A DECADE OF ADVOCATING

icbb2026

Sixth International Conference on Bioscience and Biotechnology (ICBB-2026)

CULTIVATING A RESEARCH ECOSYSTEM IN THE GLOBAL SOUTH

February 06-09, 2026
Atithi Resort and Spa, Pokhara, Nepal

Sixth International Conference on Bioscience and Biotechnology (ICBB-2026)

Theme: *Cultivating a Research Ecosystem in the Global South*

February 6–9, 2026 • Atithi Resort and Spa • Pokhara, Nepal

The primary objective of ICBB-2026 is to strengthen and cultivate a sustainable research ecosystem in the Global South by fostering meaningful collaboration among researchers, educators, entrepreneurs, policymakers, and communities. Celebrating a decade of the International Conference on Bioscience and Biotechnology (ICBB), this sixth edition marks an important milestone in ICBB's journey since its inception in 2016 as a platform for knowledge exchange and scientific cooperation. Hosted in Pokhara, Nepal: the Gateway to the Himalayas; ICBB-2026 underscores the growing role of regional research hubs in addressing local and global challenges across human, plant, animal, and environmental health. By connecting local expertise with international perspectives, the conference highlights the importance of inclusive research ecosystems, long-term capacity building, and collective action in advancing bioscience and biotechnology in resource-constrained settings. The theme "Cultivating a Research Ecosystem in the Global South" reflects ICBB's continued commitment to empowering scientific communities, strengthening institutional sustainability, and translating research into societal impact.

6th International Conference on Bioscience and Biotechnology

(ICBB - 2026)

Program Schedule

Cultivating a Research Ecosystem in the Global South

February 6–9, 2026

Atithi Resort and Spa • Pokhara, Nepal

Day 1: Friday, February 6, 2026

Welcome Reception
Venue: Sabha Hall
Registration Coordination: Nisha Thapa, Monika Chaudhary, Rashika Ghulu & Rashmi Adhikari
IT Coordination: Utsav Dahal, Monima Karmacharya, Kriti Rajbhandri & Sabita Sedhai
Master of Ceremony: Dr. Prativa Pandey, Herveda Botanicals, Lalitpur, Nepal
Dress Code: Formal

17:45 – 18:15	**Registration / Tea & Coffee**	
18:15 – 18:25	Ms. Suvechhya Bastola, Secretary, ICBB-2026	**Welcome Remark**
18:25 – 18:40	Prof. Bhupal Govinda Shrestha, Department of Biotechnology, Kathmandu University, Dhulikhel, Nepal	**KU & Biotech Program**: An Introduction
18:40 – 20:00	**RIBB Support Seminar Series: Episode 5** (Presentation - 15 mins each + 5 mins Q&A)	
	Speaker 1: Mr. Prajwal Rajbhandari, President, Research Institute for Bioscience and Biotechnology (RIBB), Kathmandu, Nepal	**RIBB Story**: The highs and lows of doing science on the roof of the world
	Speaker 2: Rojlina Manandhar, Department Chair, RIBB, Kathmandu, Nepal	**RIBB-Extra**: Advancing research and innovation for a sustainable future
	Speaker 3: Suvechhya Bastola, Department Chair, RIBB, Kathmandu, Nepal	**RIBB Visiting Scientist Program**: Building shared resources to enhance research capacity in resource-limited settings
	Speaker 4: Ravi Bhandari Member, RIBB-EIC, Kathmandu, Nepal	**RIBB Endowment Fund:** An incubator for growth
20:00 Onwards	Outdoor Social activity, Photo Galleries (RIBB-ICBB Classics, Mithila Arts & Picture Nepal by Kusal Bista) & Welcome Reception	

Day 2: Saturday, February 7, 2026

08:15 – 09:00	**Registration / Tea & Coffee**
Registration Coordination: Nisha Thapa, Monika Chaudhary, Rashika Ghulu, Kriti Rajbhandari & Rashmi Adhikari **Food Coupon Coordination**: Rojlina Manandhar	

