MONGOLIAN ACADEMY OF SCIENCES
INSTITUTE OF BIOLOGY

The International
Biological Conference in Mongolia
IBCM25
60 YEARS OF IB, MAS | 18-19 SEPTEMBER | MONGOLIA

ABSTRACT BOOK

September 18-19, 2025
Ulaanbaatar, Mongolia

Abstract Book of the International Biological Conference in Mongolia, Ulaanbaatar, Mongolia, 18–20 September 2025. Celebrating 60 years of excellence in biological sciences, Institute of Biology, Mongolian Academy of Sciences (1965–2025).

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Gantulga Davaakhuu

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Table of Contents

Preface

Dear Colleagues,

Sixty years ago, the seeds of biological science in Mongolia were planted. Today, they have grown into a thriving community of researchers, innovators, and explorers who are shaping our understanding of life, ecosystems, and the world around us. In the Asian lunar calendar, 60 years marks the completion of a full cycle, a moment to honor what has been achieved, to reflect, and to look forward with hope toward a new chapter of discovery. It is a great honor to welcome you to the International Biological Conference in Mongolia (IBCM 2025) in Ulaanbaatar on September 18–19, a gathering that represents the broadest international participation in Mongolian biology to date.

This conference is not just a reflection on the past; it is a call to the future. Here, we come together across borders and disciplines to share ideas, challenge assumptions, and imagine new possibilities. Together, we can advance knowledge, protect our planet's biodiversity, and create solutions that improve lives for generations to come. This is our opportunity to write the next chapter in the story of Mongolian science, a chapter defined by collaboration, innovation, and ambition.

The abstracts in this volume offer a glimpse of that story. They capture the creativity, rigor, and forward-looking spirit of our community, showcasing the discoveries that will shape the future of biological sciences both in Mongolia and around the world. I extend my heartfelt thanks to all the researchers, reviewers, and organizers who made this conference possible. Let us embrace this moment, learn from one another, and move boldly toward the future.

With appreciation,
Gantulga Davaakhuu
Director, Institute of Biology
Mongolian Academy of Sciences

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AGENDA

THURSDAY I 2025.09.18
CORPORATE CONVENTION HALL

TIME	ACTIVITY
10:30 – 11:00	**REGISTRATION & MORNING COFFEE**
11:00 – 11:30	**OPENING REMARKS** Minister of Economy and Development President of Mongolian Academy of Sciences Director of Institute of Biology
11:30 – 11:40	Group Photo
11:40 – 12:10	**Dr. LUDOVIC ORLANDO** The horse that changed the world: Revisiting the domestication narrative
12:10 – 12:40	**Dr. JOHN L. KOPROWSKI** How do we make a difference? The importance of partnership in conservation
12:40 – 13:10	**LUNCH BREAK & NETWORKING**
13:10 – 13:40	**Dr. JOSEP CALL** Reconstructing the evolution of cognition
13:40 – 14:10	**Dr. WILLIAM SUTHERLAND** Making conservation more effective
14:10 – 14:30	**MOU SIGNING & ALLIANCE FORMATION**
14:30 – 14:50	**COFFEE BREAK**
14:50 – 15:20	**Dr. DAVID TOLLERVEY** Lighting up RNA-protein interactions
15:20 – 15:50	**Dr. CSABA VÁGVÖLGYI** Microbial Inoculants: A Green Technology for Multiple Agricultural Crises
15:50 – 16:20	**Dr. LAURENT KREMER** Mycobacterium abscessus pathogenesis and treatment using the zebrafish model of infection
16:20 – 17:20	**AWARD GIVING CEREMONY**

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AGENDA

FRIDAY I 2025.09.19
BOLOR PREMIUM RESORT

TIME	ACTIVITY	ROOM A	
08:30 -09:00		**REGISTRATION & MORNING COFFEE**	
09:00- 09:15		**OPENING REMARKS DIRECTOR DR. GANTULGA DAVAAKHUU**	
09:15 -09:50	Keynote Speech (30 min + 5 min Q&A)	**BIOMEDICAL & HEALTH SCIENCES (MODERATOR: SHIMAKAMI TETSURO, GERELSUREN.B)**	
		Development of Nutraceuticals for Targeting Fatty Liver Diseases by using Natural Products	Chu Won Nho
09:50 -10:25		Roles of Hepatitis B and C Viruses in Hepatocellular Carcinoma and Mortality: Evidence from Long-Term Cohorts in Taiwan	Yen-Tsung Huang
10:25 - 10:50	Invited Talks (20 min each + 5 min Q&A)	Development of Reporter-based Hepatitis B Virus Infection Monitoring System in Cell Culture and its Application for Antiviral Compound Screening	Shimakami Tetsuro
10:50 - 11:10		**COFFEE BREAK AND POSTER SESSION**	
11:10 - 11:25	Oral Presentations (12 min each + 3 min Q&A)	Construction of Lentiviral Vectors for CAR-T Cell Applications in Mongolia	Gansukh Choijilsuren
11:25 - 11:40		Targeted disruption of the Orthohepadnavirus hominoidei S Gene Using CRISPR/Cas9 in HepG2 Cells	Lkhagvasuren Damdindorj
11:40 - 11:55		Neurotoxic smog: a systematic review and meta-analysis of long-term ambient air pollution xposure's impact on MRI biomarkers of brain structure	Khulan Ganzorig
11:55 - 12:30	Keynote Speech (30 min + 5 min Q&A)	**BIODIVERSITY & ECOSYSTEM CONSERVATION (MODERATOR: GABOR SRAMKO, SUKHCHULUUN.G)**	
		50 years of ichthyological and hydrobiological research in Mongolia - a review.	Dgebuadze Yuri Yulianovich
12:30 - 13:30		**LUNCH BREAK & NETWORKING**	
13:30 - 13:55	Invited Talks (20 min each + 5 min Q&A)	Genomics for Endangered Species – Insights from Mongolia and Beyond	Gabor Sramko
13:55 - 14:20		Overyielding effects in sand-fixing vegetations reseeding	Yong Zhang
14:20 - 14:35	Oral Presentations (12 min each + 3 min Q&A)	Return of the Wild Horses – a new reintroduction project of Przewalski's horse in the Eastern Mongolia	Jaroslav Šimek
14:35 - 14:50		Mongolian desert living mazaalai bear (Ursus arctos gobiensis, Sokolov and Orlov 1992) behavior	Delgerchimeg Davaasuren
14:50 - 15:05		Grazing effects on insect communities in Western Mongolia	Enkhnasan Davaadorj
15:05 - 15:20		**COFFEE BREAK & POSTER VIEWING**	
15:20 - 15:55	Keynote Speech (30 min + 5 min Q&A)	**EMERGING TECHNOLOGIES IN BIOLOGY (MODERATOR: KALAISELVI SENTHIL, MARJANGUL.N)**	
		Lipid Synthetase Inhibitors from Natural Products	Kenji Monde
15:55 - 16:20	Invited Talks (20 min each + 5 min Q&A)	Metabolomic background of the volatile communications between Aspergillus flavus and Pseudomonas strains	András Szekeres
16:20 - 16:45		Validation of traditional medicinal practices using modern tools and techniques	Kalaiselvi Senthil
16:45 - 17:10		Bio-nano interface controlling stem cells fate and application forregenerative medicine	Hexig Bayar
17:10 - 17:25	Oral Presentations (12 min each + 3 min Q&A)	Synchronization Methods for Artificial Insemination and Embryo Transfer in Mongolian Goats and ewes: A mini Review	Myagmarsuren Purevdorj
17:25 - 17:45		Study of Enzyme- Active Bacteria Potentially Usable in Leather Production	Enkhtsatsral Elbegbayar
17:45 - 17:55		BAIGALI	GIZ, SPACE II project
17:55 - 18:00		**CLOSING REMARKS & GROUP PHOTO**	
19:00 -21:00		**RECEPTION**	

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FRIDAY I 2025.09.19
BOLOR PREMIUM RESORT

TIME	ACTIVITY	ROOM B	
08:30 –09:00		**REGISTRATION & MORNING COFFEE**	
09:00- 09:15		**OPENING REMARKS DIRECTOR DR. GANTULGA DAVAAKHUU**	
09:15 –09:50	Keynote Speech (30 min + 5 min Q&A)	**CLIMATE CHANGE & ENVIRONMENTAL ADAPTATION (MODERATOR: NIKITA CHERNETSOV, IDERBAT.D)**	
		From Migratory Waterbird Telemetry to Basin-Scale Wetland Research and Conservation	Cao Lei
09:50 –10:25	Invited Talks (20 min each + 5 min Q&A)	East Asian – Australasian flyway of migratory landbirds: what do we know?	Nikita Chernetsov
10:25 - 10:50		Global Insect diversity pattern and biodiversity declining monitoring – SITE100 International Big Science Action	Bai Ming
10:50 - 11:10		**COFFEE BREAK AND POSTER SESSION**	
11:10 - 11:25	Oral Presentations (12 min each + 3 min Q&A)	Generalized Spatiotemporally Weighted Boosted Regression to Predict the Occurence of Grassland Fires in the Mongolian Plateau	Duwala
11:25 - 11:40		Strategies for Grassland Soil Health Improvement: Carbon Sequestration, Restoration and Sustainable Management	Shiming Tang
11:40 - 11:55		Behavioural and Ecological Monitoring in Przewalski's Horse Reintroductions: Standardised Research Methodologies for the New Projects	Anna Bernátková
11:55 - 12:30	Keynote Speech (30 min + 5 min Q&A)	**BIOTECHNOLOGY & MICROBIOLOGY (MODERATOR: MIKLOS TAKO, ENKH-AMGALAN.J)**	
		Breeding of oleaginous yeast Rhodotorula for lipid production	Kazuhito Fujiyama
12:30 - 13:30		**LUNCH BREAK & NETWORKING**	
13:30 - 13:55	Invited Talks (20 min each + 5 min Q&A)	Unveiling the Ecological Roles of Novel Marine Gliding Bacteria	Song-Gun Kim
13:55 - 14:20		Plant-derived NCR peptides are potent antifungals against Cryptococcus neoformans	Illona Pfeiffer
14:20 - 14:35		Advanced enzyme-assisted strategies for the recovery of bioactive phenolics from grape residues	Miklos Tako
14:35 - 14:50	Oral Presentations (12 min each + 3 min Q&A)	Detection of new peptaibiotics from Mongolian Trichoderma isolates	Nomuun Oyunbat
14:50 - 15:05		Advancing cryptogamic botany in Mongolia: addressing knowledge gaps	Vlasenko Anastasia V
15:05 - 15:20		Diversity and Plant Growth-Promoting Properties of Endophytic Microorganisms from Saussurea bogedaensis and Its Newly Recorded Distribution Site in Mongolia	Enkh-Amgalan Jigjiddorj
15:20 - 15:35		**COFFEE BREAK & POSTER VIEWING**	
15:35 - 16:10	Keynote Speech (30 min + 5 min Q&A)	**AGRICULTURAL & FOOD BIOTECHNOLOGY (MODERATOR: OKAZAWA ATSUSHI, ALTANZUL.KH)**	
		Development of high beta carotene Sweet Corn Hybrid through Marker-assisted breeding to address the vitamin A deficiency	Senthil Natesan
16:10 - 16:35	Invited Talks (20 min each + 5 min Q&A)	Discovery of chemicals for control of root parasitic weeds focusing on germination metabolism	Okazawa Atsushi
16:35 - 17:00		Antimicrobial and antibiofilm activity of essential oils on food-borne microbes	Judit Krisch
17:00 - 17:15	Oral Presentations (12 min each + 3 min Q&A)	Establishment of an in vitro propagation protocol for Spongiocarpella grubovii Ulzij.,subendemic species of Mongolia	Oyunbileg Yungeree
17:15 - 17:30		Biological activities of purified xylooligosaccharides derived from food industry by-products	Odgerel Chinbat
17:55 - 18:00		**CLOSING REMARKS & GROUP PHOTO**	
19:00 –21:00		**RECEPTION**	

PLENARY SESSION

Plenary Talk 1

Title: The horse that changed the world: Revisiting the domestication narrative

Dr. Ludovic Orlando

Centre for Anthropobiology and Genomics of Toulouse, CAGT, CNRS UMR 5288, Université de Toulouse, France

Short Bio: Ludovic Orlando is CNRS Research Director and Founder of the Centre for Anthropobiology and Genomics of Toulouse (CAGT) at Université de Toulouse. He previously led the Molecular Archaeology group at the University of Copenhagen and holds advanced training in molecular biology and genetics. His pioneering research in paleogenomics has produced landmark discoveries, including sequencing the first Middle Pleistocene genome, reconstructing ancient epigenomes, and uncovering the domestication history of horses and donkeys. He leads the international AnimalFarm research program and ERC-funded projects such as PEGASUS and HorsePower. Prof. Orlando has authored over 200 scientific publications, serves on editorial boards, and received the CNRS Silver Medal in 2023.

Abstract: The domestication of the horse marked a turning point in human history, accelerating travel, cultural exchange, and gene flow across continents. In Western countries, this long partnership endured until the 20th century, when combustion engines reshaped human mobility. Recent advances in ancient DNA research have helped refine the timeline of horse domestication, revealing that, while early horse husbandry emerged in Central Asia ~5,500 years ago, the lineage of modern domestic horses originated over 1,000 years later in the Pontic-Caspian steppes. Expanding genome time-series, our more recent work uncovers how Late Pleistocene climate change contributed to shape the genetic diversity of wild horse populations near the time of domestication. We refine the timeline of lineage replacement as domestic horses suddenly spread beyond their homeland and identify key genetic adaptations that facilitated their success. Functional validation in model organisms highlights a specific genetic modification likely linked to the rise of horseback-riding and horse-driven mobility.

Plenary Talk 2

Title: How do we make a difference? The importance of partnership in conservation

Dr. John L. Koprowski

Dean and Professor Haub School of Environment and Natural Resources 201 Bim Kendall House 804 E Fremont St Laramie, WY 82072 USA

Short Bio: Professor John Koprowski is a globally recognized conservation biologist whose research has advanced the understanding of mammal ecology, biodiversity conservation, and human–wildlife coexistence. Over the course of his career, he has led long-term international collaborations and training initiatives across North America, Europe, Asia, and beyond, emphasizing the application of science to conservation practice and policy. He has authored numerous scientific publications and books on mammalogy and wildlife management, and his leadership extends to service as President of the American Society of Mammalogists. He is a Fellow of the American Association for the Advancement of Science, The Wildlife Society, and The Explorers Club.

Abstract: We all desire to maximize our impact and generate sustainable solutions to our grand challenges through the discovery and application of our efforts. Most often, this requires that we partner with others to create opportunities for win:win scenarios. Finding connections between conservation and local prosperity are critical to the development of sustainable conservation strategies. I will discuss examples of win:win partnerships around the world where my research group and I have found ways to connect conservation efforts for mammals, ranging from squirrels to tigers, to local communities. International partnerships have continued to increase during that last 60 years and this increase is reflected in the number of papers with authors from multiple nations continuing to grow across all disciplines of science. The building of partnerships has also occurred over these years in Mongolia as the country’s wild and working lands represent one of the world’s largest relatively intact landscapes where the vast majority of wildlife species also remain. The value of partnership continues to grow and I will relate these efforts to a purple bike in a remote village in Nepal that serves as a powerful metaphor for collaboration in conservation. Collaboration in research continue to provide critical data and sustainable solutions for the conservation and management of wildlife and landscapes in addition to providing exceptional opportunities for education and intercultural exchange.

Plenary Talk 3

Title: Reconstructing the evolution of cognition

Dr. Josep Call

Evolutionary Origins of Mind, University of St Andrews, St Andrews, Fife, KY16 9TH, United Kingdom

Short Bio: Prof. Josep Call is Wardlaw Professor in Evolutionary Origins of Mind at the University of St Andrews and Co-Director of the Wolfgang Köhler Primate Research Centre at the Max Planck Institute for Evolutionary Anthropology. He earned his Ph.D. in Psychology from Emory University and has previously served as Senior Scientist at Max Planck and Lecturer at the University of Liverpool.
His research centers on the evolution of cognition in great apes, focusing on technical and social problem-solving, causal inference, tool use, gestural communication, and mind-reading. He has co-founded the Wolfgang Köhler Primate Research Centre and published nearly 200 research articles and several influential books, including *Primate Cognition* and *The Gestural Communication of Apes and Monkeys*.
Prof. Call is a Fellow of the American Psychological Association, the Royal Society of Edinburgh, and the British Academy.

Abstract: Much progress has been made in the last century on the question of animal cognition. Currently, we know (among other things) that some species can memorize multiple types of information, use different encoding mechanisms to solve spatial problems, plan to meet future needs and make inferences about the visual perspective of others. Much less is known about how and when those abilities may have evolved. The comparative method, based on contrasting the similarities and differences between both closely and distantly related species, is a key component for answering these questions. In this talk, I will outline the logic of this method and present some of the recent progress that has been made in areas such as spatial encoding, memory and planning and perspective taking. In the last part of my talk I will suggest some future research directions.

