a critical host factor required for efficient viral propagation. Subcellular analyses reveal that RSV infection induces a redistribution of EGFR and alters mitochondrial organization, accompanied by changes in key regulators of mitochondrial dynamics and metabolic control. These findings suggest that EGFR signaling contributes to virus-induced remodeling of mitochondrial function, linking viral replication to host energy metabolism. Comparative transcriptional profiling demonstrates that inhibition of the host EGFR pathway and treatment with the nucleoside analog ribavirin elicit distinct antiviral signatures, reflecting divergent mechanisms between host-targeted and direct-acting antivirals. Our findings identify intracellular EGFR signaling as a pivotal host pathway exploited during the early stages of RSV infection, whose inhibition activates a unique host-directed antiviral program, uncovering an underappreciated role of EGFR in coordinating viral replication and organelle homeostasis, and providing a mechanistic foundation for host-targeted therapies against RSV.

PVM-21

Epidemiological and genectic analysis of the 2023 adenovirus outbreak in Gwangju, South Korea

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Background: Adenovirus is significant pathogens causing a wide range of clinical symptoms such as respiratory, intestinal infection, and conjunctivitis. Adenovirus occur year-round without specific epidemic season, accompanying clinical and socio-economic burden. We have been participating in the Korea Respiratory virus Integrated Surveillance System(K-RISS) by monitoring suspected acute respiratory virus samples in Gwangju area. This study aimed to examine the trends of adenovirus and analyze the genotypes.

Method: We collected a total of 3,438 throat or nasal swabs from outpatients with Acute Respiratory infections(ARIs) in Gwangju area in 2023. We extracted nucleic acids from the samples and detected 9 target pathogens(Influenza virus, Parainflueanza virus, human Coronavirus, Metapneumovirus, Rhinovirus, Adenovirus, Bocavirus, COVID19). Adenovirus Positive samples were carried out Next Generation Sequencing and phylogenetic analysis was performed using whole genome.

Result: In 2023, adenovirus was the most detected of the nine respiratory viruses with 688 adenovirus positive detections out of 3,438 samples. The detection rate of adenovirus began to rise sharply to 44.4% in Week 33 of 2023, reaching 60.0% in Week 40. Phylogenetic analysis of whole genome of 35 specimens selected randomly showed that the number of species B was 20(57.1%) and species C was 15(42.9%). In addition, Phylogenetic analysis of each of major antigenic regions of adenovirus-Penton, Hexon, and Fiber- showed that there were type 1, type 2, type 5, type 89, type 108 and type 114. From July to December, during outbreak, type 114 was the most detected.

Conclusion: The timing of the increase in detection rates coincided with the period when adenovirus type 114 was the dominant strain suggesting that Adenovirus type 114 was responsible for the 2023 outbreak in Gwangju. Continuous surveillance of respiratory virus is important for tracking trends in virus activity, seasonality, and geographic spread. Furthermore surveillance data of adenovirus guide strategy of developing vector for vaccine or genome therapy.

PVM-22

Whole-Genome Analysis of SFTSV isolated from Ticks in Gyeongju, South Korea

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Sever fever with thrombocytopenia syndrome virus(SFTSV), a tickborne phlebovirus first identified in China in 2009, has since been reported across East Asia, including Japan and South Korea, posing a significant public health threat. In South Korea, *Haemaphysalis longicornis* is recognized as the predominant tick vector, frequently associated with SFTSV transmission. In this study, we analyzed the complete genome of an SFTSV strain (GJGB-J, GJGB-A) isolated from a female *H. longicornis* tick collected in Gyeongju, Gyeongbuk Province, South Korea. Whole-genome sequencing revealed that the L segments of the GJGB-J and GJGB-A are most closely related to the Japanese strain SPL030A, the M segments clustered with SPL105A, and the S segments exhibited the highest similarity to Korean strains (KAGWH3 and KAGWT), while still showing genetic proximity to SPL030A. These findings suggest that both GJGB-J and A belong to an East Asian lineage with evidence of segment-specific diversity, potentially reflecting historical reassortment events among circulating strains. Our results provide insights into the molecular epidemiology of SFTSV in South Korea and highlight the importance of continuous genomic surveillance to better understand viral evolution and cross-border transmission dynamics.