Inauguration Ceremony **Venue:** Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya / Sabita Sedhai **Master of Ceremony**: Dr. Prativa Pandey, Herveda Botanicals, Lalitpur, Nepal		
09:00 – 9:20	**Inaugural Welcome Remark**: Prof. Dr. Dhurva Prasad Gauchan Co-Chair, ICBB-2026 (5 min)	Head, Department of Biotechnology, Kathmandu University, Dhulikhel, Nepal
	Special Remark I: Dr. Niraj Dhital, Director, Research & Scholarship Division (7 min)	University Grant Commission (UGC), Bhaktapur, Nepal
	Special Remark II: TBD (8 min)	

9:20 – 09:30	**Guest of Honor I**: Er. Ganesh Shah, Former Minister, Ministry of Environment, Science and Technology, Government of Nepal, Nepal
9:30 – 10:00	**Keynote I**: Prof. Richard Burchmore, University of Glasgow, Glasgow, UK **Title:** The extended phenotype of intracellular *Leishmania* parasites (Presentation - 25 mins each + 5 mins Q&A)
ICBB-2026 Group Picture (Resort Garden)	

SESSION I: Science, Research, Innovation, Economy, and Higher Education (10:10 – 12:00) **Venue**: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Sabita Sedhai (Presentation - 20 mins each + 5 mins Q&A)		
Co-Chairs: Dr. Sunil Pokhrel & Dr. Prativa Pandey		
Session Overview (10:10 - 10:20): Dr. Sunil Pokhrel, Principal, Kathford International College, Kathmandu, Nepal		
10:20 – 10:45	**Speaker 5**: Dr. Krishna Raj Adhikari	Vice Chancellor, Gandaki University (GU), Pokhara, Nepal
10:45 – 11:10	**Speaker 6**: Prof. Thomas F. Krauss	University of York, York, UK

11:10 – 11:35	**Speaker 7**: Dr. Rajendra Pokharel	Member, Curriculum Development Committee, University of Nepal (UNepal), Kathmandu, Nepal
11:35 – 12:00	**Speaker 8**: Dr. Dhaka Ram Bhandari	Center for Environmental and Sustainable Agricultural Research (CESAR), Pokhara, Nepal
12:00 – 13:30	**Lunch, Poster Session, RIBB Endowment Stall for Charity & Photo Galleries (RIBB-ICBB Classics, Mithila Arts & Picture Nepal by Kusal Bista)** **Poster Coordinator:** Daisy Awale, Rashika Ghulu, Monima Karmacharya, Monika Chaudhary & Kriti Rajbhandari **Stall Coordination:** Sabita Sedhai & Ravi Bhandari	

SESSION II: Human Health (13:30 – 15:20) **Venue**: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Sabita Sedhai (Presentation - 15 mins each + 5 mins Q&A)		
Co-Chairs: Prof. Arjan Narbad & Prof. Sangita Shakya		
Session Overview (13:30 - 13:40): Prof. Arjan Narbad, Quadram Institute, Norwich, UK		
13:40 – 14:00	**Speaker 9**: Dr. Anurag Adhikari, La Trobe University, Melbourne, Australia	**Title**: Integrated antibody and T-cell profiling to identify cross-reactive immune signatures
14:00 – 14:20	**Speaker 10**: Dr. Martina Vidmar, Quadram Institute, Norwich, UK	**Title**: Fermented coconut: a tasty remedy for gut health
14:20 – 14:40	**Speaker 11**: Dr. Sakhila Ghimire, University Hospital Regensburg, Regensburg, Germany	**Title**: Interplay between gut microbiome and immune cells in health and disease
14:40 – 15:00	**Speaker 12**: Stephan Harper, Quadram Institute, Norwich, UK	**Title**: The impact of wheat arabinoxylan fermentation in the gut microbiota
15:00 – 15:20	**Speaker 13**: Gopiram Syangtan, Amrit Campus, Kathmandu, Nepal.	**Title**: Development of Data Transfer Ethics Framework (daTEF): a participatory approach to delivering evidence-based guidelines for healthcare data transfer
15:20 – 15:50	**Coffee Break**	