Plenary Talk 4

Title: Making conservation more effective

Dr. William Sutherland

Department of Zoology, University of Cambridge, Downing Street, Cambridge
CB2 3EJ, United Kingdom

Short Bio: William J. Sutherland, CBE, FRS is Director of Research in the Department of Zoology at the University of Cambridge. Formerly the Miriam Rothschild Chair of Conservation Biology, he founded the influential *Conservation Evidence* platform and pioneered the evidence-based conservation movement. His work centers on linking behavioral and population ecology with policy through methods like horizon scanning and evidence synthesis, transforming how global conservation decisions are made. Prof. Sutherland has authored or edited numerous books and over 400 papers, and his leadership has been recognized with major honors—including the Royal Society Fellowship, a CBE, the International Ecology Institute Prize (2023), and the International Cosmos Prize (2024).

Abstract: Conservation has made extraordinary progress over recent decades, with some greatly improved populations of rare species and improved habitats. Yet alongside this there are many populations and habitats that have deteriorated. The lessons from other fields such as aircraft safety, medicine and building design is that embedding learning into practice can be hugely beneficial. In this lecture I will describe how conservation is being transformed through the use of evidence.

Our work entails collating evidence at an industrial scale. We have read 1.3 million paper titles in 17 languages. We then collate these and extract the key information. This is all made available through the website www.conservationevidence.com.

We are busy working with practitioners, policy makers and funders to develop tools for improving practice. The tools are summarised here https://about.conservationevidence.com/2023/09/20/the-evidence-toolkit-supporting-evidence-based-decision-making-in-conservation/

A key challenge is the creation of learning from practice. I will describe the problems arising from traditional monitoring and evaluation and the thinking needed to embed testing into practice. The experimental design used really matters with the worse design (after monitoring) being only slightly better than tossing a coin yet are the commonest design in conservation and social science.

There is a need to draw upon diverse knowledge systems and consider how to make decisions with a diversity of knowledge.
Artificial Intelligence is rapidly changing how conservationists work. For example, we have been using this to synthesise the literature at scale. This has many exciting possibilities but also serious challenges, such as the ease with which entirely fake studies can be created and how this places the power into the hands of the few.

Plenary Talk 5

Title: Lighting up RNA-protein interactions

Dr. David Tollervey

Wellcome Centre for Cell Biology, University of Edinburgh, Michael Swann Building, King's Buildings, Edinburgh EH9 3BF, United Kingdom

Short Bio: David Tollervey is a leading RNA biologist at the University of Edinburgh and Wellcome Trust Principal Research Fellow. He is internationally recognized for his work on RNA processing, ribosome assembly, and RNA surveillance, including pioneering studies on small nucleolar RNAs (snoRNAs) and the RNA exosome. His research combines genetics, molecular biology, and high-throughput genomic approaches to understand RNA–protein interactions and cellular stress responses.

He has held positions at the Institut Pasteur and EMBL, and has served as Director of the Wellcome Centre for Cell Biology. Professor Tollervey is a Fellow of the Royal Society, the Royal Society of Edinburgh, and the Academy of Medical Sciences, and an EMBO member. He has also served as President of the RNA Society and received awards including the Biochemical Society's Novartis Medal (2016) and the Mendel Medal (2017).

Abstract: Over the past decades, our knowledge of the range and significance of RNAs and RNA–protein binding has greatly increased. We have developed techniques to characterize dynamic changes in RNA–protein interactions in living cells, and are applying these during infection, ncRNA-linked disease, aging, and stress. This talk will focus on response to stress. Organisms must constantly cope with variable and stressful environments. This problem is especially acute for unicellular organisms such as the budding yeast *Saccharomyces cerevisiae*, but human cells must also frequently respond to diverse stresses.

Cells respond to stress by altering protein expression at both the transcriptional and translational levels, and RNA-binding proteins (RBPs) are at the heart of stress adaptation. Yeast growing in glucose medium utilize aerobic fermentation, generating ATP only from glycolysis. Following glucose withdrawal, very rapid translational silencing is driven by a specialized metabolic mechanism. Intracellular NTP levels drop drastically over 30 sec, before stabilizing at a regulated, post-stress set-point. Programmed translational control results from the differential NTP

affinities of key enzymes; ATP falls below the (high) binding constants for DEAD-box helicase initiation factors, including eIF4A, driving mRNA release and blocking 80S assembly. Contrastingly, GTP levels always greatly exceed the (low) binding constants for elongation factors, allowing ribosome run-off and orderly translation shutdown. Translation initiation is immediately lost on all pre-existing mRNAs, before being preferentially re-established on newly synthesized, upregulated stress-response transcripts. We conclude that enzymatic constants are tuned for metabolic remodeling, allowing hierarchical inhibition of energy-consuming processes on very rapid timescales.

Aerobic fermentation has evolved repeatedly, and initial results indicate ATP depletion to ~200 μM (similar to yeast) within 5 min after glucose withdrawal in a human, activated T cell model, followed by polysome run off. Our results may therefore be relevant to human cells, and potentially many other systems.

Plenary Talk 6

Title: Microbial Inoculants: A Green Technology for Multiple Agricultural Crises

Csaba Vágvölgyi[1], Jelena Živančev[2], Nataša Đurišić-Mladenović[2], László Kredics[1]

[1] University of Szeged, Szeged. Hungary
[2] University of Novi Sad, Faculty of Technology Novi Sad, Novi Sad, Serbia
csaba@bio.u-szeged.hu

Short Bio: Prof. Dr. Csaba Vágvölgyi is full professor at the Department of Biotechnology and Microbiology, Faculty of Science and Informatics, University of Szeged. A leading microbiologist, his research spans agricultural microbiology, microbial biotechnology, fungal taxonomy, and bacterial cellulose production. He has authored over 400 scientific papers, 12 books, and 50 book chapters, with more than 16,000 citations and an h-index of 49.

Prof. Vágvölgyi has held numerous academic leadership roles, including Head of Department and Head of the Doctoral School of Biology at the University of Szeged, and he has served prominently on scientific committees of the Hungarian Academy of Sciences and the Hungarian Microbiological Society. He has supervised more than 20 PhD theses and mentored numerous young scientists and postdoctoral fellows.

His achievements have been recognized with prestigious national and international awards, including the Order of Merit of the Hungarian Republic, the Széchenyi István Research Award, the Szentágothai National Excellence Award, and multiple university distinctions. He is currently Editor-in-Chief of *Acta Biologica Szegediensis* and serves on several editorial and scientific boards.

Abstract: The global agricultural sector is currently facing a "triple crisis" - climate change, biodiversity loss, and environmental pollution - which collectively threaten food security and the stability of ecosystems. These challenges are deeply interconnected and require holistic, sustainable solutions. At the same time, consumer demand for healthy, pesticide-free food is rising, while the widespread use of agrochemicals poses increasing risks to both human health and the environment.

Microorganism-based products - microbial inoculants - offer a promising, multifunctional approach to mitigating this complex crisis. These bioinoculants contribute to sustainable agriculture by promoting plant growth, enhancing nutrient uptake, increasing resistance to abiotic stress (such as drought), and serving as

environmentally friendly alternatives to chemical fertilizers and pesticides. Additionally, they hold significant potential for bioremediation, including the degradation of herbicide residues, thereby helping to reduce soil and water contamination.

This presentation will highlight research findings demonstrating the diverse applications of microbial products, both as soil inoculants and foliar treatments. Their capabilities include the biological control of plant pathogens, the stimulation of plant growth, and the potential to reduce the xenobiotic burden in agricultural ecosystems.

We argue that microbial inoculants should not be viewed merely as tools for organic farming, but rather as central components of a new paradigm in agriculture, one that meets ecological, agronomic, and public health challenges through microbiological innovation.

This research is supported by the Interreg VI-A IPA Hungary-Serbia Interreg Programme (HUSRB/23S/11/027).

Keywords: biological control, plant growth promoting bacteria, *Bacillus*, *Trichoderma*.

Plenary Talk 7

Title: *Mycobacterium abscessus* pathogenesis and treatment using the zebrafish model of infection

Dr. Laurent Kremer

Centre National de la Recherche Scientifique UMR 9004, Institut de Recherche en Infectiologie de Montpellier (IRIM), Université de Montpellier, 1919 route de Mende, 34293, Montpellier, France

Short Bio: Laurent Kremer is a Research Director at CNRS and head of the "Mycobacterial Pathogenesis and Novel Therapeutic Targets" team at the Institut de Recherche en Infectiologie de Montpellier (IRIM), CNRS UMR 9004, University of Montpellier, France. He holds a Ph.D. in Molecular Microbiology from INSERM–Pasteur Institute, Lille, and has held postdoctoral positions in the USA and UK before joining IRIM. His research explores the biochemistry and pathogenicity of mycobacteria—especially their lipid metabolism, cell envelope components, and mechanisms of drug activation and resistance—using innovative models including zebrafish. Dr. Kremer has authored around 150 peer-reviewed publications and has been recognized with the European Respiratory Society Innovation Award for research on non-tuberculous mycobacterial diseases and is a leader in microbiology in France.

Abstract: The number of non-tuberculous mycobacterial (NTM) infections has increased recently and even surpassed tuberculosis as a public health concern in many countries. These infections require long treatment periods that are often unsuccessful. Among the NTM commonly isolated from clinical respiratory specimens, *Mycobacterium abscessus* has emerged as one of the most difficult-to-manage NTM pathogens. *M. abscessus* is often found to be the underlaying cause of pulmonary infections, especially in patients with cystic fibrosis (CF) or with other lung disorders. The natural resistance of this species to most commonly available antibiotics seriously limits chemotherapeutic treatment options, which is particularly challenging for treating CF patients. New drugs with novel molecular targets are urgently needed against this emerging pathogen. In addition, very little is known regarding pathogenesis of *M. abscessus* and its virulence factors. We have exploited zebrafish to study the chronology of the infection and pathogenesis of smooth (S) and rough (R) variants of *M. abscessus*, both in wild-type and CFTR-deficient larvae. This model allowed to demonstrate the increased virulence of the R variant over the

S variant. Infection with the R strain is characterized by the formation of extracellular cords, representing a mechanism of immune evasion. Infection of larvae lacking CFTR unraveled the link between a dysfunctional CFTR with increased pathology/inflammation, allowing to better aprehend the particular vulnerability of CF patients to *M. abscessus* infection. In addition, the zebrafish model was used to evaluate the therapeutic efficacy of several antimycobacterial agents at a spatio-temporal level. Our recent work validated also the usefulness of this model to test the efficacy of phage treatment against infections caused by a multi-drug resistant strain of *M. abscessus*. In summary, the zebrafish model has allowed to decipher new immunopathologial aspects specific to *M. abscessus* infections and to highlight therapeutic innovations for future treatments against *M. abscessus* lung diseases.

SESSION 1:

BIODIVERSITY & ECOSYSTEM CONSERVATION

Keynote Speech

Title: 50 years of ichthyological and hydrobiological research in Mongolia

Dgebuadze Yu.Yu.[1,2]**, B. Mendsaikhan**[3]

[1] Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, 33 Leninsky pr., 119071 Moscow, Russia
[2]Lomonosov Moscow State University, Moscow, Russia
[3]Institute of Geography and Geoecology, Mongolian Academy of Sciences, Ulaanbaatar-15170, Mongolia

Short Bio: Yury Y. Dgebuadze is a Professor and Academician of the Russian Academy of Sciences. He serves as Head of the Laboratory at the Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, and Head of the Department of General Ecology and Hydrobiology at Lomonosov Moscow State University. He is also the Scientific Leader of the ichthyology and hydrobiology team of the Joint Russian–Mongolian Complex Biological Expedition.

Professor Dgebuadze has authored more than 300 scientific papers and books, with research interests spanning biodiversity, ecology, biological invasions, fish fauna, speciation, fish ecology, microevolution, and nature conservation. He has presented at over 80 international and Russian scientific conferences and has supervised 11 doctoral dissertations, including two by Mongolian scholars.

In addition to his academic and research leadership, he is Head of the General Biology Section of the Department of Biological Sciences of the Russian Academy of Sciences, a member of the Presidium of the Russian Academy of Sciences, and Editor-in-Chief of the Russian Journal of Biological Invasions.

Abstract: Exactly 50 years ago, an ichthyological and hydrobiological team was established in frame of the Joint Soviet-Mongolian Complex Biological Expedition by the Academy of Sciences of the USSR and the Mongolian Academy of Sciences. All these years, this team has been conducting regular ichthyological and hydrobiological research in Mongolian waters. During this work in aquatic ecosystems of Mongolia by Mongolian and Russian scientists, a number of breakthrough results were obtained that were fundamentally new for biological science. These include diversity and adaptations of aquatic organisms to the specific conditions of waters in the semi-arid zone, the dynamics of ecosystems during cyclic climate changes, the microevolution of living organisms, and the peculiarities of the formation of ecosystems of reservoirs in semi-arid regions. For the first time, the abundance and biomass of bacterioplankton, phototrophic picoplankton, and

heterotrophic nanoflagellates has been determined in lakes, rivers, and reservoirs of Central Asian Internal Drainage Basin As a result of joint research, it was concluded that the waters of Mongolia are inhabited by 78 species of fish, and one species of lamprey; four new for science species of fish from the family Balitoridae and mechanisms of formation and adaptations of intraspecific "forms flocks" of fish of the genus *Oreoleuciscus* have been described. Studies of planktonic organisms, in particular Cladocera (Crustacea), have helped to clarify the taxonomy and distribution of a number of species. The ecosystems of periodically drying lakes in the semi-arid zone have been studied in detail. Unique cyclical microevolution of O. humilis have been discovered.

Prospects team's studying are seen in continuing research into aquatic ecosystems in Mongolia in the context of climatic and anthropogenic impacts. Work will continue on the problem of providing Mongolian people with clean water. In terms of fundamental research, genetic, epigenetic and ecological studies of aquatic organisms are of great interest.

Keywords: Mongolia, aquatic ecosystems, aquatic organisms, fishes, adaptations, cyclic diversification

Invited Talk 1

Title: Formation and Dynamics of Planktonic and Benthic Communities in Taishir Reservoir (Western Mongolia)

Alexander V. Krylov, A.A. Prokin, D.B. Kosolapov, L.G. Korneva, N.G. Kosolapova*

I.D. Papanin Institute for Biology of Inland Waters, Russian Academy of Sciences, 152742, Borok, Nekouz District, Yaroslavl Region, Russia

krylov@ibiw.ru

Short Bio: Alexander V. Krylov is Director of the I.D. Papanin Institute for Biology of Inland Waters, Russian Academy of Sciences, where he has worked since 1989 and leads the Laboratory of Aquatic Invertebrate Ecology. He received his Doctor of Science in Biology (2004) and became Professor of Hydrobiology (2014). With 35 years of research experience, he has authored 17 books and over 150 peer-reviewed papers. His work focuses on freshwater planktonic communities in Russia, Mongolia, and Armenia, with particular emphasis on the structural and functional responses of zooplankton to keystone species such as beavers and waterbirds. Prof. Krylov has advanced the concept of zoogenic eutrophication as distinct from natural and anthropogenic processes, contributing significantly to freshwater ecology and ecosystem theory.

Abstract: This study presents the results of investigations on planktonic algae and cyanobacteria, heterotrophic bacteria and nanoflagellates, rotifers, crustaceans, and benthic macroinvertebrate communities in Taishir Reservoir (Gegennur) during the initial stages of its ecological establishment. The research examined community composition, spatial distribution, and interannual dynamics under fluctuating hydrological conditions.

Worldwide, large-scale reservoir construction was most active in the 1950s–1970s. Construction slowed in industrialized nations but increased in arid and developing regions to meet energy demands for socio-economic development. Mongolia’s natural environment and resource base are highly vulnerable to anthropogenic impacts, a factor increasingly relevant under globalization and climate change. In Western Mongolia, one of the largest hydropower stations of the 21st century created Taishir Reservoir on the upper reaches of the Dzabkhan River. The reservoir’s dam is 50 m high and 190 m long, with filling beginning in 2007; the reservoir is ~35 km long and ~6 km wide at its maximum. Planktonic and benthic communities have been studied within the framework of a Russian-Mongolian joint biological expedition since 2010.

At the studied sites in Taishir Reservoir and the Dzabkhan River, 212 algal taxa below the genus level were recorded in the phytoplankton. In the first years after reservoir formation, floristic diversity doubled compared with the river, average abundance increased fourfold, and biomass doubled, although average cell size decreased threefold, reflecting enhanced trophic conditions. Over time, the reservoir's trophic status shifted from oligotrophy to mesotrophy. Cyanobacteria and mixotrophic phytoflagellates, particularly dinoflagellates, increased in abundance and biomass. Dominant species included representatives of the limnoplankton complex, such as centric diatoms adapted to high nitrogen conditions. Maximum phytoplankton abundance and biomass were observed near the dam, associated with increased mineralization and reduced flow, while species richness and community diversity declined from upstream to downstream.

The reservoir exhibited high levels of bacterioplankton typical of meso- and eutrophic waters. Five bacterial phyla dominated: Bacteroidetes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Cyanobacteria. Reservoir bacterioplankton displayed greater stability and diversity than unregulated river sections. Thirty flagellate species and forms were recorded in the reservoir, compared to 18 in the Dzabkhan River. Heterotrophic flagellates selectively grazed on large and active cells, shaping bacterial community structure and dominance patterns.