PVM-23

Two-Year Community-Wide Monitoring of Respiratory Virus Trends Using Wastewater-Based Epidemiology in Jeju

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Purpose: This study systematically investigated the seasonal and periodic dynamics of eight major respiratory viruses -including Influenza virus, Parainfluenza virus, Rhinovirus, human Metapneumovirus, human Coronavirus, Adenovirus, human Bocavirus, and Respiratory Syncytial virus (RSV)-over 123-week period from week 7 of 2023 to week 22 of 2025 in Jeju's island-type metropolitan environment. The research considered Jeju's unique geographic characteristics and the influence of substantial tourist influx to assess the effectiveness of wastewater-based epidemiology for monitoring and detecting respiratory virus outbreaks.

Methods: Weekly composite influent samples were systematically collected from municipal wastewater treatment plants serving approximately 670,000 residents. Viral RNA was simultaneously detected and quantified using a TaqMan Array Card-based multiplex RT-qPCR assay, in which positive signals were determined based on validated cycle threshold (Ct) and strict quality controls. Temporal distributions of viral concentrations were statistically analyzed alongside clinical incidence data using Pearson correlation and time-series forecasting models.

Results: Over the 123-week observation period, wastewater signals from multiple respiratory viruses showed clear seasonal and periodic patterns that closely aligned with clinical surveillance data in Jeju. Increases in viral RNA concentrations in wastewater consistently preceded surges in clinical cases by approximately 1-2 weeks, demonstrating the early warning potential of wastewater-based epidemiology (WBE). Strong negative correlations were observed between wastewater viral loads and clinical cases, exemplified by influenza (*Pearson r* = - 0.87), parainfluenza (*Pearson r* = - 0.80), and human metapneumovirus (*Pearson r* = - 0.82), all statistically significant with p-values < 001. Time-series forecasting models achieved 76-89% accuracy in predicting clinical case increases across all virus types, confirming the monitoring approach's robustness and predictive reliability in Jeju's community-level respiratory virus surveillance.

Conclusions: This two-year, city-wide wastewater-based surveillance study provides robust evidence that monitoring eight major respiratory viruses through RT-qPCR analysis of municipal wastewater is a reliable and scalable approach for tracking community transmission dynamics in Jeju. Wastewater viral loads were consistently and strongly correlated with clinical incidence data, with viral load peaks in wastewater preceding clinical case surges by approximately one to two weeks across all viruses studied. This early warning capability was demonstrated repeatedly through multiple epidemic cycles and seasonal variations. The study highlights the significant potential of wastewater-based epidemiology to supplement and enhance traditional clinical surveillance systems. Continuous development of integrated surveillance models and leveraging regional characteristics such as tourist traffic are recommended for enhanced outbreak detection and public health intervention.

PVM-24

Sequence variation between SFTSV F and B strains influences recombinant Gn protein expression and solubility

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Severe fever with thrombocytopenia syndrome virus (SFTSV) or Dabie bandavirus has been considered an emerging threat to human owing to its high fatality (~20%) since fisrt discovered in China in 2012. Mainly, the Gn glycoprotein of *Phlebovirus* in *Phenuiviridae*, including SFTSV, is a critical target for antibody therapeutics, vaccine development, and serological diagnostics. Thus, strain-specific production optimization is essential to obtain the functional Gn protein required for these applications. In this study, we transiently expressed recombinant Gn proteins from two SFTSV strains (F and B) in Expi293F cells using a plasmid construct incorporating both Avitag and His-tag sequences. Following purification via nickel affinity chromatography and size-exclusion chromatography, protein quality and yield were assessed by SDS-PAGE, Western blot, and ELISA using both a commercial SFTSV Gn-specific antibody and an in-house developed monoclonal antibody. Notably, expression yields differed between the F and B strains, suggesting strain sequence-dependent variation in protein production efficiency and solubility. These findings provide a platform for further structural and immunological characterization of SFTSV Gn and support its application in antibody therapeutics, vaccine design, and sero-diagnostics.

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PVM-25

Antiviral Activity Analysis of *Humulus japonicus* Extract

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Both influenza virus and coronavirus are viruses that have caused worldwide pandemic diseases. In this study, we investigated the antiviral efficacy of evergreen conifers growing in Gyeonggi-do to develop antiviral agents for coronaviruses for which there are no antiviral agents. Cell viability was measured by MTT assay (Modified ISO 10993-5), and antiviral activity was measured by a modification of ASTM E1052-20. To investigate the effect of *Humulus japonicus* extract on cells, the cell viability of the host cells of H1A1 influenza virus and coronavirus was measured. As a result, it did not show cytotoxicity in the influenza host cells, but cytotoxicity was shown in the host cells of coronavirus at high concentrations. As a result of measuring the antiviral activity of *Humulus japonicus* extract against H1A1 and coronavirus, it showed a virus reduction rate of 99.996% in the case of H1A1, and 92.06% and 96.84% in the case of FCoV and HCoV, respectively. Accordingly, *Humulus japonicus* extract is expected to be used as a substance for the treatment or prevention of infections caused by H1A1, FCoV, and HCoV.