Panel Discussion (Parallel): Research Ecosystem in the Global South (16:00 – 17:30) **Venue**: Sabha Hall **IT**: Coordinated by PRI **Gifts Coordination**: Sabita Sedhai & Kriti Rajbhandari	
Moderator: Dr. Ashim Dhakal, Phutung Research Institute (PRI), Kathmandu, Nepal	
Panelist 1 – Prof. Neil Mabbott	University of Edinburgh, Edinburgh, UK
Panelist 2 – Prof. Niraj Dhital	University Grant Commission, Bhaktapur, Nepal
Panelist 3 – Dr. Ravindra Mohan Sapkota	Shikhar Biotech, Lalitpur, Nepal
Panelist 4 – Dr. Santosh Koirala	Center for Environmental and Sustainable Agricultural Research (CESAR), Pokhara, Nepal

Focus Group Discussion (Parallel) (16:00 – 17:30) **High School Science Curriculum - Grade 11 & 12** **Venue**: Bhela Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Monika Chaudhary
Round Table Overview: Dr. Sunil Pokhrel (Presentation 10 mins)
Participants: 12 - 15 (Schools Teachers & Educators from Physics, Chemistry, Biology and Zoology)

Day 3: Sunday, February 8, 2026

08:15 – 8:45	**Registration Tea & Coffee**
Registration Coordination: Nisha Thapa, Monika Chaudhary, Kriti Rajbhandari, Rashika Ghulu & Rashmi Adhikari **Food Coupon Coordination**: Rojlina Manandhar	
Venue: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Sabita Sedhai **Master of Ceremony**: Suvechhya Bastola, RIBB, Kathmandu, Nepal **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Sabita Sedhai	

8:45 – 9:00	**Guest of Honor II:** Prof. Achyut Prasad Wagle, Vice Chancellor, Kathmandu University, Dhulikhel, Nepal
9:00 – 9:30	**Keynote II:** Prof. Arjan Narbad, Quadram Institute, Norwich, UK **Title:** Modification of human gut microbiome for combating disease and improving human health (Presentation - 25 mins each + 5 mins Q&A)

Policy Seminar I (Parallel): National Biotechnology Policy, Nagoya Protocol and ICGEB Membership (09:30 – 11:00) **Venue**: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Monika Chaudhary	
Co-Chairs: Suvechhya Bastola & Prajwal Rajbhandari	
Session Overview (09:30 - 09:40): Suvechhya Bastola, RIBB, Kathmandu, Nepal	
Case Presentation I: Prof. Dr. Tribikram Bhattarai,	Nepal Biotechnology Association (NBA) (Presentation 10 mins)
Case Presentation II: Prof. Dr. Krishna Das Manandhar	Tribhuvan University (Presentation 10 mins)
Commenter I: Prof. Dhurva Ghauchan	Kathmandu University (KU), Dhulikhel, Nepal
Commenter II: Nabin Munakarmi	Biotechnology Society of Nepal (BSN), Kathmandu, Nepal
Discussion/Q&A: 30 mins	