Zooplankton included 38 invertebrate species (22 Rotifera, 6 Copepoda, 10 Cladocera) in the reservoir, versus 7 in the river (5 Rotifera, 1 Copepoda, 1 Cladocera). Highest abundances occurred in middle and lower reservoir zones due to longer residence times and stable environmental conditions. Interannual variation was largely driven by weather and hydrological factors, including precipitation, air and water temperature, and water level. Zooplankton formation followed a floodplain-type succession and was completed within four years.

Benthic macroinvertebrate surveys recorded 112 species across the Dzabkhan River and reservoir. Species richness was highest downstream of the reservoir (61) and lowest upstream (37), with 59 species in the reservoir itself. Accumulation of terrigenous plant-derived organic matter in mid-depth zones supported gradual colonization, while high sediment movement limited shallow-water settlement and macrophyte development. Overall, benthic biomass remained relatively stable after reservoir regulation, reflecting the region's gravelly substrates, which act as a "landscape filter" slowing successional processes.

Further details on planktonic and benthic communities, as well as fish population dynamics and parasitofauna, are presented in the collective monograph *Reservoirs in Semi-Arid Zones* (2023).

Keywords: reservoir, semi-arid zone, plankton communities, benthic communities

Invited Talk 2

Title: Genomics for Endangered Species – Insights from Mongolia and Beyond

Gábor Sramkó[1,2]

[1] Evolutionary Genomics Research Group, Department of Botany, University of Debrecen, Egyetem tér 1., 4032 Debrecen, Hungary
[2] HUN-REN–UD Conservation Biology Research Group, 4032 Debrecen, Hungary
sramko.gabor@science.unideb.hu

Short Bio: Gábor Sramkó is an Assistant Professor of Botany at the University of Debrecen, Hungary, specializing in phylogenomics, phylogeography, and conservation genetics of steppe biota. He pioneered the use of DNA-based and genome-wide methods in Hungarian plant systematics and published the first whole-genome sequence of a non-model Hungarian plant. He leads international collaborations in Central Asia and Europe, contributes to biodiversity conservation, and actively trains young researchers in genomic approaches.

Abstract: The increasing availability of genomic data has revolutionized evolutionary research. This is particularly true for conservation genetics, where genomic approaches offer significant advances over classical methods (e.g., mitochondrial DNA sequencing, microsatellite genotyping). A major leap in understanding endangered species' genetic structure comes from the order-of-magnitude improvement in phylogenetic resolution. Taxonomic instability, often caused by shallow population divergence, can complicate decisions about appropriate conservation levels, especially when closely related taxa are not endangered. While such shallow divergence often remains undetected by classical techniques, the enhanced resolution of genomic approaches provides critical insight into fine taxonomic distinctions. Similarly, resolving population structure often requires the higher resolution provided by genomic data. The saiga antelope exemplifies these advantages. Similarly, comparing microsatellite and RADseq data from the same population of Hungarian birch mice revealed far greater structural detail with the genomic approach. A unique strength of genomics is its capacity to sample adaptive genetic variation, which would otherwise remain hidden. By sampling genomic regions underlying adaptation to local conditions, we gain a powerful tool for defining management units in endangered populations. Siberian taimens from Mongolia provide a compelling example of how genomics, particularly insights into local adaptation, can shed new light on conservation.

Keywords: adaptive variation, evolutionary genomics, *Hucho taimen*, phylogenetic resolution, *Saiga tatarica*, *Sicista trizona*.

Invited Talk 3

Title: Overyielding effects in sand-fixing desert vegetations

Yong Zhang

Institute of Plant Protection, Chinese Academy of Agricultural Sciences
Zhangyong@caas.com

Short Bio: Yong Zhang is a researcher at the Institute of Plant Protection, Chinese Academy of Agricultural Sciences. His work focuses on plant protection, pest management, and sustainable agricultural practices. He has contributed to numerous studies on crop health, integrated pest control strategies, and the ecological interactions between plants and pests, advancing both theoretical and applied aspects of agricultural science.

Abstract: Biodiversity plays important roles in driving plant community dynamics and ecosystem functioning. Biodiversity is also crucial in controlling desertification, for example in the Kubuqi Desert replanting schemes. However, due to the high-water consumption of the vegetation planted during previous desertification control programmes, as well as the poor economic performance of these vegetations, the Kubuqi Desert replanting schemes require science-based criteria to select species for sowing and establishment. We therefore conducted mixed planting and intercropping experiments with plant species that were selected on the basis of their drought tolerance and high economic value. We investigated the vegetation characteristics of 12 replanted species combinations in a desert region in China. The experiment provided evidence that the species had different characteristics after seeding. Leguminous plants can grow rapidly in the first year and improve the average coverage, height and above-ground biomass of the replanting plant community. Gramineous plants grow slowly and play a complementary role. Gramineous species were dominated by interspecific competition in 2021 and Leguminosae were dominated by interspecific competition in 2022, showing that the relationship between Gramineous and Leguminosae changed over time. Our results showed that the species combinations *Hedysarum laeve* Maxim. + *Agropyron cristatum* (L.) Gaertn. + *Astragalus adsurgens* Pall. and *Caragana microphylla* Lam. + *Agropyron cristatum* (L.) Gaertn. / *Glycyrrhiza uralensis* Fisch. had a strong interspecific facilitation, and they would be the best combinations to combat desertification in our research region. Through this study, we provide new designs for desertification control programmes in the Kubuqi Desert, with improved long-term effectiveness and stability of desert control.

PP-01: MOLECULAR CHARACTERIZATION OF *LYSIPHLEBUS FABARUM* (HYMENOPTERA: BRACONIDAE, APHIDIINAE) BASED ON THE mtCOI BARCODING GENE

Michidmaa Enkhtsog[1]*, Enkhjargal Bayanjargal [1], Chuluuntsetseg Nyamsuren[1], Byambasuren Mijidsuren[1]
[1] Institute of Plant Protection Research, Ulaanbaatar, Mongolia
*Email: michidmaaenkhtsog@gmail.com

Aphids (family Aphididae) are sap-feeding insects that can transmit viruses from plant to plant. Endoparasitoids are significant natural enemies of aphids and play an important role in regulating aphid populations. The study aims to identify some aphid species associated with forest plants in Mongolia and detect endoparasitoids within aphids using molecular biological methods. In this study, 12 aphid specimens were collected from forested areas in Khuvsgul and Zavkhan provinces in Mongolia during June 2024. The specimens were preserved in 70% ethanol for subsequent analysis. The mitochondrial cytochrome C oxidase subunit I (mtCOI) gene was utilized as a molecular marker for DNA barcoding to help identify aphid species. Polymerase chain reaction (PCR) amplification was performed using universal and specific primers. The results of the sequences were analyzed using the National Center for Biotechnology Information (NCBI) database. The sequence analysis identified one endoparasitoid species, which was 94.3% similar to *Lysiphlebus fabarum* (Hymenoptera: Braconidae, Aphidiidae). It was found to be associated with the aphid *Cinara sp.* (Hemiptera: Aphididae, Lachninae), which exhibited 99.3% similarity. The study has significant implications for guiding laboratory research into potential applications of this endoparasitoid as a control agent for aphids in Mongolia.

Keywords: aphid, endoparasitoid, DNA barcoding, molecular identification

PP-02: GROUPING OF HOUSEHOLDS ON THE DESERT STEPPE IN INNER MONGOLIA UNDER GRASSLAND ECOLOGICAL COMPENSATION POLICY

Bai Haihua[1,2], Chun Liang[1,2]*, Zhao Yongzhuo[1,2], Teregel[1,2]
[1] Institute of Grassland Research, Chinese Academy of Agricultural Sciences, Hohhot, China
[2] Key Laboratory of Grasslands & Agriculture Ecological Remote Sensing, Ministry of Agriculture and Rural Affairs, Hohhot, China
Email: chunliang@caas.cn

Studies indicate that households were showing group-level variations based on their specific characteristics under the Grassland Ecological Compensation Policy (GECP). In this study, a household survey in Darhan-Momingan Joint Khushuu and Durbud Khushuu of Inner Mongolia was conducted including the data of household income, GECP income, grassland area and livestock number, to group herders considering the effects of GECP on their income and stocking rates. The results show that stocking rates of household decrease with rising compensation amounts and compensation proportions, showing steeper declines at lower compensation levels, while the downward trend gradually stabilizes as these compensation metrics rise further. After a calculation, 29297 CNY of amount of eco-compensation payments and 24% of proportions of compensation payment to household income were as the thresholds. Then, the households were divided into four groups with different characteristic on livestock number and stocking rate: (A) larger herd sizes and higher stocking rates, (B) smaller herd sizes and higher stocking rates, (C) smaller herd sizes and lower stocking rates, and (D) larger herd sizes and lower stocking rates. The methodology of household grouping provides valuable references due to the different response of the households in different group on the GECP.

Keywords: Grassland policy, household survey, stocking rate, grassland, ecological compensation

PP-03: HYPERSPECTRAL GROUND-BASED IDENTIFICATION METHODS FOR LARCH NEEDLE PEST INFESTATION

Luo Xiaohua[1] and Huang Xiaojun[1,2,3]*
[1] College of Geographical Science, Inner Mongolia Normal University, Hohhot 010022, China
[2] Inner Mongolia Key Laboratory of Remote Sensing & Geography Information System, Hohhot 010022, China
[3] Inner Mongolia Key Laboratory of Disaster and Ecological Security on the Mongolia Plateau, Hohhot 010022, China
*Email: 20244016002@mails.imnu.edu.cn

In this study, the sensitivity of canopy-scale spectral features to pest indicator indicators and their potential to identify the degree of larch damage were investigated based on ground-based hyperspectral combined with measured data for the damage to larch forests by the Mongolian Plateau's Erannis Jacobsoni Djak (EJD) and Dendrolimus Sibiricus Tschtv (DST) on the Mongolian Plateau in the larch forests of the Hangai and Khanty Mountains of Mongolia. By obtaining features such as smoothed spectral reflectance (SSR), differential spectral reflectance (DSR), spectral index (GSI) and continuous wavelet coefficient (CWC), we analyzed their response relationships with leaf loss rate (LLR) and forest canopy colour (FCC), and constructed a pest assessment system using regression models (PLSR, SVMR) and classification models (RF, SVC). It was found that: Hyperspectral features were sensitive to both FCC and LLR pest indicators, with the most significant being CWC, especially in the visible (400-680 nm), red-edge (680-750 nm) and short-wave infrared (1400-1780 nm) bands; It was followed by GSI and DSR, and finally by SSR. The accuracy of the leaf loss rate estimation models based on PLSR and SVMR and the canopy colour discrimination models based on RF and SVC established by using spectral continuous wavelet coefficients were improved. The optimal models for LLR estimation of Erannis jacobsoni djak and Dendrolimus sibiricus tschtv infestation were bior3.5-SVMR and sym5-SVMR, respectively. The differences in discriminative accuracy between CWC-RF and CWC-SVC models were not obvious, and both of them were improved over the accuracy of Fisher's model.

Keywords: Ground level hyperspectral, spectral features, *Erannis jacobsoni djak*, *Dendrolimus sibiricus tschtv*

PP-04: SENTINEL-2A IMAGE REFLECTANCE SIMULATION ENHANCES RETRIEVAL ACCURACY FOR PEST INDUCED FOREST

Yang Le[1]*，Huang Xiaojun[1,2,3]， Dorjsuren Altanchimeg[4], Davaadorj Enkhnasan[4], Dashzebeg Ganbat[5] and Mungunkhuyag Ariunaa[5]
[1] College of Geographical Science, Inner Mongolia Normal University, Hohhot 010022, China
[2] Inner Mongolia Key Laboratory of Remote Sensing & Geography Information System, Hohhot 010022, China
[3] Inner Mongolia Key Laboratory of Disaster and Ecological Security on the Mongolia Plateau, Hohhot 010022, China
[4] Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar 13330, Mongolia
[5] Institute of Geography and Geoecology, Mongolian Academy of Sciences, Ulaanbaatar 15170, Mongolia
*Email: 1433713407@qq.com

This study addresses critical challenges in forest pest remote sensing monitoring, including mixed pixel interference, insufficient cross-platform data synergy, and the lack of pest-specific models. Focusing on pest-infested forest areas in Khentii and Selenge Provinces of Mongolia, we propose a novel multi-source remote sensing collaborative approach for retrieving key physiological parameters of forest pests. The methodology integrates Sentinel-2A satellite imagery, UAV-RGB images, and ground hyperspectral data to develop a hybrid pixel decomposition model. By combining spectral response functions with downscaling strategies, we effectively mitigated non-target feature interference. Through successive projections algorithm (SPA), we identified sensitive spectral indices (SIs) and derivative spectral features (SDFs), subsequently establishing partial least squares regression (PLSR) models for estimating chlorophyll content (CHLC), leaf water content by dry weight (LWCD), and leaf water content by fresh weight (LWCF).Key findings include:(1) Simulated Sentinel-2A data significantly enhanced model performance, achieving mean cross-validation R^2 values (mR2CVmRCV2) of 0.8159, 0.7297, and 0.7596 for CHLC, LWCD, and LWCF respectively, with the model performance index (MPI) reaching up to 0.8959;(2) Pest species exhibited distinct spectral sensitivity patterns: *Erannis jacobsoni Djak.* showed CHLC sensitivity to SAVI (Soil-Adjusted Vegetation Index) and EVI2 (Enhanced Vegetation Index 2), while *Dendrolimus sibiricus Tschtv.* demonstrated primary sensitivity to PSRI (Plant Senescence Reflectance Index) and CHL_RED_EDGE (Chlorophyll Red Edge Index); (3) Integration of UAV texture features with multispectral data effectively captured pest-induced physiological changes, with the SDF-PLSR model improving accuracy by 4.04%–11.69% compared to non-simulated data approaches.

Keywords: *Erannis jacobsoni Djak, Dendrolimus sibiricus Tschtv*, hybrid image decomposition, Estimation of physiological parameters, Sentinel-2A

PP-05: ASSESSING ANTIMICROBIAL RESISTANCE IN SOIL AND WATER WITHIN ULAANBAATAR'S FOOD SYSTEM

Anumandal Orgil[1]*, Khishigmaa Batsaikhan[1], Mend-Amar Mendbayar[1], Uuriintuya Munkhbayar[1],
Erdenee Batzorig[2], Rentsenkhand Tserennadmid[1], Suvdantsetseg Balt[3]
[1] Institute of Biology, MAS, Ulaanbaatar, Mongolia
[2] Mongolian Remote Sensing Society, Ulaanbaatar, Mongolia
[3] Presidium office, MAS, Ulaanbaatar, Mongolia
*Email: anumandalo@mas.ac.mn

The rapid urbanization in Ulaanbaatar has increased the challenge of proper waste management, contaminating soil and water with pathogens and antimicrobial-resistant bacteria (ARBs), threatening urban ecosystem resilience. The current study explored the prevalence and antimicrobial resistance (AMR) of bacteria in 42 soil and water samples from five food system nodes: processing, production, retailing, consumption, and waste management. The microbiological analysis followed Mongolian National Standards, and the antibiotic susceptibility was determined by the Kirby-Bauer disc diffusion test. Findings showed *Shigella* spp. in 100% of all nodes; *E. coli* in retail, processing, and consumption (100%), waste (65%), and production (50%); STEC in consumption and production (100%); *Salmonella* spp. in retail (100%) and waste (65%); *S. aureus* highest in retail (100%) and processing (65%); MRSA only in processing and waste (35%); and *C. perfringens* was not detected. In processing and retailing, *E. coli* isolates indicated resistance to all eight tested antibiotics, including ampicillin, gentamicin, doxycycline, tetracycline, ciprofloxacin, chloramphenicol, penicillin, and erythromycin. In processing, *S. aureus* isolates demonstrated resistance to erythromycin, ampicillin, penicillin, and chloramphenicol. *E. coli* isolates from retailing and processing had the highest MAR index (1.0), followed by production (0.88), waste management (0.75), and consumption (0.62); *S. aureus* isolates from processing exhibited the MAR index of 0.50. In conclusion, the potential presence of multidrug-resistant bacteria, particularly *E. coli* and *S. aureus*, in Ulaanbaatar's food system nodes indicated the critical antimicrobial resistance in all five food nodes, raising awareness of the need for integrated waste management, AMR surveillance, and hygiene interventions to preserve the resilience of urban ecosystems.

Keywords: Microbiological Contamination, Antibiotic Resistance, Public Health

PP-06: SPECIES AT RISK: ILLEGAL EXPLOITATION OF MAMMALS IN MONGOLIA BASED ON FORENSIC INVESTIGATIONS

Gantulga Gankhuyag*, Undrakhbayar Enkhbat, Sukhchuluun Gansukh, Adiya Yansanjav
Institute of Biology, Mongolian Academy of Sciences, Mongolia
*Email: gantulga_g@mas.ac.mn

Illegal hunting and trade pose significant threats to biodiversity in Mongolia, especially among mammalian species that are ecologically and economically important. This study analyzes 215 forensic wildlife crime cases involving mammals submitted to the Institute of Biology of the Mongolian Academy of Sciences between 2016 and 2022. The cases encompass 5 taxonomic orders, with *Carnivora* (50.2%) and *Artiodactyla* (37.2%) comprising the majority, followed by *Rodentia* (5.6%), *Perissodactyla* (2.3%), and others (4.7%). However, the distribution of affected individual animals tells a different story: *Rodentia* accounts for a striking 73.9% of all individuals, despite only 5.6% of total cases, primarily due to large-scale harvests of marmots and muskrats. In contrast, *Carnivora* and *Artiodactyla*, which together comprise nearly 90% of the cases, make up just 7.6% and 18.2% of the individual animals, respectively. This discrepancy highlights the mass-harvest nature of rodent-related crimes versus more targeted but frequent offenses involving carnivores and ungulates.