PVM-26

Development and Immunogenicity Evaluation of a Recombinant Envelope Protein-Based Vaccine Candidate Against Chikungunya Virus

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Chikungunya virus (CHIKV) is a mosquito-borne, positive-sense RNA virus belonging to the Alphavirus genus within the Togaviridae family, first identified in Tanzania in 1952. Since its reemergence in the Indian Ocean region in 2004, CHIKV has caused large-scale outbreaks across Africa, Asia, and Europe, becoming a global public health concern. Transmitted by infected Aedes mosquitoes, CHIKV is classified as a biosafety level 3 pathogen and causes chikungunya fever, which is characterized by high fever and prolonged joint pain. Among its structural proteins, the envelope proteins (E1, E2, E3, and 6K) are critical for viral entry and serve as primary targets for neutralizing antibodies. Based on the structural and functional properties of CHIKV envelope proteins, we designed a recombinant protein vaccine antigen with improved production efficiency. Immunization studies in C57BL/6 mice confirmed that the CHIKV vaccine candidate elicited strong immune responses. In addition, we established multiple efficacy evaluation methods to comprehensively analyze the immunogenicity of CHIKV vaccines. These methods will be applied not only to the development of CHIKV vaccine candidates but also as a platform to support efficacy evaluation of vaccines against emerging infectious diseases in the private sector.

PVM-27

Impacts of Climate Change on Mosquito Ecology and Vector-Borne Disease Risk in Jeollanam-do (2021-2024)

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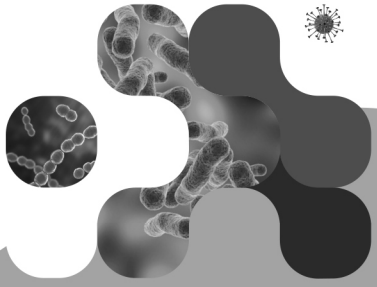
According to the World Health Organization (WHO), approximately 720,000 people die each year from mosquito-borne infectious diseases. With the acceleration of climate change, concerns about the spread of vector-borne infectious diseases are growing as the mosquito activity period is advancing and the number of mosquitoes is increasing. This study analyzed the distribution and ecological characteristics of mosquitoes in the Jeollanam-do region from 2021 to 2024 and evaluated the impact of environmental and climatic factors. Mosquitoes were collected from various environments, including urban area, bird sanctuary, and Cattle shed sites, and their density was analyzed using various types of traps. A total of 168,312 female mosquitoes belonging to 16 species were collected, with the main species identified as *Culex pipiens, Aedes albopictus, Aedes vexans*, *Anopheles* spp. and *Culex tritaeniorhynchus.* In particular, the population of *Culex tritaeniorhynchus*, the primary vector for Japanese encephalitis, showed a notable increase. Additionally, differences in mosquito species distribution were observed depending on environmental factors such as urbanization and habitat changes. Mosquitoes are generally known to be observed mainly at temperatures of 25~27℃ and humidity levels of 60%; however, In this study, an increasing trend in mosquito survival was observed under temperatures exceeding 30℃ and high humidity conditions of up to 80%. Mosquito density was found to be significantly influenced by rising temperatures ($r=0.72$, $p<0.001$) and relative humidity ($r=0.43$, $p<0.001$). However, no significant correlation was observed with precipitation. Although flavivirus infection was not detected during the four-year monitoring period, the risk of infectious disease outbreaks may increase in the future due to the possibility of invasive mosquito species being introduced as a result of climate change. These results emphasize that changes in the mosquito ecosystem due to climate change could pose a public health threat in Korea, underscoring the need for continuous surveillance and targeted vector control strategies. Key words: Vector-borne disease; *Culex tritaeniorhynchus*; Japanese encephalitis virus.

Keywords Index



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감염병기술전략센터

감염병 대응역량 강화를 위한 기술-전략-산업 연계 플랫폼 구축

글로벌 경쟁력을 갖춘 감염병 대응 기술 확보를 위해 핵심유망기술을 집중 지원하고 기술전략을 수립하는 감염병 대응 싱크탱크 역할을 수행하겠습니다.

미션 글로벌 시장 선도를 위한 기술 주도 혁신

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