SESSION III (Parallel): Environmental Health (09:30 – 11:20) **Venue**: Bhela Hall **IT**: Coordinated by PRI **Gifts Coordination**: Sabita Sedhai & Kriti Rajbhandari (Presentation - 15 mins each + 5 mins Q&A)		
Co-Chairs: Prof. Thomas Krauss & Dr. Amol Dahal		
Session Overview (09:30 - 09:40): Prof. Thomas F. Krauss, University of York, York, UK		
09:40 – 10:00	**Speaker 14:** Hari Krishna GC, SNV, Kathmandu, Nepal	**Title**: Area-wide approach to improving environmental health
10:00 – 10:20	**Speaker 15**: Lokesh Sapkota, SWAT Lab, Kathmandu, Nepal	**Title**: Environmental monitoring and environmental health: a private laboratory perspective
10:20 – 10:40	**Speaker 16**: Dr. Rijan Maharjan & Sadikshya Dahal, Phutung Research Institute (PRI), Kathmandu, Nepal	**Title**: Real-time fluorometric quantification of residual chlorine at sub-PPM levels using the WAS device
10:40 – 11:00	**Speaker 17**: Dr. Nabin Aryal, University of South-Eastern Norway, Notodden, Norway	**Title**: Biofilm based technologies for chemical synthesis and environmental remediation
11:00 – 11:20	**Speaker 18**: Prof. Thomas F. Krauss, University of York, York, UK	**Title**: Technologies for detecting bacterial contamination in water: a critical review

SESSION IV: Plant Health (11:00 – 12:30) **Venue**: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya & Sabita Sedhai (Presentation - 15 mins each + 5 mins Q&A)		
Co-Chairs: Dr. Namraj Dhami & Rojlina Manandhar		
Session Overview (11:00 - 11:10): Dr. Namraj Dhami, PU, Pokhara, Nepal		
11:10 – 11:30	**Speaker 19**: Dr. Pablo D. Cardenas, University of Copenhagen, Copenhagen, Denmark	**Title**: From wild to tamed: Reimagining novel crops through Omics and local plant diversity
11:30 – 11:50	**Speaker 20**: Mr. Ashok Limbu, Temperate Horticulture Development Center, Mustang, Nepal	**Title**: Enhancing high-density apple plantations in Mustang through tissue culture production of M9 dwarf rootstock
11:50 – 12:10	**Speaker 21**: Mr. Prasodhan Niraula, Apex Biotech, Jhapa, Nepal	**Title**: Plant Tissue Culture, quality seed, and yield: A strategic imperative for Nepal's potato sector
12:10 – 12:30	**Speaker 22**: Prof. Bhupal Govinda Shrestha, Kathmandu University, Dhulikhel, Nepal	**Title**: Merger of ayurveda and biotechnology for study of anti-cancer activity of medicinal plants of Nepal
12:30 – 14:00	**Lunch, Poster Session, RIBB Endowment Stall for Charity & Photo Galleries (RIBB-ICBB Classics, Mithila Arts & Picture Nepal by Kusal Bista)** **Poster Coordinator**: Daisy Awale, Rashika Ghulu, Monima Karmacharya, Monika Chaudhary & Kriti Rajbhandari **Stall Coordination**: Sabita Sedhai & Ravi Bhandari	

Lightning Talks (14:00 – 14:15) **Venue**: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Sabita Sedhai & Monika Chaudhary (Presentation - 3 mins each, Q&A during Poster Session)		
Co-Chairs: Dr. Neha Shrestha & Dr. Prayan Pokharel		
14:00 – 14:03	**Speaker 23**: Dipak Paudel, Prithivi Narayan Campus, Pokhara, Nepal	**Title**: Time and altitude variation of cinnamaldehyde and anticancer potential of *Cinnamomum tamala* from different locations of Nepal
14:03 – 14:06	**Speaker 24**: Asim Maharjan, Phutung Research Institute, Kathmandu, Nepal	**Title**: A multiparameter, low cost and portable fluorometer for drinking water monitoring

14:06 – 14:09	**Speaker 25**: Monima Karmacharya, RIBB, Kathmandu, Nepal	**Title**: *Enterococcus* detection and microbial safety assessment of vegetable- and legume-based fermented foods from Nepal
14:09 – 14:12	**Speaker 26**: Jamie Tuibeo, La Trobe University, Melbourne, Australia	**Title**: Investigating the mechanism of viral control in HIV-infected individuals
14:12 – 14:15	**Speaker 27**: Kriti Rajbhandari, KU, Dhulikhel, Nepal	**Title**: Circulating miR-1246 as a diagnostic and prognostic biomarker in dengue infection: A Case-Control study