This study emphasizes the ongoing pressure on Mongolia’s wildlife from poaching, fur trade, and unregulated market demand. Strengthening enforcement, improving interagency collaboration, and increasing public awareness are critical to mitigating these crimes. Furthermore, the findings provide a foundation for evidence-based conservation planning and targeted policy reform aimed at protecting Mongolia’s mammalian biodiversity.

Keywords: Illegal hunting, wildlife trade, mammals

SESSION 2:

EMERGING TECHNOLOGIES IN BIOLOGY

Keynote Speech

Title: Lipid Synthetase Inhibitors from Natural Products Toward Obesity, SARS-CoV-2 and Alzheimer's Disease

Enkhmaa Enkhbat[1,3], Othman, M. Aqmal[1], Mahadeva M. M. Swamy[1], Mutmainah[1], Yuta Murai[2], Kohei Yuyama[2], and Kenji Monde[2]

[1] Graduate School of Life Science, Hokkaido University, Japan 001-0021
[2] Faculty of Advanced Life Science, Hokkaido University, Japan 001-0021
[3] Laboratory of Mammalian Ecology, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
kmonde@sci.hokudai.ac.jp

Short Bio: Kenji Monde is Professor of Bioorganic Chemistry at the Faculty of Advanced Life Science and Vice Executive Director at Hokkaido University, and currently serves as Senior Science and Technology Policy Fellow at the Cabinet Office of the Government of Japan. He earned his Ph.D. in Bioorganic Chemistry from Hokkaido University in 1993 and has since held academic and research appointments at Columbia University, Tohoku University, RIKEN, and Hokkaido University.

Professor Monde’s research focuses on chiroptical analysis of biologically active compounds, the chemical biology of sphingolipids, and the development of fluorescence imaging probes in the shortwave infrared region for biomedical applications. He has authored more than 200 publications and supervised over 70 graduate students. His contributions have been recognized with major awards, including the 2025 SPSJ Award for Outstanding Achievement in Polymer Science and Technology and the 2018 Molecular Chirality Award. Professor Monde also an Editorial Board Member of *Chirality* (Wiley) and has served on multiple international scientific committees.

Abstract: Sphingomyelin (SM) is a lipid classified as a sphingolipid, found in high concentrations in the outer layer of cell membranes, where it accounts for 5–15% of the total lipids. Its synthetic enzyme, sphingomyelin synthase (SMS) membrane protein family consists of two functional isozymes, SMS1 and SMS 2. Both SMS 1 and 2, catalyze ceramide and phosphatidylcholine (PC) as substrates to produce sphingomyelin (SM) and diacylglycerol (DAG). The SMSs modulate SM and other sphingolipids levels, thereby regulating membrane fluidity, ceramide-dependent apoptosis, lipid metabolism and signal transduction. The increasing levels of SM and DAG produced by the SMSs will lead to obesity and insulin resistance. SMS

knockout mice are resistant to Alzheimer's disease, tumorigenesis, diet-induced obesity, type 2 diabetes mellitus and are also known to exhibit decreased levels of plasma inflammatory cytokines. Therefore, the inhibition of the SMS 1 and SMS 2 enzymes would be an ideal approach in reducing the levels of SM and DAG.

In our group, we have been investigating the SMS2 inhibitors studies from natural resources, such as medicinal plants, and have discovered useful inhibitors1),2),3). In this talk, I will give an overview of the process of searching for these inhibitors and their application to drugs for obesity2)3), SARS-CoV-25) and Alzheimer's Disease4).

Keywords: Sphingomyelin, Inhibitor, SMS, obesity, SARS-CoV-2.

Invited Talk 1

Title: Validation of traditional medicinal practices using modern tools and techniques

Kalaiselvi Senthil

Professor, Department of Biochemistry, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, India
kalaiselvi_bc@avinuty.ac.in

Short Bio: Kalaiselvi Senthil is Professor of Biochemistry at the Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, India, with over 25 years of research and 20 years of teaching experience. She has held academic positions in India, Japan, Korea, and Indonesia, including five years of postdoctoral research at the National Institute of Crop Science (Japan) and Konkuk University (Korea), and has served as Visiting Professor in South Korea and Indonesia.

Her research focuses on metabolic engineering of medicinal plants, plant tissue culture, and molecular biology, with significant contributions to secondary metabolite augmentation in *Withania somnifera* and gene identification for stress tolerance in soybean. She has supervised six doctoral students, mentored several international scholars, and established key laboratory facilities for plant biotechnology.

She has authored more than 60 international publications, co-authored five textbooks, and had an h-index of 20. She has also played an active role in institution building, international collaborations, and academic leadership, including service as Assistant Dean of Research and Development.

Abstract: Traditional medicinal practices were developed by human communities based on long-term interactions with the environment, plants, animals, and other natural resources. The co-evolution of humans with traditional medicinal practices reflects a dynamic interplay between societies and the natural world inclusive of cultural and biological diversity. These practices were passed on to generations orally, with minimal documentation, leading to difficulty in replicating the process and products. While the effectiveness of home remedies and traditional medicines has been acknowledged sufficiently through experiential knowledge, the advances of modern science have always tried to understand and explain these practices scientifically. The scientific community has developed several assays and tools to systematically evaluate and confirm the therapeutic potential of traditional medicines including pharmacological assays, bioassay guided fractionation of active principles,

identifying biomarkers and conducting clinical trials. Advanced computational methods to identify the bioactive compound and its potential target in treating a disease are gaining immense momentum in the present days. The application of these tools at the appropriate level and development of a one stop solution for validation of traditional medicinal practices will be discussed in detail. The integration of traditional knowledge and new technology will not only preserve traditional practices, but also enrich modern medicine with newer therapeutic agents.

Invited Talk 2

Title: Bio-nano interface controlling stem cells fate and application for regenerative medicine

Bayar Hexig

School of Life Science, Inner Mongolia University, P. R. China
bhexig@imu.edu.cn

Short Bio: Bayar Hexig is Professor at the State Key Laboratory of Reproductive Regulation and Breeding of Grassland Livestock, School of Life Science, Inner Mongolia University, China. He received his Ph.D. in Biomolecular Engineering from Tokyo Institute of Technology, M.Sc. in Biological & Chemical Engineering from Gunma University, and B.Sc. in Physics from Inner Mongolia Normal University. He previously worked as Postdoctoral Researcher at the National Institute of Health Science, Japan, and Assistant Professor at Tokyo Institute of Technology before joining Inner Mongolia University in 2012. His research interests include stem cell biology, developmental biology, biomaterials, regenerative medicine, and tissue engineering. Prof. Hexig is an active member of international societies including ISSCR, TERMIS, CSCB, JSRM, and JSBM, and serves as Vice Director of the Inner Mongolia Neuroscience Society.

Abstract: Pluripotent stem cells (Embryonic stem cell (ESCs) and induced pluripotent stem cell (iPSCs)) are one of the most promising stable seed cell sources for achieving regenerative medicine and clinical cell therapy. Due to its unique *in vitro* infinite self-renewal characteristics and the ability to differentiate into all types of cells and achieve renewable tissues or organs like functional structures in a specific inducing environment in vitro. Since the 1990s, the novel concept of tissue engineering has been proposed, in which the three basic elements of cells, scaffold materials, and some physiologically active substances such as growth factors and cytokines are appropriately combined to create artificial organs or tissues. Therefore, the biological-nano interface between cells and scaffold materials plays an important role in maintaining cellular function and facilitating large-scale expansion. However, the two main issues of cell quantity and purity required for the implementation of regenerative medicine and clinical treatment have not yet been resolved. To address the low efficiency of seed cells derived from pluripotent stem cells, we have developed several biological-nanointerfaces in our laboratory to establish a system for directed-differentiation of pluripotent stem cells to functional hepatocytes, nerve

cells, and hematopoietic stem cells (HSCs). Here, I will introduce the results demonstrated that fibronectin plays a role in HSC expansion in the foetal liver. The application of fibronectin and specific stimulatory factors, combined with the hanging drop method, was found to significantly increase the entry of murine embryonic stem (ES) cell-derived mesodermal cells into haematopoietic lineages. This study will provide a useful conceptual framework for the role of ECM in HSC induction, which will support future research toward the efficient *in vitro* induction and expansion of HSCs for regenerative medicine.

PP-07: EVALUATION OF EGCG AND A-TOCOPHEROL CO-ENCAPSULATION IN LIPOSOMAL SYSTEMS TO IMPROVE ANTIOXIDANT ACTIVITY, CELLULAR PROPERTIES, AND STABILITY

Hyeon Gyu Lee[1]*, Hyeonju Song[1], Youjin Baek[1], Beomkyu Choi[1], Enkhtsatsral Elbegbayar[2]
[1] Department of Food and Nutrition, Hanyang University, Korea
[2] Laboratory of Microbial Synthesis, Institute of Biology, Mongolian Academy of Sciences,
Ulaanbaatar, Mongolia
*Email: hyeonlee@hanyang.ac.kr

Epigallocatechin gallate (EGCG) and α-tocopherol (AT) are nutraceuticals with strong antioxidant properties. However, both compounds have limited application in the food industry due to their poor bioavailability and stability. In this study, we investigated the effects of co-encapsulation of EGCG and AT in liposomal systems (EGCG/AT LPs) on antioxidant activity, cellular properties, and stability. The optimal EGCG:AT ratio was 1:5, yielding the lowest antioxidant combination index of 0.935. The EGCG/AT LPs showed well-controlled particle size and stable properties with an average size of 112.58 ± 4.84 nm, PDI of 0.238 ± 0.017, and zeta potential of -75.49 ± 4.56 mV. In addition, the entrapment efficiency (EE) of EGCG and α-tocopherol in EGCG/AT LPs was 72.69% and 93.52%, respectively. The relatively lower EE of EGCG than α-tocopherol is attributed to its hydrophilic nature, which results in a higher binding affinity for the surrounding aqeous medium. However, both compounds exhibited high EE values above 70%, which is similar to the values reported in previous co-encapsulation studies. Morphology characteristics confirmed successful formation of spherical EGCG/AT LPs. The DPPH, ABTS, and FRAP assays for measuring *in vitro* antioxidant activity confirmed successful co-encapsulation of both nutraceuticals without reducing their antioxidant activity. In cellular antioxidant activity, EGCG/AT LPs exhibited 1.23 times higher antioxidant activity than the free mixture ($p<0.05$). TBARS assay showed that EGCG/AT LPs had the lowest levels compared to the blank and single antioxidant-loaded LPs ($p<0.05$). EGCG/AT LPs maintained higher antioxidant activity retention than free mixtures and stable physical properties during thermal and storage stability analysis ($p<0.05$). These results indicate that the EGCG/AT LPs can be effectively applied in the food industry by enhancing the antioxidant activity, cellular properties, and stability of both antioxidants.

Keywords: Epigallocatechin gallate, α-tocopherol, Liposome, Co-encapsulation, Antioxidant activity

PP-08: POSSIBILITY OF PRODUCING PACKAGING MATERIAL FOR DRIED FOOD PRODUCTS

Batnasan Narmandakh[1], Baljinnyam Joosh[1], Enkhtsatsral Elbegbayar[2*]
[1] School of Food, Light Industry, and Design, Department of Food Engineering, Mongolian University of Science and Technology, Ulaanbaatar, Mongolia
[2] Laboratory of Microbial Synthesis, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
*Email: enkhtsatsrale@mas.ac.mn

The packaging method is crucial in food production, preservation, transportation, product quality, safety, and customer satisfaction. In Mongolia, the packaging industry is supported by companies that produce retail and shipping films, mainly relying on imported raw materials. This study aimed to develop and evaluate a new packaging material, called Multipack (MP), made entirely from polyethylene (PE), tailored explicitly for dried food products. The research focused on characterizing the physical and chemical properties of MP. Physical properties such as thickness, elongation, and the ratio of PE to polypropylene (PP) were assessed according to ASTM D374-99 (2020) standards, using Differential Scanning Calorimetry (DSC) for composition analysis. MP was compared to 11 widely used dried food packaging materials. The tested packaging materials had thicknesses ranging from 69 to 133 microns, with MP measuring 82.3 microns. Chemical analysis confirmed that MP is composed of 100% PE. Furthermore, toxic element testing showed that MP contained lead and cadmium levels below 0.015 mg/kg and 0.001 mg/kg, respectively, two and ten times lower than the maximum allowable limits defined by Mongolian standards MNS ISO 8124-3:2011 and MNS ISO 5576:2005. These results demonstrate that MP not only meets established safety standards but also has the potential to enhance the shelf life and overall quality of dried food products. In conclusion, MP represents a safe, efficient, and locally manufacturable alternative to conventional packaging for dried foods in Mongolia.

Keywords: Plastic, Dried products, Packaging materials, Food packaging, Polyethylene, Polypropylene

SESSION 3:

AGRICULTURAL & FOOD BIOTECHNOLOGY

Keynote Speech

Title: Development of high beta carotene Sweet Corn Hybrid through Marker-assisted breeding to address the vitamin A deficiency

Senthil Natesan*, Shivakumar Ravichandran

Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore – 641003, Tamil Nadu, India
senthilnatesan1969@gmail.com

Short Bio: Senthil Natesan is an agricultural scientist and molecular breeder at Tamil Nadu Agricultural University (TNAU), specializing in genome-assisted breeding and crop improvement. Over two decades, he has developed multiple high-yielding and nutritionally enhanced crop varieties, including ragi, samai, thenai, kuthiraivali, wheat, and maize, and contributed over 20 crop genome sequences to international databases. Prof. Natesan has guided numerous graduate students, established international collaborations, and facilitated patents and MoUs connecting academia and industry. His research achievements include publication in *CELL*, recognition as a highly cited agriculture scientist, and election as Fellow of the National Academy of Agricultural Sciences (FNAAS) in 2022.

Abstract: Biofortification offers a cost-effective and sustainable strategy to combat micronutrient deficiencies. This study reports the development of a novel biofortified sweet corn hybrid, CSBH 23003, enriched with a provitamin A carotenoid. The hybrid was developed by crossing beta-carotene–enriched inbred lines, DBT 23 and DBT 15, both carrying the crtRB1 gene associated with enhanced beta-carotene biosynthesis. Hybridization was carried out in Summer 2023, followed by evaluations during Kharif 2023 (Preliminary Yield Trial) and Summer 2024 (Comparative Yield Trial). The hybrids were assessed for sugar and carotenoid content. Total sugars were quantified using the Anthrone method, reducing sugars via the Nelson-Somogyi method, °Brix with a digital refractometer, and beta-carotene concentration by High-Performance Liquid Chromatography (HPLC). Marker analysis confirmed the presence of the crtRB1 allele in the inbreds. In the Kharif 2023 trial, CSBH 23003 recorded 0.90% reducing sugars, 18.00% non-reducing sugars, 18.89% total sugars, 19.50° Brix, and 10.977 µg/g beta-carotene (fresh weight). During the Summer 2024 trial, it showed 2.99% reducing sugars, 15.22% non-reducing sugars, 18.21% total sugars, 17.00° Brix, and 8.78 µg/g beta-carotene at 75 days after pollination. Given its agronomic stability and enhanced

nutritional profile, CSBH 23003 has been nominated for multi-location trials (MLT) in Kharif 2024 to evaluate its broader adaptability and yield performance.

Keywords: Biofortification, Beta-Carotene, Sweet Corn Hybrid, Vitamin A Deficiency, Micronutrient Enhancement

Invited Talk 1

Title: Discovery of chemicals for control of root parasitic weeds focusing on germination metabolism

Atsushi Okazawa

Osaka Metropolitan University, 1-1 Gakuen-cho, Naka-ku, Sakai 599-8531, Japan
Okazawa.atsushi@omu.ac.jp

Short Bio: Dr. Atsushi Okazawa is a Professor at the Graduate School of Agriculture, Osaka Metropolitan University. He obtained his Ph.D. in Agriculture from Kyoto University in 1998. His career spans over two decades, beginning as an Assistant Professor at Osaka University (1997–2012), followed by appointments as Associate Professor at Osaka Prefecture University (2012–2022) and Osaka Metropolitan University (2022–2024), before assuming his current professorship in 2024. Dr. Okazawa's research focuses on pesticide science and plant chemical regulation, areas in which he has made significant contributions. He is the recipient of the Japanese Society for Chemical Regulation of Plants Award for Young Scientists (2010) and the Pesticide Science Society of Japan Achievement Award (Research) (2025).