Policy Seminar II (Parallel): Snakebite treatment challenges and future perspectives in Nepal (14:30 – 16:00) **Venue**: Sabha Hall **IT Coordination**: Nisha Thapa & Rashika Ghulu **Gifts Coordination**: Sabita Sedhai
Co-Chairs: Dr. Ravindra Mohan Sapkota & Dr. Sunita Gautam Ghimire
Session Overview (14:30 - 14:40): Dr. Sunita Gautam Ghimire, RIBB, Kathmandu, Nepal
Case Presentation I: Dr. Chhabilal Thapa Magar, Chairman, Nepal Toxinology Association, Nepal (Presentation 15 mins)
Case Presentation II: Kamal Devkota, President, Save the Lives Society, Nepal (Presentation 15 mins)
Case Presentation III: Dr. Ashim Subedi, Manipal Teaching Hospital, Pokhara, Nepal (Presentation 15 mins)
Discussion/Q&A: 30 mins

Poster Competition (Parallel): Meet the Herbs - Young Scientists, Young Changemakers (14:30 – 16:00) **Poster Coordinator**: Daisy Awale, Kriti Rajbhandari, Rashika Ghulu, Monika Chaudhary & Monima Karmacharya **Venue**: Resort Garden **Coordinator**: Suvechhya Bastola, Amol Dahal & Rashmi Adhikari **Hands-On Activity**: Optics in our daily life
Participants: 30 - 40 (Schools Teachers & Students)

SESSION V: Animal Health (16:15 – 17:25) **Venue**: Sabha Hall **IT Coordination**: Utsav Dahal & Nisha Thapa **Gifts Coordination**: Monima Karmacharya/Sabita Sedhai (Presentation - 15 mins each + 5 mins Q&A)		
Co-Chairs: Prof. Neil Mabbott & Dr. Hitesh Kumar Bhattarai		
Session Overview (16:15 - 16:25): Prof. Neil Mabbott, University of Edinburgh, Edinburgh, UK		
16:25 – 16:45	**Speaker 28**: Wen-Chi Hsu, National Pingtung University of Science and Technology, Pingtung, Taiwan	**Title**: Fecal RNA-based profiling as a non-invasive alternative for characterizing active gut microbiota in cattle
16:45 – 17:05	**Speaker 29**: Zi-Chen Hsu, National Pingtung University of Science and Technology, Pingtung, Taiwan	**Title**: Effects of dietary tannic acid supplementation on the active gut microbiota of pigs
17:05 – 17:25	**Speaker 30**: Prof. Neil Mabbott, University of Edinburgh, Edinburgh, UK	**Title**: The impact of gastrointestinal helminths on susceptibility to co-infection with other parasite infections
17:30 – 18:00	**Closing Ceremony**	