Abstract: Orobanchaceae root parasitic weeds cause serious agricultural problems world-wide. Management of root parasitic weeds is an urgent issue for global food se-curity, but practical methods are under development. Our group focuses on the metabolism of root parasitic weeds during germination to seek molecular targets for their control. Through metabolome studies, we found that planteose is stored in the seeds of root parasitic weeds. OmAGAL2, an acidic α-galactosidase, was identified as a planteose-hydrolyzing enzyme during Orobanche minor germina-tion. We screened a chemical library of about 15,000 compounds and selected several classes of OmAGAL2 inhibitors. Among the chemical classes, we select-ed aryloxyacetylthioureas for further structural optimization as OmAGAL2 inhib-itors. The inhibitory effects of 21 derivatives synthesized in two steps on O. mi-nor radicle growth were evaluated. This structure–activity relationship study re-vealed the chemical characteristics required for their potent inhibitory activity. Other classes of growth inhibitors and their potential as practical control agents are also discussed in the presentation.

Keywords: Metabolic Inhibitors, Parasitic Plants, Storage Carbohydrates.

Invited Talk 2

Title: Antimicrobial and anti-biofilm activity of essential oils on food-borne microbes

Judit Krisch

Department of Food Engineering, University of Szeged

Short Bio: Dr. Judit Krisch is an Associate Professor at the Institute of Food Engineering, University of Szeged, Hungary. She earned her Ph.D. in Molecular Biology from József Attila University in 1996, following her M.Sc. in Biology in 1985. Her academic career includes research and teaching appointments in biochemistry and microbiology, as well as clinical laboratory supervision at the Municipal Hospital of Szeged.

Her research focuses on food microbiology, food safety, and bioactive natural compounds, with particular interest in plant-derived antimicrobials, antioxidants, probiotics, and biofilms. Dr. Krisch has published extensively in international journals and continues to contribute to advancing safe and sustainable food systems.

Abstract: Essential oils (EOs) have excellent antimicrobial and anti-biofilm activity which empowers their use in the food industry as preservatives or sanitizing agents against food-borne microbes. Most of the EOs has the GRAS status by the FDA and are on the list of flavoring substances by the EFSA. The strong aroma, low water solubility, and changing composition of essential oils limit their use in the food industry. Extensive work is established to overcome these problems. Essential oils as food preservatives can be used directly or incorporated into active packaging. Efficient dose of EOs could change the sensorial characteristics of foods therefore they are often combined with other preservatives utilizing the synergistic effect among these substances. Other application of EOs is their use as sanitizing or disinfection agents. In this aspect EOs has several advantages compared to commercial disinfectants: they are able to eliminate matured and multi-species biofilms from industrial and domestic surfaces and need no rinsing. Considering all pros and cons essential oils have their place in the food industry or in households.

PP-9: GROWTH AND DEVELOPMENT OF DOMESTIC BACTRIAN CAMEL CALVES RAISED IN GUCHIN-US SUM, UVERKHANGAI PROVINCE

Purevdolgor D[1]*, Suvdaa G[1], Saranchimeg M[2], Altantuya D[3], Bat-Erdene D[1]
[1] Animal Science Sector, Research Institute of Animal Husbandry, Ulaanbaatar, Mongolia
[2] Agricultural Division, Guchin-Us Soum, Uvurkhangai Province, Mongolia
[3] "Tüseg Khairkhan" LLC, Guchin-Us Soum, Uvurkhangai Province, Mongolia
*Email: Dagviipurev@gmail.com

This study was conducted in 2023 on a herd of domestic Bactrian camels raised in the "Mongolyn Khooloi" area of Guchin-Us sum, Uvurkhangai province. A total of 40 calves were selected, and their live weight and body measurements were recorded at birth, 3, 6, 9 months, and 1 year of age. Daily weight gain, absolute and relative growth were calculated accordingly. At birth, the local camel calves of Guchin-Us weighed on average 42.3 ± 0.49 kg, increasing to 52.7 ± 0.54 kg at one month, 97.7 ± 0.82 kg at three months, 146.5 ±1.44 kg at six months, and reaching 219.1 ± 4.85 kg at one year of age. The relatively abundant rainfall during spring (April–May) improved the quality of maternal milk, resulting in higher birth weights (36–46 kg) and steady weight gain during the first month (48–58 kg). This indicates sufficient forage growth and nutrient availability during that period. Despite the dry, hot, and windy summer (June–August), organized herding, proper management, and availability of feed and water contributed to uninterrupted growth, with calves reaching 138–156 kg by six months of age. Rainfall increased again in early autumn (September–October), improving pasture conditions and accelerating weight gain. By one year of age, male calves reached up to 295 kg, which is 11.9% higher than female calves-attributable to sex-specific physiological differences and better feed conversion efficiency. Regarding body measurements, at birth the average values were as follows: height between humps 102.3 ± 0.09 cm, oblique body length 59.4 ± 0.12 cm, chest girth 83 ± 0.05 cm, and cannon bone girth 11 ± 0.01 cm. These increased steadily at each measurement period, reaching at one year of age: 142.9 ± 0.27 cm, 124.7 ± 0.29 cm, 193.5 ± 0.48 cm, and 14.7 ± 0.02 cm, respectively. The consistent increase in body dimensions indicates adequate nutrition and a well-managed, comfortable rearing environment for the calves.

Keywords: live weight, growth, body measurements, calf, age

PP-10: SYNERGISTIC YEASTS AS BIOCONTROL AGENTS AGAINST FUNGAL PATHOGENS: ENZYME PROFILES AND VOLATILE COMPOUNDS

Anumandal Orgil[1]*, Urjinlkham Renchindorj[1], Mend-Amar Mendbayar[1], Uuriintuya Munkhbayar[1],
Pagmadulam Baldorj[1], Rentsenkhand Tserennadmid[1] Enkhtsatsral Elbegbayar[1]
[1] Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar 13330, Mongolia
*Email: anumandalo@mas.ac.mn

Postharvest losses of fruits and vegetables are provoked worldwide by fungal pathogens. In Mongolia, postharvest loss of fruits and vegetables accounts for approximately 20-30% due to improper storage conditions and inadequate sanitation. Although there have been widespread applications of chemical fungicides, their environmental health risks have led to increased demand for and concerns about safer alternatives. In the present work, we examine the biocontrol capacity of epiphytic yeasts preserved in our laboratory culture library against crop fungal pathogens, based on published literature that highlighted their ability to synthesize fungal cell-degrading enzymes and organic volatile compounds inhibiting spore germination. Of the 150 samples collected from vegetable and fruit crops from greenhouses and open fields in Selenge province, Mongolia, 50 pure fungal cultures were isolated and identified by molecular analysis, which included *Botrytis* spp. (2), *Aspergillus* spp. (7), *Fusarium* spp. (16), *Penicillium* spp. (11), *Mucor* spp. (10), and *Geothrichum candidum* (4). These fungi were tested in vitro against yeast strains, both singularly and in combination, using the dual-culture method. The two yeasts, *Wickerhamomyces anomalus* 80 and *Pichia jadinii*, showed the strongest antagonism by means of volatile (93.8% and 91.46%) and non-volatile inhibitory (40% and 48%) compounds. *W.anomalus* 80 showed chitinase, lipase, and amylase; *P.jadinii* exhibited chitinase and cellulase activity. Both strains were biofilm producers and could stand stress conditions, such as a pH range of 4-9, a temperature range of 8–37°C, and a salinity range of 1 to 4%. These results indicate that *W. anomalus* 80 and *P. jadinii* have a synergy with each other and could be potential environmentally friendly biocontrol agents against postharvest fungal pathogens.

Keywords: Postharvest Fungal Diseases, Epiphytic Yeasts, Biocontrol Mechanisms

PP-11: COMPARATIVE EXPRESSION ANALYSIS OF *C4H* AND *CYP98A* GENES IN WILD, CULTIVATED, AND *IN VITRO*-REGENERATED *SAPOSHNIKOVIA DIVARICATA*

Khaliunaa Tuvshinjargal[1], Oyunbileg Yungeree[2], Altanzul Khorolragchaa[2]*
[1] Laboratory of Molecular Biology, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
[2] Laboratory of Plant Biotechnology, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
*Email: Altanzulkh@mas.ac.mn

Saposhnikovia divaricata is a well-known medicinal plant valued for its bioactive secondary metabolites, including chromone and coumarins, which contribute significantly to its therapeutic properties. The biosynthesis of these compounds is regulated by key genes, notably *C4H* (*Cinnamate-4-hydroxylase*) and *CYP98A* (*Cytochrome P450-like protein*), both of which play essential roles in phenylpropanoid metabolism. This study investigates the expression of these genes in *S. divaricata* grown under three different conditions: *in vitro*, cultivated (grown from seed in the field), and in wild environments. To optimize seed germination for the establishment of *in vitro* propagation protocol, various sterilization treatments were tested, with a 0.1% H_2O_2 treatment for 12 hours, resulting in the highest germination rate (86.6%) and minimal contamination. Samples were separately collected from leaves, stems, and roots of *in vitro*-regenerated, cultivated, and wild-grown plants. These samples were subsequently used for genetic stability assessment and gene expression analysis. Genetic stability was evaluated using RAPD markers, while the expression levels of *C4H* and *CYP98A* genes were quantified by RT-qPCR using the $2^{-\Delta\Delta CT}$ method. Murashige and Skoog (MS, 1962) medium supplemented with 0.5 mg/L 6-benzylaminopurine (BAP) and 2.0 mg/L α-naphthaleneacetic acid (NAA) was found to be the most effective for shoot regeneration from leaf explant – induced callus. Genetic fidelity analysis indicated a high degree of similarity among the plant groups (similarity coefficient: 0.88–1.00), suggesting minimal genetic variation occurred in tissue-cultured plants. The expression levels of *C4H* and *CYP98A* in the leaves and stems of *in vitro* plants were 2.3–2.5-fold higher compared to wild plants.. However, ANOVA analysis indicated that the observed differences were not statistically significant ($p > 0.05$). The preliminary findings confirm that *S. divaricata* can be successfully regenerated in vitro while preserving both genetic stability. The ability to propagate this species under controlled conditions presents a sustainable approach to producing medicinal biomass, thereby alleviating harvesting pressure on wild populations. Moreover, insights into gene expression patterns of key biosynthetic genes may guide future efforts in phytochemical enhancement, selective breeding, and biotechnological propagation. Therefore, this study provides valuable guidance for optimizing cultivation techniques and supporting conservation strategies for this important medicinal species.

Keywords: *S. divaricata*, expression analysis, C4H, CYP98A, *in vitro* regeneration

PP-12: ISOLATION AND CHARACTERIZATION OF INDIGENOUS STRAINS OF *SACCHAROMYCES CEREVISIAE* FOR THEIR PROMISING POTENTIAL AS EFFECTIVE BAKER'S YEAST

Munguntuya Bataa[1], Bolor-Oyut Batbayar[2], Gerelmaa Zorigtbaatar[2], Rentsenkhand Tserennadmid[2], Enkhtsatsral Elbegbayar[2]*,
[1] School of Animal Science and Biotechnology, Mongolian University of Life Sciences, Ulaanbaatar, Mongolia
[2] Laboratory of Microbial Synthesis, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
*Email: enkhtsatsrale@mas.ac.mn

Indigenous *Saccharomyces cerevisiae* (*S. cerevisiae*) strains play a vital role in baking; however, their diverse fermentation traits and stress tolerance require thorough evaluation to identify the best candidates. This study aimed to isolate and characterize local yeast strains adapted to Mongolia's environment, with the broader goal of reducing dependence on imported baker's yeast. Five strains (Sc01–Sc05) were isolated from Mongolian fruit and soil samples and assessed for key physicochemical and fermentative properties, including dough leavening ability and resistance to osmotic and thermal stress. None of the isolates produced H_2S, and all strains tolerated temperatures up to 45°C and ethanol concentrations of 15%. At pH 4, Sc04 exhibited the highest growth activity and significantly increased dough volume compared to other strains ($p< 0.05$). Both Sc01 and Sc04 reached peak growth in high-sugar media (40–50%) at 24 and 48 hours, respectively ($p< 0.05$). Under optimized conditions, Sc04 produced significantly more biomass than the others ($p< 0.05$). Based on bread leavening efficiency and characterization of five promising baker's yeast strains, Sc04 was selected as a potential baker's yeast. The Sc04 strain was identified as *S. cerevAA__3366isiae* through biochemical properties, API kit analysis, and PCR-based molecular methods. Its performance was compared with commercial baker's yeast (Angel), and fermentation parameters were optimized accordingly. Based on these findings, Sc04 demonstrates strong potential as a locally sourced alternative for baking in Mongolia. However, larger-scale trials and pilot production are needed before industrial adoption can be recommended. This study provides valuable insights into the development of indigenous microbial resources for sustainable food biotechnology.

Keywords: baker's yeast, *Saccharomyces cerevisiae*, indigenous yeast, yeast fermentation, bread

PP-13: ISOLATION OF BIOACTIVE COMPOUNDS PRODUCING ACTINOBACTERIA FROM SOIL IN MONGOLIA

Pagmadulam Baldorj[1]*, Yoshifumi Nishikawa[2], Rentsenkhand Tserennadmid[1], Mendamar Mendbayar[1], Erdenechimeg Shagdar[1]
[1] Laboratory of Microbial Synthesis, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
[2] National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Hokkaido 080-8555, Japan
*Email: pagmadulam_b@mas.ac.mn

Toxoplasmosis is caused by *Toxoplama gondii*, which is an intracellular protozoan parasite classified in the phylum *Apicomplexa*, capable of infecting various warm-blooded animals, including humans. Currently, no ideal drugs are available. Therefore, screening for more effective drugs targeting protozoan infections is critically required. Natural products, mainly microorganisms and medicinal plants, play a vital role as a major source of bioactive compounds against infectious diseases. Therefore, the proposed research aims to identify potent antiprotozoal agents from Mongolian natural resources against protozoan diseases. The specific objective is to screen and evaluate active compounds from natural resources such as actinobacteria (*Streptomyces* sp.). Soil samples were collected from the Ulaanbaatar and Tuv provinces of Mongolia, and 30 cultures of actinomycetes were isolated on ISP 1,2,4,5,7 (International Streptomyces Project). The cultures were grown in ISP2 broth at 28°C for 7 days with shaking (200 rpm) as a production medium. The supernatant and mycelia were separated by centrifugation. Each supernatant was extracted with an equal volume of ethyl acetate and evaporated. Crude extracts were dissolved in DMSO for testing antibacterial and antiprotozoal activities. Antibacterial activity was determined by agar diffusion method, and the results were evaluated by the clear zone. For antiprotozoal activities, human foreskin fibroblast (HFF) cells were grown on a 96-well plate at 37°C for 48h and infected with 100 µl of *Toxoplasma gondii* (RH-GFP) and evaluated with fluorescence intensity by a microplate reader. The phylogenetic analysis was conducted using 16S RNA gene sequences. In the present study, 30 crude extracts were extracted from actinomycetes. The 11 crude extracts showed antibacterial activity against the pathogenic bacteria *Staphylococcus aureu*s and *Escherichia coli.* The crude extracts from all the samples were evaluated against *T.gondii* (RH-GFP) growth *in vitro*. Ten crude extracts (Belh hulemj1-6, 7-HBU-3^2) inhibited *T. gondii* growth by >50%. However, crude extract Belh hulemj1-6 and 7-HBU-3^2 had significant anti-protozoan activities with IC_{50}: 13 µg/ml and IC_{50}: 21.9 µg/ml. The phylogenetic study of Belh hulemj1-6 and 7-HBU-3^2 cultures revealed they had the highest similarity (99.3% and 99.9%) with the actinomycete strains *Streptomyces badius* and *Streptomyces bacillaris*. Further, it is important to continue the research in this field to discover microorganisms that can be used for the control of infectious diseases.

Keywords: Actinobacteria, Toxoplasmosis, Bioactive compounds

PP-14: COMBATING CLIMATE STRESS IN LEGUME FARMING: DROUGHT-TOLERANT RHIZOBIA FOR FABA BEAN CULTIVATION IN HUNGARY

Sándor Jenei[1], Ágota Domonkos[2], Alexandra Pál[1], Rózsa Máté[3], Beatrix Horváth[2], Zsolt Bereczky[3], Péter Kaló[1,2] and Gabriella Endre[1]
[1]HUN-REN Biological Research Centre, Institute of Plant Biology, Hungary, Szeged 6726, Temesvári krt. 62.
[2]MATE Hungarian University of Agriculture and Life Sciences, Institute of Genetics and Biotechnology
[3]BioFil Microbiological, Gene-technological and Biochemical Ltd.
E-mail: endre.gabriella@brc.hu

Leguminous crops are essential contributors to sustainable agriculture due to their capacity for biological nitrogen fixation via symbiotic interactions with soil-dwelling rhizobia. This symbiosis not only fulfills the nitrogen demands of the host plant but also enhances soil fertility, facilitating improved yields in other crops within intercropping and crop rotation systems. Vicia faba (faba bean) is among the earliest domesticated legumes and historically served as a principal food source in Europe.

This study aims to develop a prototype microbial inoculant comprising drought-tolerant rhizobia and co-inoculant soil bacteria to enhance faba bean resilience under water-deficit stress. We collected plant samples from eight different locations, from which we isolated bacteria from root nodules, root tissue, root surface and the soil region around the roots. More than 500 bacteria were isolated and cleaned further to single colonies. PCR amplification of rDNA ITS region followed by sequencing were done, and the genus and, in many cases, species level identification was performed on 235 strains using bioinformatic methods based on sequence polymorphisms. As expected, most of the strains identified from the root nodule belonged to the Rhizobium leguminosarum species, while Priestia, Bacillus, Peribacillus and Pseudomonas bacteria were predominantly in the endophytic samples. The research involves their phenotypic characterization, evaluating their plant growth-promoting (PGP) effects under controlled and field conditions, and screening for drought tolerant strains. Promising strains are selected based on symbiotic efficiency, stress resilience, followed by optimization of inoculant formulation and production parameters. The outcomes are expected to contribute to the development of climate-resilient legume cropping systems.

The project is done in collaboration with Moroccan partners at the Cadi Ayyad University, Marrakech and the Sultan Moulay Slimane University, Beni-Mellal. The project is supported by the Hungarian National Office for Research, Development and Innovation (NKFIH) through the grant 2021-1.2.6-TÉT-IPARI-MA-2022-00005.

SESSION 4:

BIOTECHNOLOGY & MICROBIOLOGY

Keynote Speech

Title: Breeding of oleaginous yeast *Rhodotorula* for lipid production

Fujiyama Kazuhito [1, 2*], Misaki Ryo [1, 2] Kajiura Hiroyuki [1, 2]

[1] International Center for Biotechnology, The University of Osaka,
[2] Institute for Open and Transdisciplinary Research Initiatives (OTRI), The University of Osaka
fujiyama@icb.osaka-u.ac.jp

Short Bio: Kazuhito Fujiyama is a Professor at the International Center for Biotechnology, Osaka University, Japan, and former Director of ICBiotech. His research focuses on applied microbiology for sustainable development goals and glyco-engineering of heterologously produced proteins.
Prof. Fujiyama has extensive international research experience, including positions at Arizona State University, Cornell University, and University of Zurich. He has authored over 160 publications, contributed to plant- and microbe-based bioproduction, and received awards such as the Osaka University Prize (2021) and Honorary Professorship at Institut Teknologi Bandung (2019).

Abstract. *Rhodotorula* strains are oleaginous yeasts and represent an attractive microbial platform for lipid production. These microbial lipids are considered a promising alternative source for renewable fuels. High oleic acid (OA; C18:1) content in plant-derived oils offers advantages such as improved oxidative stability and suitability across a wide range of temperatures. In this presentation, two case studies involving *Rhodotorula* strains are introduced. First, *R. mucilaginosa* DMKU3-TK16 (TK16), isolated in Thailand, was metabolically engineered. TK16 strains were modified to express the Delta-9 fatty acid desaturase (Δ9FAD) gene, resulting in enhanced lipid production enriched in OA. Second, *R. toruloides* NBRC0880 was utilized for lipid production using crude glycerol, a bio-waste byproduct. This strain successfully accumulated lipids at levels comparable to those observed when glucose or pure glycerol was used as the carbon source. Overall, *Rhodotorula* strains were engineered to produce OA-enriched lipids, providing a desirable feedstock for the production of tailored biodiesel and other value-added lipid-based chemicals.

Keywords: Oleaginous yeast; *Rhodotorula*; lipid production; Delta-9 fatty acid desaturase

Invited Talk 1

Title: Unveiling the Ecological Roles of Novel Marine Gliding Bacteria

Song-Gun Kim

Biological Resource Center/Korean Collection for Type Cultures (KCTC), Korea Research Institute of Bioscience and Biotechnology, Jeongeup, Jeonbuk 56212, the Republic of Korea

Short Bio: Dr. Song-Gun Kim is Principal Research Scientist at the Biological Resource Center, Korea Research Institute of Bioscience & Biotechnology (KRIBB) and Professor at the University of Science and Technology, Daejeon, Korea. He earned his Ph.D. in Environmental & Molecular Microbiology from KAIST and completed postdoctoral training in Environmental & Molecular Phycology at KRIBB and X-ray Protein Crystallography at Louisiana State University.

His research focuses on microbial resources, prokaryotic taxonomy, comparative genomics, and phylogenetic analysis. As Head of KRIBB's Biological Resource Center, he has curated bacterial collections and discovered and characterized numerous novel marine microbial species. He leads national research projects advancing microbial resource infrastructure and applications. Dr. Kim received a commendation from the Minister of Science & ICT of the Republic of Korea in 2019. He also received a commendation from the Minister of Environment of the Republic of Korea in 2021.

Abstract: Marine gliding bacteria play important roles in marine ecosystems through their motility and metabolic versatility. We isolated novel gliding strains from diverse marine substrates, enabling the cultivation of taxa rarely obtained by conventional methods. Taxonomic analyses, integrating phenotypic, chemotaxonomic, and phylogenomic data, led to the description of a novel genus and several new species, expanding the phylogenetic diversity of marine Bacteroidota.

Genome sequencing and functional annotation revealed extensive carbohydrate-active enzyme (CAZyme) repertoires, indicating adaptation to polysaccharide-rich environments such as macroalgal surfaces and detrital material. Biochemical assays confirmed the degradation of diverse marine polysaccharides, linking genomic potential with ecological function. Additionally, predatory activity against co-occurring marine bacteria was observed, suggesting these microorganisms contribute both to organic matter turnover and microbial community regulation.

This study demonstrates the ecological significance and functional diversity of gliding bacteria, highlighting their dual roles as decomposers and predators in marine

nutrient cycling. Our findings emphasize the value of targeted isolation strategies in uncovering novel microbial diversity and elucidating their roles in ocean ecosystems.

Invited Talk 2

Title: Plant-derived NCR peptides are potent antifungals against *Cryptococcus neoformans*

Bettina Szerencsés[1], Gabriella Endre[2], Éva Kondorosi[2] and Ilona Pfeiffer[1*]

[1] Department of Biotechnology and Microbiology, Faculty of Sciences and Informatics, University of Szeged; Szeged, Hungary;
[2] Institute of Plant Biology, HUN-REN Biological Research Centre, Szeged, Hungary;

Short Bio: Ilona Anikó Pfeiffer is an Associate Professor at the University of Szeged, Faculty of Science and Informatics, Department of Biotechnology and Microbiology. She earned her Ph.D. in Biology from Attila József University in 1997 and completed her habilitation at the University of Szeged in 2023. Her research focuses on microbiology and mycology, with more than 50 publications, two patents, and over 1,300 independent citations.

Dr. Pfeiffer has held several leadership roles, including Vice Dean for Education (2020–present) and Deputy Head of the Institute of Biology for Education (2013–2021). Her honors include the Hungarian Academy of Sciences Academic Youth Award (1998), the Hungarian Microbiological Society Best Youth Lecturer Award (1999), and the Hungarian Golden Cross of Merit (2019). She is an active member of professional societies and has served on numerous national and international conference organizing committees.

Abstract: *Cryptococcus neoformans* is an opportunistic fungal pathogen in humans, capable of inducing severe and potentially fatal meningitis in individuals with compromised immune systems (1). Considering the increased incidence and severe consequences of the infection, coupled with the restricted array of therapeutic options, cryptococcosis represents a substantial global public health concern. The management of cryptococcal infections remains problematic, as the available drugs are limited to three primary agents: amphotericin B, fluconazole, and flucytosine; however, the pronounced toxicity associated with amphotericin B, along with the growing resistance observed against fluconazole and flucytosine, significantly complicates the therapy (2). Consequently, the exploration of novel therapeutic approaches is needed. Antimicrobial peptides are promising candidates, given that many displays antifungal characteristics while maintaining minimal cytotoxic effects (3). In our study, the anti-cryptococcal efficacy of *Medicago truncatula* NCR247, NCR335, and NCR169C derivatives, as well as three synthetic chimera peptides was assessed, utilizing the micro-dilution technique and flow cytometry. The concentration- and time-dependent efficacy of one chimera peptide was determined

through colony-forming unit enumeration. The cytotoxicity of the peptides was evaluated by MTT assay, whereas their impact on the phagocytic function of macrophages was monitored using flow cytometry. Confocal laser scanning microscopy was employed to examine the intracellular distribution of NCR peptide. Fifteen peptide derivatives, along with all three chimeras, demonstrated notable effectiveness against *Cryptococcus neoformans.* Among these, the X1-NCR247C chimera exhibited the highest efficacy, with its effectiveness being contingent on both concentration and time. Notably, the attachment of X1-NCR247C to yeast cells augmented their uptake by murine macrophages. The results of our study underscore the effectiveness of NCR peptide derivatives as anti-cryptococcal agents, thereby emphasizing the potential for enhancing their activity through the development of chimera peptides.

Invited Talk 3

Title: Advanced enzyme-assisted strategies for the recovery of bioactive phenolics from grape residues

Miklós Takó[1], Tamás Kovács[1], Endre Surman[1], Zsófia Sára Kasziba[1], Marija Petrović[2], Judit Krisch[3], Csaba Vágvölgyi[1], Tamás Papp[1,4]

[1] Department of Biotechnology and Microbiology, Faculty of Science and Informatics, University of Szeged, Közép fasor 52, H-6726 Szeged, Hungary
[2] Institute of General and Physical Chemistry, Studentski trg 12, 11070 Belgrade, Serbia
[3] Institute of Food Engineering, Faculty of Engineering, University of Szeged, Mars tér 7, H-6724 Szeged, Hungary
[4] HUN-REN-SZTE Pathomechanisms of Fungal Infections Research Group, University of Szeged, Közép fasor 52, H-6726 Szeged, Hungary

Short Bio: Miklós Takó is an Assistant Professor at the Department of Biotechnology and Microbiology, University of Szeged, Hungary. He earned his Ph.D. in Microbiology from the University of Szeged in 2012, receiving summa cum laude.

Dr. Takó's research focuses on natural active ingredient-based food additives, preservation processes, and surface disinfection systems. His work includes studying the effects of essential oils, phenolic antioxidants, and other bioactive compounds on foodborne microorganisms, biofilm formation, and quorum sensing mechanisms. He also investigates environmentally friendly production of saccharides and fatty acid esters through enzymatic processes and fermentation, and analyzes bioactive effects using both in vitro and in silico approaches.

He has received numerous awards and fellowships, including the János Bolyai Research Scholarship (2017), the New National Excellence Program Scholarship (2018, 2019), and the NKFIH Young Researchers' Excellence Programme (2020–2025). Dr. Takó is a member of the Hungarian Society for Microbiology and the Hungarian Academy of Sciences.

Abstract: Grape pomace represents a valuable source of antioxidant phenolic compounds with well-documented health benefits. However, the majority of these phenolics are bound to plant cell wall polymers, resulting in their limited bioavailability. Although solvent extraction is frequently used to liberate bound phenolics, it poses environmental concerns and may compromise extract quality. Enzyme-assisted extraction using hydrolytic enzymes (e.g., cellulase, pectinase) produced by filamentous fungi provides an eco-friendly and effective alternative.

This approach enhances phenolic yields by disrupting plant cell wall structures and cleaving ester and glycosidic bonds. In this study, we aimed to enhance the free phenolic content of grape pomace residues from Blaufränkisch and Cabernet Sauvignon varieties through enzymatic treatments utilizing hydrolytic enzymes derived from filamentous fungi. Based on prior research, cellulolytic and lipolytic extracts, alongside commercial pectinase and tannase preparations, were selected for treatments. The extracts were subsequently analyzed for bioactivity through assays measuring total phenolic and flavonoid contents, antioxidant capacity, and enzyme inhibitory activities. Combined enzymatic treatments significantly increased the total phenolic content and improved the antioxidant activity of the residues. The extracts demonstrated inhibitory effects against the activity of diabetes-related key enzymes. These findings highlight the potential of enzymatically derived extracts from grape pomace as bioactive functional additives for the development of health-promoting food and feed products. This research was supported by the projects HUN-REN 2001007 and TKP2021-EGA-28.

PP-15: BIOPROSPECTING OF POLYHYDROXYALKANOATES-PRODUCING BACTERIA FROM MARINE ENVIRONMENT

Sondor Ganbat[1], Dariimaa Ganbat[2], Yujin Son[3], Dong-Woo Lee[4], Sung Tae Kim[5,6], Seong-Bo Kim[2,7], Mi Hwa Park[8] and Sang-Jae Lee[1]*
[1] Department of Bioscience and Research Center for Extremophiles and Marine Microbiology, Silla University, South Korea
[2] Department of Applied Biosciences, Kyungpook National University, South Korea
[3] Department of Integrative Biotechnology (IBT), Yonsei University, South Korea
[4] Department of Biotechnology, Yonsei University, South Korea
[5] Department of Nanoscience and Engineering, Inje University, South Korea
[6] Department of Pharmaceutical Engineering, Inje University, South Korea
[7] Bio-Living Engineering Major, Global Leaders College, Yonsei University, South Korea
[8] Department of Food and Nutrition, College of Human Ecology, Silla University, South Korea
*E-mail: sans76@silla.ac.kr

Polyhydroxyalkanoates (PHAs) are a group of biopolymers with various applications and excellent biodegradability; however, their widespread use has been limited by high production costs. To overcome this limitation, strains with high PHA yield, the ability to grow in low-cost media, and susceptibility to simple cell lysis for efficient recovery are of great interest. This study aimed to explore PHA-producing microorganisms isolated from marine environments in South Korea for their potential in cost-effective PHA production. A diverse group of bacteria was isolated and screened by Sudan Black B and Nile Red A staining. A total of 27 potent PHA-producing bacteria belonging to the genera *Halomonas* spp., and *Cobetia* spp. were characterized. PHA granules in the cells were visualized using a confocal microscope. The presence of a PHA synthase gene (*phaC*) was confirmed by PCR. Gas chromatography analysis was performed to confirm the PHA fractions, and the extracted polymers were identified as polyhydroxybutyrate (PHB). Preliminary analysis revealed that the selected marine bacteria exhibit high salinity tolerance (up to 13–15% NaCl) and notable PHA accumulation, with PHA content reaching 67.1 ± 3.54 wt%. Therefore, complete bacterial genome sequencing and de novo assembly were performed using the PacBio Sequel II platform and the Microbial Genome Assembly pipeline to predict metabolic pathways of *Halomonas* spp. and to identify genes involved in PHA metabolism, carbohydrate metabolism, fatty acid metabolism, and stress tolerance. Moreover, the complete genome sequence of *Halomonas* spp. revealed the presence of an extracellular PHA depolymerase gene, and its PHA-degrading activity was experimentally confirmed. These findings suggest a high potential not only for PHA production but also for the biodegradation and recycling of PHA by halophilic bacteria isolated from the marine environment.

Keywords: Polyhydroxyalkanoates (PHAs), Halophiles, Marine Environment

PP-16: ISOLATION AND CHARACTERIZATION OF KERATINASE-SECRETING MICROORGANISMS

Bolor-Oyut Batbayar[1*], Tumen-Erdene Unurtsetseg[2], Khulan Janchiv[2], Ochirkhuyag Baldorj[2]
[1] Laboratory of Microbial Synthesis, Institute of Biology, Mongolian Academy of Sciences, Mongolia
[2] Department of Biology, School of Sciences, National University of Mongolia, Mongolia
*Email: khulan@num.edu.mn

The main factors of environmental pollution are often considered to be industry, energy, and transportation. Furthermore, huge livestock complexes and industrial poultry farming also have a significant and far-reaching impact on ecosystems. Feathers produced in large quantities during the growing and slaughtering of poultry pose a threat to the environment due to the presence of the complex degradable structural protein keratin. In addition, the presence of a large number of microbiological pathogens in the feathers poses a threat to the environment. Nowadays, processing such protein-containing wastes requires technology that consumes high energy, which is also an unfriendly process to the environment. The main method of feather waste dismantling is the production of feather meal with pressurized steam. The significant costs incurred by this method of hydrothermal degradation of waste contribute to the search for alternative options for poultry waste recycling. In this study, we aimed to isolate and characterize keratinase-producing bacteria from wool and soil samples and test their ability to degrade feathers *in vitro*. A total of 9 pure cultures of proteolytic bacteria were isolated by forming clear zones on skim milk agar. When the activities of protease and keratinase enzymes were determined using L-tyrosine and soluble keratin as substrates, isolate D2-23 exhibited the highest activity, with protease enzyme activity of 462 U/ml and keratinase enzyme activity of 294 U/ml, respectively. From the laboratory scale feather-degrading activity test, it was found that the bacterial culture D2-23 showed a remarkable 93% feather decomposition and was characterized as *Bacillus pumilus* by 16S rRNA gene sequencing and biochemical tests. Studying the enzymatic capacity of bacteria provides a sustainable method to add value to poultry waste and expands our understanding of the role of microbial keratinases in bioconversion processes. Overall, our results indicate that the isolated strain of *Bacillus pumilus* D2-23 is a promising and environmentally effective biological tool for converting feather waste into valuable products through natural biodegradation.