Day 4: Monday, February 9, 2026

ICBB Retreat: KORA (Cycling 22 Km around Fewa Lake) **Route**: Atithi Resort & SPA - Lakeside - Pame - Lairak - Siddha Baba - Ghatichinna - Pallo Bhitta - Pame - Lakeside - Atithi Resort & SPA 09:00 – 11:00		
10:00 – 16:00 (Phutung Research Institute Group Meeting) **Venue**: Sabha Hall		
Celebrating 10 years of ICBB **Photo Gallery**: (RIBB-ICBB Classics, Mithila Arts & Picture Nepal by Kusal Bista) **Venue**: Sabha Hall & Resort Garden 18:00 Onwards **Dress Code**: Formal		
Master of Ceremony: Ravi Bhandari, RIBB, Kathmandu, Nepal		
18: 00 – 18:35	Introduction to Mithila Arts Presentation by Manisha Shah, Modern Mithila Artist (10 mins Presentation)	
	A decade of advocating (Celebrating Glorious 10 Years of ICBB) by Prajwal Rajbhandari, RIBB, Kathmandu, Nepal (20 mins)	
	Closing Remark: Prof. Bed Mani Dahal, Dean, School of Science, KU, Dhulikhel, Nepal	
18: 45 – 19:15	Cultural Show I (Dance)	
	Cultural Show II (Song)	
	Cultural Show III (Song)	
	Cultural Show IV (Dance)	
Gifts Coordination: Monima Karmacharya / Sabita Sedhai		
19: 30 – 20:00	RIBB-SAB Members	Felicitation
	Friends of RIBB (Endowment Donors)	Felicitation
	Token of Love (Sponsors)	Felicitation
	Token of Love (Volunteers)	Felicitation
20:00 Onwards	**RIBB Endowment Stall for Charity** **Photo Galleries (RIBB-ICBB Classics, Mithila Arts & Picture Nepal by Kusal Bista)** **Closing Banquet**	

TABLE OF CONTENTS

Keynote Presentation 01

Prof. Richard Burchmore

University of Glasgow, Glasgow, United Kingdom

Richard Burchmore is Professor of Pathogen Phenomics at the University of Glasgow (Glasgow, UK). He obtained his PhD in Biochemistry from the University of London. Richard was an early adopter of mass spectrometry for proteomics and metabolomics and, over 20 years, has been instrumental in establishing both these research areas at the University of Glasgow. His research group was among the first to apply proteomic approaches to parasites and, with colleagues in Glasgow, pioneered the use of Orbitrap mass spectrometry for untargeted metabolomic analyses. His current research employs -omic approaches to understand the molecular basis of pathogen phenotypes. His primary focus is on the protozoan parasite *Leishmania*, which can survive phagocytosis by macrophages to establish an intracellular niche. *Leishmania* multiply within macrophages, resulting in a spectrum of chronic pathologies in millions of infected individuals. Leishmaniasis, a disease associated with poverty, is poorly understood and difficult to diagnose and to treat. Richard has studied *Leishmania* throughout his research career, focusing on proteins at the surface of the parasite that mediate interaction with the host. He has developed and applied various approaches, such as proteomics, metabolomics and membrane transport assays, to understand the expression and function of surface proteins. Richard has active collaborations with Leishmaniacs in Colombia, Brazil, Thailand, Saudi Arabia and Iran.

The extended phenotype of intracellular *Leishmania* parasites

Richard Burchmore
University of Glasgow, Glasgow, United Kingdom
richard.burchmore@glasgow.ac.uk

Abstract

Leishmania are intracellular protozoan parasites that are responsible for a spectrum of chronic human pathologies. Millions are infected but available therapies are limited and sub-optimal. *Leishmania* parasites are able to thrive within a phagolysosomal compartment in macrophages, an environment that is typically lytic. The pathways that *Leishmania* exploit to establish a permissive niche in the macrophage host cell are incompletely understood but present potential targets for disease control. We are employing a multifaceted approach to elucidate the intimate interactions between intracellular *Leishmania* parasites and their host cells. Using proteomics, we have identified proteins that are secreted by the parasite, and we are currently employing microscopy and proteomics to investigate the fate of secreted proteins in the host macrophage. We are also investigating changes in the proteome and transcriptome of macrophages upon infection with *Leishmania*, and we are using transport assays and metabolomics to understand how *Leishmania* acquire nutrients for which they are auxotrophic. In a related project, we are seeking to understand the phenotype of drug-resistant Leishmania. We aim to find strategies to perturb niche modification by the parasite, to allow the host to gain the upper hand in the interaction with *Leishmania*.