Keywords: keratin, feather degradation, keratinase, proteolytic bacteria, industrial strain

PP-17: ISOLATION AND CHARACTERIZATION OF ENDOPHYTIC *METSCHNIKOWIA* YEASTS FROM THE MEDICINAL PLANT *ACORUS CALAMUS* LINN. IN MONGOLIA

Bumtsend Byambasuren[1], Amarbayasgalan Maidarjav[1], Enkh-Amgalan Jigjiddorj[1]*
[1] Laboratory of Microbiology, Institute of Biology, Mongolian Academy of Sciences, Enkhtaivan avenue 54b, Ulaanbaatar 13330, Mongolia
*Email:enkhamgalanj@mas.ac.mn

The inner tissues of plants are colonised by endophytic microorganisms, which benefit the host both directly and indirectly. Members of the genus *Metschnikowia* are prevalent endophytic yeasts encountered in various plant parts, including fruits, nectar, and roots. *Acorus calamus* Linn., otherwise classified as sweet flag, is a medicinal plant species that is endangered in Mongolia. It is traditionally employed for its digestive and anti-inflammatory properties. In this study, 24 culturable endophytic microbial strains were isolated from *A. calamus*, of which five were identified as yeasts. The results of the BLAST analysis of the ITS regions and D1/D2 domains of the LSU rRNA gene indicated that the strains P6-K1 and P6-K1-1 exhibited the highest degree of similarity to *Metschnikowia* species, with sequence similarities of 92.45% and 87.02%, respectively. Strains P6-K1-3 and P6-K1-5 exhibited 93.79% and 92.98% similarity to *Meira* species, respectively, while P6-K1-2 demonstrated 99.82% similarity to *Pseudozyma aphidis* DSM 101929. Phylogenetic analysis based on the D1/D2 domain confirmed that strains P6-K1 and P6-K1-1 formed a separate clade, suggesting they may represent a novel *Metschnikowia* species. All five yeast strains exhibited the capacity to solubilise inorganic phosphate, resulting in the formation of clear zones measuring 13–15 mm. Furthermore, all strains were found to produce indole-3-acetic acid (IAA), with the strains P6-K1-1 and P6-K1-4 displaying the highest levels, as indicated by intense pink colouration. This study is the first to report the isolation of endophytic yeasts from *A. calamus*. Two of the isolates appear to represent novel species of *Metschnikowia*, and their phosphate solubilisation and IAA production highlight their potential as plant growth-promoting endophytes.

Keywords: ITS region, D1/D2 domain, indole acetic acid, phosphate solubilization

PP-18: PROBIOTIC POTENTIAL AND LEAD TOLERANCE OF INDIGENOUS LACTIC ACID BACTERIA ISOLATED FROM MONGOLIAN TRADITIONAL FERMENTED CAMEL MILK, KHOORMOG

Batsaikhan Batbileg[1], Khasbaatar Gantuya[1], Erdenetugs Enkhtugs[1], Gankhuyag Angarag[1], Jigjiddorj Enkh-Amgalan[1]*
[1] Laboratory of Microbiology, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia
*Email: enkhamgalanj@mas.ac.mn

Camel milk is highly nutritious, rich in minerals and vitamins, and low in sugar and cholesterol. It also contains antibacterial and antiviral components. In Mongolia, traditionally fermented camel milk, *khoormog,* is widely consumed and known for its various health benefits, including antidiabetic, anticancer, and antituberculosis effects. Lead (Pb) exposure poses a serious public health concern, primarily affecting the nervous system, but also impacting hematopoietic, renal, reproductive, immunological, cardiovascular, and respiratory systems. Recent research has highlighted the ability of certain lactic acid bacteria (LAB) to remove lead from contaminated environments. The objective of this study was to isolate and identify probiotic LAB strains from khoormog and to assess their probiotic activity, lead tolerance, and lead absorption capacity. A total of 26 LAB strains were isolated from six khoormog samples. Proteolytic activity ranged from 16.3 to 21.6 mm in clear zones on skim milk agar. The strains were capable of coagulating milk within 24 to 48 hours and producing lactic acid at concentrations ranging from 0.59% to 2.61%. Most strains also showed growth in the presence of 0.3% bile salts. Nine bacilli strains exhibited strong antagonistic activity against *Escherichia coli*, *Staphylococcus aureus*, and *Bacillus subtilis*. 16S rRNA gene sequencing results revealed that the strains were most closely related to representatives of *Lacticaseibacillus paracasei*, *Lactiplantibacillus argentoratensis*, *Lactiplantibacillus pentosus*, *Lactococcus lactis*, *Lactococcus petauri, Enterococcus hirae*, and *Enterococcus faecium*. All isolates showed tolerance to MRS agar containing lead at concentrations of 100 mg/L, 500 mg/L, 1000 mg/L, 2000 mg/L, 3000 mg/L, and 5000 mg/L. Among them, *Lacticaseibacillus paracasei* Kh2-5 was selected for further analysis due to its notable probiotic properties and lead resistance. This strain was able to reduce Pb^{2+} concentration in HEPES buffer by 73.4% (from 15.2 mg/L to 4.03 mg/L) within 24 hours as detected by atomic absorption spectroscopy (AAS). In conclusion, the identified lactobacilli strains, particularly *L. paracasei* Kh2-5, demonstrate significant probiotic potential and lead-binding capabilities, making them promising candidates for both environmental bioremediation of lead-contaminated sites and development of functional probiotic products.

Keywords: *Lacticaseibacillus paracasei,* 16S rRNA gene sequencing, Antimicrobial Activity, Proteolytic Activity, Lead Absorption and Tolerance

PP-19: CHARACTERIZATION AND PLANT GROWTH PROMOTING ACTIVITIES OF ENDOPHYTIC BACTERIA ASSOCIATED WITH ROOT NODULES OF *SPONGIOCARPELLA GRUBOVII* ULZIJ

Munkhjargal Sengenorov[1], Marjangul Nuramkhaan[1], Munkhtsetseg Tserendagva[1], Selenge Munkhtsetseg[1], Batbileg Batsaikhan[1], Bolorbuyan Batsansar[1], Altanzul Khorolragchaa[1], Oyunbileg Yungeree[1] and Enkh-Amgalan Jigjiddorj[1]*
[1] Institute of Biology, Mongolian Academy of Sciences, Enkhtaivan avenue 54b, Ulaanbaatar 13330, Mongolia
*Email: enkhamgalanj@mas.ac.mn

Spongiocarpella grubovii Ulzij., a member of the *Fabaceae* family, is an endangered, subendemic, and relict plant species in Mongolia. It is facing a population decline due to the combined effects of climate change and poor seed germination. The utilization of plant micropropagation methods, employing the endophytes, is of paramount importance. These endophyte microorganisms have been demonstrated to promote plant growth by facilitating nutrient acquisition, synthesizing phytohormones, and activating systemic resistance. In this study, a total of 18 strains were isolated from the root nodules of *S. grubovii*. The identification results based on the 16S rRNA gene sequence revealed that the isolates belonged to four genera: *Rhizobium* (6)*, Priestia* (10)*, Peribacillus* (1), and *Neobacillus* (1)*,* respectively. Six strains belonging to the genus *Priestia* produced significant amounts of indole-3-acetic acid (IAA) when cultured in Luria-Bertani (LB) medium supplemented with 5 mM L-tryptophan. Among them, strain UN1-1 exhibited the highest IAA production, reaching 335.6 µg/mL at 72 hours. Three *Priestia* strains, Gr2-3, Gr3-3, and UN2-5, demonstrated phosphate solubilization activity on solid Pikovskaya (PVK) medium with a solubilization index (SI) of 2.1 ± 0.02, 2.3±0.02, and 2.5±0.02, respectively. Cell suspensions of all 18 strains were tested to evaluate their effects on plantlet growth and development in *ex vitro*. The assay was conducted using 2–3 cm *in vitro*-grown shoots. After 60 days, plantlet roots treated with Gr3-2-1 and UN2-3 suspensions reached 1.28 ± 0.5 cm and 1.42 ± 0.8 cm, respectively, both significantly longer than the indole butyric acid (IBA)-treated control (0.54 ± 0.5 cm). Additionally, the numbers of lateral roots induced by the two treatments were 6.0 ± 2.9 and 2.6 ± 1.0, respectively, compared to 2.2 ± 1.98 in the IBA-treated control. These results indicate that, despite the high IAA production and phosphate-solubilizing abilities of the *Priestia* strains, strains G3-2-1 and UN2-3, assigned to the genus *Rhizobium*, which is known for its nitrogen fixation in legume root nodules, were the most promising candidates for promoting both root elongation and lateral root formation. Experiments investigating the combined effects of *Priestia* and *Rhizobium* strains on plantlet growth and development are currently underway to identify the most effective strains and combinations for application in the propagation of *S. grubovii*.

Keywords: *Spongiocarpella grubovii* Ulzij; endophytes; rhizobia; indole acetic acid; phosphate solubilization; plant micropropagation

SESSION 5:

BIOMEDICAL & HEALTH SCIENCES

Keynote Speech

Title: Development of Nutraceuticals for Targeting Fatty Liver Diseases by using Natural Products

Chu Won Nho

Natural Products Research Institute, Korea Institute of Science and Technology, South Korea
cwnho@kist.re.kr

Short Bio: Chu Won Nho is a researcher at the Natural Products Research Institute, Korea Institute of Science and Technology (KIST), South Korea. His work focuses on the discovery, characterization, and application of bioactive natural compounds, with an emphasis on developing innovative solutions in biotechnology and pharmacology.

Abstract: Metabolic dysfunction-associated steatotic liver disease (MASLD) which encompasses patients who have hepatic steatosis and have at least one of five cardiometabolic risk factors. Metabolic dysfunction-associated steatohepatitis (MASH) is a progressive form of MASLD that combines steatosis with inflammation and fibrosis in the liver. In this talk, the research results from two studies using natural products for targeting MASLD will be presented. The first example of study is about root of Sanguisorba officinalis L. (SO), which is a plant known to have anti-inflammatory, antioxidant effects and has beneficial effects related to metabolic diseases such as obesity and diabetes. This study aimed to confirm the efficacy and molecular mechanism of inhibiting MASH and fibrosis in vivo using 95% ethanol SO extract (SOEE) and its three compounds. SOEE was administrated orally to C57BL/6J mice fed a Choline-deficient, L-amino acid-defined, high-fat diet (CDAHFD) for 10 weeks. In the present study, three main effects of SOEE on MASH-related markers were derived. First, SOEE showed the potential to inhibit MASH by modulating markers in CDAHFD-fed mice. SOEE decreased malondialdehyde levels in liver and controlled oxidative stress-related gene expression. Simultaneously, SOEE regulated fatty acid oxidation-related genes including, Ppara and Lpl. Second, SOEE effectively suppressed fibrosis and related markers both in vivo and in vitro. SOEE suppressed the deposition of extracellular matrix, hydroxyproline, and collagens in liver. Moreover, fibrosis-related gene expression was significantly decreased by SOEE. Thirdly, SOEE and its active compounds inhibited the activation of hepatic stellate cells (HSCs) by regulating SMAD signaling in HSCs. In LX-2 cells, TGF-β was treated to induce activation of

HSCs. SOEE and three active compounds reduced greatly mRNA expressions of fibrosis-related genes. In- depth, SOEE inhibited phosphorylation of SMAD2/3, the transcription promoter of collagen. Thus, our study suggests that SOEE has the potential to inhibit MASH and fibrosis by regulating oxidative stress and fatty acid oxidation. The second example of study is about Artemisia argyi (AA), a herbal medicine traditionally used in Asian countries, totreat inflammatory conditions such as eczema, dermatitis, arthritis, allergic asthma and colitis. However, the mechanism of action of this plant with regard to hepatitis and other liver-related diseases is still unclear. This study aimed to investigate the effects of AA ethanol extract on MASH-related fibrosis and gut microbiota in a choline-deficient, L-amino acid- defined, high-fat diet (CDAHFD)-induced mouse model. Male C57BL/6J mice were fed CDAHFD, with or without AA ethanol extract treatment. Biochemical markers, lipid profiles, hepatic mRNA expression levels of key genes, and the fibrosis area were assessed. In vitro,TGF- β-stimulated human hepatic stellate LX-2 cells and mouse primary hepatic stellate cells (mHSCs) were used to elucidate the effects of AA ethanol extract on fibrosis and steatosis. 16S rRNA sequencing, QIIME2, and PICRUST2 were employed to analyze gut microbial diversity, composition, and functional pathways. Treatment with the AA ethanol extract improved plasma and liver lipid profiles, modulated hepatic mRNA expression levels of antioxidant, lipolytic, and fibrosis-related genes, and significantly reduced CDAHFD-induced hepatic fibrosis. Gut microbiota analysis revealed a marked decrease in Acetivibrio ethanolgignens abundance upon treatment with the AA ethanol extract, and its functional pathways were significantly correlatedwith MASH/fibrosis markers. The AA ethanol extract and its active components (jaceosidin, eupatilin, andchlorogenic acid) inhibited fibrosis-related markers in LX-2 and mHSC. The AA ethanol extract exerted therapeutic effects on CDAHFD-induced liver disease by modulating MASH/fibrosis-related factors and gut microbiota composition. Notably, AA treatment reduced the abundance ofthe potentially profibrotic bacterium (A. ethanolgignens). These findings suggest that AA is a promising candidatefor treating MASH-induced fibrosis.

Keynote Speech

Title: Roles of Hepatitis B and C Viruses in Hepatocellular Carcinoma and Mortality: Evidence from Long-Term Cohorts in Taiwan

Yen-Tsung Huang

MD, ScD, Institute of Statistical Science, Academia Sinica, Taiwan

Short Bio: Yen-Tsung Huang is a Research Fellow at the Institute of Statistical Science, Academia Sinica, and Professor at National Taiwan University and National Sun Yat-sen University. He earned his M.D. from National Taiwan University and Sc.D. in Epidemiology and Biostatistics from Harvard University. His research bridges statistical science, epidemiology, and genomics, with applications in population health and precision medicine.

Dr. Huang has held faculty positions at Brown University and visiting appointments at Harvard, and has received numerous honors, including the Academia Sinica Presidential Scholar Award (2022–2025), the Outstanding Research Award from the Ministry of Science and Technology (2020, 2025), and the Foundation for the Advancement of Outstanding Scholarship Young Scholar Award (2023).

Abstract: Hepatitis B virus (HBV) and hepatitis C virus (HCV) cause hepatocellular carcinoma (HCC) and mortality through intrahepatic and extrahepatic pathways, but lifetime risk, sex differences, and viral interactions remain unclear.

Data from community-based cohorts in Taiwan (n=23,820; follow-up >25 years) were linked to national registries. Serum HBV/HCV seromarkers and viral loads were measured at baseline/follow-up. Cox models and causal mediation analyses evaluated lifetime HCC risk, sex- and age-specific effects, viral interplay, and mediating diseases for HCV-related mortality.

Lifetime HCC incidence (age 30–75) was highest in HBV+HCV coinfection (men 38.35%, women 27.40%). HBV carriers showed male predominance, while HCV-related risk was similar by sex. In HBV carriers, HCV increased HCC risk directly (HR≈2.5) but reduced it indirectly by suppressing HBV load (HR≈0.75). Higher HBV or HCV load increased HCC risk. For HCV-related mortality, 54.1% was mediated by intrahepatic diseases and 45.9% by extrahepatic conditions (notably septicemia, renal and blood/immune disorders), with hypertension, metabolic syndrome, and type 2 diabetes prominent in women. Mediation effects showed a dose–response with HCV load.

HBV and HCV exert complex, interacting, sex- and age-specific effects on HCC risk and mortality. Extrahepatic disease contributes nearly half of HCV-related deaths, highlighting the need for integrated hepatic and systemic interventions.

Invited Talk 1

Title: Development and Application of HiBiT-Tagged Hepatitis B Virus for High-Throughput Antiviral Screening and Identification of Skimmianine as an Entry Inhibitor

Tetsuro Shimakami

Department of Gastroenterology, Kanazawa University Hospital, Kanazawa, Ishikawa, Japan

Short Bio: Tetsuro Shimakami is a clinician-scientist with expertise in hepatology and gastroenterology, combining patient care, education, and molecular virology research. His work focuses on the biology of hepatitis B and C viruses, including virus-host interactions, RNA replication, antiviral therapeutics, and the role of microRNAs in viral regulation. He has conducted postdoctoral research at leading U.S. institutions and currently leads studies on antiviral strategies, viral replication mechanisms, and translational approaches to improve HBV/HCV treatment. Prof. Shimakami also collaborates with local governments to implement effective screening programs, contributing to public health initiatives in Ishikawa Prefecture.

Abstract: Approximately 290 million people worldwide are infected with hepatitis B virus (HBV). Antiviral therapies comprising nucleos(t)ide analogs and/or interferon are used in active chronic HBV carriers. These therapies can delay the progression of HBV-related diseases such as liver cirrhosis and hepatocellular carcinoma but cannot completely eliminate HBV due to the persistence of HBV covalently closed circular DNA (cccDNA) in hepatocytes. Therefore, novel antiviral agents that can eliminate cccDNA from HBV-infected hepatocytes are urgently needed to cure HBV infection. For the development of such agents, efficient HBV cell culture systems are needed that mimic the entire life cycle of HBV and can be used to easily monitor HBV infection and/or replication. We engineered a replication- and infection-competent HBV carrying an 11–amino acid HiBiT reporter (HiBiT-HBV), inserted at the N-terminus of the preS1 domain of genotype C, enabling quantitation of infection and replication by extracellular luciferase activity in primary human hepatocytes (PXB cells).

Methods: HiBiT-HBV was generated by transfection of HepG2-NTCP cells with the HiBiT-HBV genome, and infectious cell culture–derived virus (HBVcc) was purified. HiBiT activity correlated with intracellular viral markers (cccDNA, pgRNA, HBsAg, HBcrAg, HBV DNA) and responded to entry (heparin, Myrcludex B) and replication inhibitors (entecavir, IFN-α2b). HiBiT-HBV supported

consecutive rounds of infection and yielded Dane particles identical in density and morphology to wild-type HBV. Leveraging its luminescent readout, we performed high-throughput screening of FDA-approved (n=760) and natural product (n=502) compound libraries in PXB cells infected with genotype C HiBiT-HBV, selecting 172 hits for secondary dose–response assays.

Results: HiBiT-HBV enabled rapid, sensitive quantitation of viral entry and replication and proved suitable for large-scale antiviral screens. Secondary screening identified the furoquinoline alkaloid skimmianine as a potent HBV entry inhibitor (entry EC_{50} = 0.36 pM; selectivity index $>5\times10^6$), with negligible activity when added post–entry. Time-lapse imaging of ReAsH-labeled HBV capsids demonstrated that skimmianine blocks retrograde trafficking after internalization without affecting attachment or uptake. Skimmianine showed no direct effect on viral replication in HepG2.2.15 cells.

Conclusions: HiBiT-HBV provides a robust platform for monitoring the entire HBV life cycle and for high-throughput antiviral discovery. Using this system, we identified skimmianine as a novel HBV entry inhibitor targeting post-internalization trafficking steps. HiBiT-HBV will accelerate the development of next-generation HBV therapeutics.

PP-20: IMMUNE CHECKPOINT INHIBITORS IN RECURRENT GLIOBLASTOMA: A SYSTEMATIC REVIEW AND META-ANALYSIS OF THERAPEUTIC EFFICACY AND THE ROLE OF PD-1 MUTATIONS IN TREATMENT OUTCOMES

Khulan Ganzorig[1]*, Nominzul Ganbold[1], Solongo Tsogoo[1]
[1] School of Medicine, Mongolian National University of Medical Sciences, Ulaanbaatar, Mongolia
*Email: chrystalkhulan@gmail.com

Glioblastoma (GBM) is an aggressive brain tumor with poor prognosis due to frequent recurrence despite standard treatment. Immune checkpoint inhibitors (ICIs) offer promising therapeutic options and are being studied in recurrent GBM (rGBM). This systematic review followed PRISMA guidelines and analyzed seven clinical trials from 2010 to 2024, involving 209 rGBM patients previously treated with the Stupp protocol. The ICIs assessed included anti-PD-1 agents (nivolumab, pembrolizumab, tislelizumab), anti-CTLA-4 (ipilimumab), and anti-PD-L1 agents (durvalumab, avelumab), used alone or combined with radiotherapy (RT), temozolomide (TMZ), or bevacizumab. The combination of nivolumab + RT + TMZ showed the longest median overall survival (OS) of 28.9 months and progression-free survival (PFS) of 14.1 months. Tislelizumab monotherapy resulted in an OS of 14.3 months, while other regimens showed OS between 8.8-16.7 months. The hazard ratio for OS at 6 months favored nivolumab + RT + TMZ (HR=1.28, p=0.04). PFS HR was 2.32, suggesting increased progression risk. Grade 3/4 adverse events were most frequent with nivolumab + RT + TMZ (52.4%). Immune-related adverse events included pneumonitis and hypothyroidism. A moderate negative correlation was found between PD-1 mutation and 12-month OS (r = –0.36). No publication bias was detected. These findings highlight the potential of ICIs in managing rGBM.

Keywords: recurrent glioblastoma, immune checkpoint inhibitor, treatment regimen efficacy

PP-21: GREEN SYNTHESIZED ZINC OXIDE NANOPARTICLES USING AQUEOUS EXTRACTS FROM *DRACOCEPHALUM FOETIDUM BUNG* AND IT'S IN VITRO ANTIOXIDATIVE ACTIVITY

Bolor Tsolmon[1]*, Tansarmaa Munkhjargal[2], Suvdmaa Tuvaanjav[2], Sarangerel Oidovsambuu[1]
[1] Institute of Chemistry and Chemical Technology, Mongolian Academy of Sciences, 13330, Mongolia
[2] National University of Mongolia, Ulaanbaatar 14201, Mongolia
*Email: bolor_ts@mas.ac.mn

Zinc oxide nanoparticles (Df-ZnONPs) were synthesized using aqueous extracts from the Mongolian medicinal plant *Dracocephalum foetidum* Bunge. The green-synthesized Df-ZnONPs, both before and after calcination, as well as chemically synthesized ZnONPs, were characterized and compared using UV-Vis spectroscopy, Fourier-transform infrared spectroscopy (FTIR), scanning electron microscopy (SEM), X-ray diffraction (XRD), and in vitro antioxidant assays. The UV-Vis absorption peaks appeared as a broad band between 290 and 450 nm. SEM analysis revealed that the synthesized ZnONPs were roughly spherical in shape with an average particle size of 111.63 ± 33.66 nm. FTIR analysis confirmed that alkanes, alkenes, and alcohols present in the plant extract (DfAE) played a major role in nanoparticle formation. Df-ZnONPs exhibited significantly higher antioxidant activity than both the original extract and the calcinated Df-ZnONPs in $DPPH^{\bullet}$ and $ABTS^{\bullet+}$ assays. However, the original extract (DfAE) demonstrated higher antioxidant activity than Df-ZnONPs in the FRAP assay.

Keywords: zinc oxide nanoparticle, *Dracocephalum foetidum* Bung, aqueous extract, green synthesis, antioxidant

SESSION 6:

CLIMATE CHANGE & ENVIRONMENTAL ADAPTATION

Keynote Speech

Title: From Migratory Waterbird Telemetry to Basin-Scale Wetland Research and Conservation

Cao Lei[1], [2]

[1]State Key Laboratory of Regional and Urban Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China.
[2]University of Chinese Academy of Sciences, Beijing 100049, China.
leicao@rcees.ac.cn

Short Bio: Lei Cao is Professor at the State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing. She received her Ph.D. in Biology from Lanzhou University and her B.S. in Biology from Hunan Normal University. Her research focuses on wetland and biodiversity ecology, conservation, and movement ecology, with particular expertise in developing and applying advanced GPS/BDS tracking technologies to study migratory waterbirds. Prof. Cao has published over 100 international journal articles, including in *Nature*, *Nature Communications*, and *Current Biology*, and has led more than 20 national and international research projects. She serves as Associate Editor for *Ibis*, *Wetlands*, *Avian Research*, and *Bird Conservation International*, and is an active member of international ornithological societies. Her contributions have been recognized with multiple awards, including the prestigious British Ornithologists' Union Godman-Salvin Prize (2023) and the Alfred Newton Lecture Prize (2019).

Abstract: Asian wetlands are undergoing the most dramatic changes on Earth, yet basin-scale evidence for conservation remains scarce. Drawing on the Sino BON--Bird Diversity Monitoring Network, we combined satellite telemetry from 2,866 individuals of 42 migratory waterbird species with twenty years of hydrological and land-use data spanning six major Chinese river basins. Results show that grassland–wetland complexes on the Mongolian Plateau form the principal breeding grounds and migration-corridor hub for several keystone taxa—such as Swan Goose, Bean Goose, Greylag Goose and Whooper Swan—linking Siberian breeding areas with wintering sites in China, the Korean Peninsula and Japan, and thus serving as a mid- to high-latitude breeding grounds. In China, less than 1.5 % of the national territory—concentrated in floodplain wetlands of the Yangtze, Yellow, Pearl, Liao, Heilong and Songhua rivers—supports the stopover and wintering needs of waterbirds from more than twenty countries. We further reveal that the extent of drawdown zones is the primary factor shaping species composition and abundance

at the basin scale; case studies of the Three Gorges Reservoir and Dongting Lake demonstrate that water-level regulation can either impair or enhance habitat suitability. Emphasizing the pivotal role of hydrological processes in sustaining migratory networks, we propose a coupled monitoring framework that integrates waterbird telemetry with basin-wide hydrological observation, providing evidence-based strategies for wetland restoration and transboundary conservation across Mongolia and the wider Asian region.

Keywords: Migratory waterbirds, Watershed wetlands, Telemetry technology, Hydrological processes, Cross-border conservation, Basin-scale research

Invited Talk 1

Title: East Asian – Australasian flyway of migratory landbirds: what do we know?

Nikita Chernetsov[1,2]*, Mikhail Markovets[3], Pavel Ktitorov[4]

[1] Zoological Institute RAS, St. Petersburg
[2] St. Petersburg University, St. Petersburg
[3] Biological Station Rybachy of the Zoological Institute RAS, Rybachy
[4] Institute of Biological Problems of the North FEB RAS, Magadan

nikita.chernetsov@gmail.com

Short Bio: Dr. Nikita Chernetsov is Director of the Zoological Institute of the Russian Academy of Sciences, St. Petersburg, Russia, and Professor at the Department of Vertebrate Zoology, St. Petersburg State University. He earned his Ph.D. in Zoology from the Zoological Institute RAS in 2000 and completed his Habilitation in 2009.

Dr. Chernetsov's research focuses on avian migration, including orientation and navigation mechanisms, stopover ecology, and magnetic compass systems in migratory birds. He has conducted extensive field studies and international research on migratory strategies, satellite tracking, and navigation of passerines across Europe and Asia.

He has directed the Biological Station Rybachy, secured multiple grants from the Russian Science Foundation and the Russian Foundation for Basic Research, and serves on editorial boards of journals including Journal for Ornithology, Frontiers in Physiology, and Avian Research.

Abstract: Whereas relatively much is known about migratory routes of waders and waterbirds breeding in NE Siberia and in the Russian Far East and wintering in eastern and southeastern Asia and in Australia, information on landbirds is much more limited. The reason is obvious: many waterbirds are hunted; therefore, traditional ringing (banding) is a relatively efficient tool for studying their flyways. For shorebirds, marking by leg flags resulted in relatively many refighting's in the recent decades. However, data for landbirds have been extremely scarce until the advent of satellite tags and light-level geolocators. Here we review the data that have recently become available and the trends that start to emerge from these data.

Tracking studies of East Asian landbirds showed that small and medium-sized species generally prefer to avoid prolonged crossings of the seas, and perform detours around water barriers even when they start migration from the islands of the Pacific Ocean, yet some species opt for direct sea crossing. Two main migration corridors of East Asian landbirds were found: first, a mainland route through

continental East Asia for populations spending the non-breeding season in India or mainland South-East Asia, and second, an island route, with birds moving from North-East Asia through a chain of islands in the Pacific to non-breeding sites in the Philippines or Indonesia [1]. Just three landbird species that breed in the Russian part of the Pacific Rim regularly winter in Australia: Pacific Swift (*Apus pacificus*), White-throated Needletail (*Hirundapus caudacutus*) and Oriental Cuckoo (*Cuculus optatus*). Tagging with light- level geolocators revealed the almost 10,000 km long journey of Pacific Swifts between Sakhalin Island (Russia) and Australia [2], and similar travel of White-throated Needletails tracked from Hokkaido, Japan [3]. Both swift species avoided prolonged sea crossings; during the southward and northward migrations they performed detours, moving from Sakhalin (or Hokkaido) to the nearest Asian continent, reaching northern Australia via Indochina and the Indonesia archipelago. Oriental Cuckoos are a remarkable exception, performing direct sea crossings from China to Indonesia and even from Japan to Papua New Guinea.

Invited Talk 2

Title: Global insect diversity pattern and biodiversity declining monitoring – site100 international big science action

Ming Bai

Ming BAI

Professor, Principal Investigator of the Group of Morphology and Evolution of Beetles, Institute of Zoology, Chinese Academy of Sciences
baim@ioz.ac.cn

Short Bio: Prof. Dr. Ming Bai is a Distinguished Professor at the Institute of Zoology, Chinese Academy of Sciences (CAS), leading research on the morphology and evolution of Coleoptera. He is also a professor at the University of the Chinese Academy of Sciences, a doctoral supervisor, and chief scientist of a National Key R&D Program project.
Prof. Bai focuses on insect evolution, morphological quantification, and intelligent identification systems for beetles, including applications in pest monitoring and rapid customs identification. He has published over 200 papers in high-impact journals, holds multiple patents, and has received awards including the 2019 CAS Young Scientist International Cooperation Award and the 2016 Chou Io Entomological Classification Award.

Abstract: Insects are widely distributed, with complex behavior and diverse feeding habits, making them the most diverse biological group. Due to climate change and human activities, insect diversity is declining around the world at about twice the declining rate of vertebrate species. However, there are some problems in insect classification and monitoring technology, which can not efficiently and comprehensively obtain insect diversity pattern. Through the research and development of new AI model (PENet), new insect monitoring hardware (e.g. Big FIT、New Pitfall trap、Portable Funnel Light Trap、Water Exclusion Trap、Mycophagy Insect Windows Trap), a series studies established several sample sites through the SITE-100 international Grand Science Program, to promote the development of next-generation entomological taxonomy and obtain the national insect diversity pattern and formation mechanism.

OP-1: STRATEGIES FOR GRASSLAND SOIL HEALTH IMPROVEMENT: CARBON SEQUESTRATION, RESTORATION, AND SUSTAINABLE MANAGEMENT

Dr. Shiming Tang

Institute of Grassland Research, Chinese Academy of Agricultural Sciences
tangshiming@caas.cn

This presentation highlights research on grassland soil health evaluation and functional enhancement conducted by the Grassland Soil Health and Cultivation Research Center at the Chinese Academy of Agricultural Sciences. Key findings include: (1) Short- to medium-term fencing significantly improves grassland ecosystem functions, particularly in high-precipitation regions (>300 mm), while long-term fencing may inhibit recovery, especially in deep soil layers. (2) Degraded grassland restoration techniques, such as low-disturbance oat production and straw grid applications, enhance soil moisture, seed retention, and biomass, achieving ecological and economic benefits. (3) Species diversification and mixed sowing boost ecosystem multifunctionality in restored grasslands. (4) Land-use management, like rotational grazing in mixed-sown grasslands, improves soil micro-food web diversity and functionality. Collaborative directions focus on degraded grassland fencing, desert steppe restoration, and soil fertility enhancement. These insights provide theoretical and practical support for sustainable grassland management and carbon sequestration strategies.

OP-2: A GENERALIZED SPATIOTEMPORALLY WEIGHTED BOOSTED REGRESSION TO PREDICT THE OCCURRENCE OF GRASSLAND FIRES IN THE MONGOLIAN PLATEAU

Professor. Duwala

Institute of Grassland Research of CAAS
duwala@caas.cn

Grassland fires are one of the main disasters in the temperate grasslands of the Mongolian Plateau, posing a serious threat to the lives and property of residents. The occurrence of grassland fires is affected by a variety of factors, including the biomass and humidity of fuels, the air temperature and humidity, the precipitation and evaporation, snow cover, wind, the elevation and topographic relief, and human activities. In this paper, MCD12Q1, MCD64A1, ERA5, and ETOPO 2022 remote sensing data products and other products were used to obtain the relevant data of these factors to predict the occurrence of grassland fires. In order to achieve a better prediction, this paper proposes a generalized geographically weighted boosted regression (GGWBR) method that combines spatial heterogeneity and complex nonlinear relationships, and further attempts the generalized spatiotemporally weighted boosting regression (GSTWBR) method that reflects spatiotemporal heterogeneity. The models were trained with the data of grassland fires from 2019 to 2022 in the Mongolian Plateau to predict the occurrence of grassland fires in 2023. The results showed that the accuracy of GGWBR was 0.8320, which was higher than generalized boosted regression models' (GBM) 0.7690. Its sensitivity was 0.7754, which is higher than random forests' (RF) 0.5662 and GBM's 0.6927. The accuracy of GSTWBR was 0.8854, which was higher than that of RF, GBM and GGWBR. Its sensitivity was 0.7459,which is higher than that of RF and GBM. This study provides a new technical approach and theoretical support for the disaster prevention and mitigation of grassland fires in the Mongolian Plateau.

Author Index

Munkhtsetseg Tserendagva
Nikita Chernetsov
Nominzul Ganbold
Ochirkhuyag Baldorj
Oyunbileg Yungeree
Pagmadulam Baldorj
Pavel Ktitorov
Péter Kaló
Purevdolgor D
Rentsenkhand Tserennadmid
Rózsa Máté
Sándor Jenei
Sang-Jae Lee
Sarangerel Oidovsambuu
Selenge Munkhtsetseg
Senthil Natesan
Seong-Bo Kim
Solongo Tsogoo
Sondor Ganbat
St. Petersburg
Sung Tae Kim
Suvdaa G
Suvdantsetseg Balt
Suvdmaa Tuvaanjav
Tamás Kovács
Tamás Papp
Tansarmaa Munkhjargal
Tumen-Erdene Unurtsetseg
Urjinlkham Renchindorj
Uuriintuya Munkhbayar
Yang Le
Yoshifumi Nishikawa
Youjin Baek
Yujin Son
Yuta Murai
Zhao Yongzhuo
Zsófia Sára Kasziba
Zsolt Bereczky

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