Keywords: *Leishmania*, macrophage, proteomics, secretomics, host:parasite interface

Keynote Presentation 02

Prof. Arjan Narbad

Quadram Institute Bioscience, Norwich, United Kingdom

Arjan graduated from Leeds University with a BSc in Microbiology. He then moved to Cardiff University and obtained a PhD in microbial metabolism of xenobiotic compounds. After a short postdoctoral position in the Biochemistry Department of Cardiff University he joined the institute in 1989 and have worked on a number of industrially-funded biotechnology projects on the engineering of lactic acid bacteria and yeast for production of novel food ingredients and antimicrobials. Currently he is a translational microbiome group leader at the Quadram Institute Bioscience where his research is focused on understanding the role of gut bacteria in the health and disease of humans and animals. Current focus of his research is on the competitive exclusion of foodborne pathogens such as *Campylobacter* and *C. perfringens* from the food chain. In collaboration with clinicians at the Norfolk and Norwich University Hospital, his group is actively involved in setting up Faecal Microbiota Transplant (FMT) service for the treatment of recurrent Clostridium difficile infections. His team is also exploring the role of gut microbiome in colonisation and persistence of the SARS-CoV-2 in the GI tract of COVID-19 patients. He has published more than 160 research papers and has filed 11 international patents. He has been appointed a Visiting Professor at Jiangnan University in China and has recently established a BBSRC funded UK-China joint centre for research on probiotics.

Modification of human gut microbiome for combating disease and improving human health

Arjan Narbad
Quadram Institute Bioscience, Norwich, United Kingdom
arjan.narbad@quadram.ac.uk

Abstract

The gut microbiome plays a critical role in our health and disease. The human and animal GI tract contain a diverse array of microbes with up to 1 x 10^{12} bacteria per gram of gut contents in the colon. Alteration or dysbiosis of the healthy gut microbiome is associated with development of a number of different disorders including inflammatory conditions of IBS, ulcerative colitis, as well as obesity, diabetes and neurodegenerative disorders of Alzheimer and Parkinson's disease. We are interested in modification of the gut microbiome structure and function for treatment of these disorders. I will discuss different strategies including the use of phage therapy, application of different dietary components such as prebiotics and the use of faecal microbiota transplant to reconstruct the entire microbiome. In the second part of my presentation, I will focus on the microbial composition of some plant based naturally fermented foods and their application for improving food safety and developing novel starter cultures for production of bioactive compounds including bacteriocins, vitamins and GABA that can be utilised for health benefits.

Keywords: gut microbiome, probiotics, fermented foods, faecal microbiota transplant, microbiome modulation

Conference Track: *Human Health*

Invited Speaker 01

Dr. Anurag Adhikari

La Trobe University, Melbourne, Australia

Kathmandu Research Institute for Biological Sciences, Lalitpur, Nepal

Dr. Anurag Adhikari is a researcher specializing in infectious diseases, particularly RNA viruses and bacterial infections. He holds a B.Tech in Biotechnology from Purbanchal University, Nepal (2015) and a PhD in Pathology from the University of New South Wales, Australia (2023). Currently, he leads a research group at the Kathmandu Research Institute for Biological Sciences (KRIBS), focusing on antibody responses and viral genomic changes during successive dengue outbreaks in Nepal. In his previous work, Dr. Adhikari managed and co-led clinical cohort studies involving over 1,400 patients with Hepatitis E Virus, HIV, and viral co-infections, contributing to more than 25 publications in high-impact journals such as Nature Medicine and The Journal of Immunology.

Integrated antibody and T-cell profiling to identify cross-reactive immune signatures

Anurag Adhikari[1,2,*], Daisy Awale[2], Stephanie Gras[1]
[1]La Trobe University, Melbourne, Australia
[2]Kathmandu Research Institute for Biological Sciences, Lalitpur, Nepal
*adhikari.a@kribs.org.np

Abstract

RNA viruses such as SARS-CoV-2, dengue, Zika, and other arboviruses continue to drive recurrent outbreaks globally. Recent studies highlight substantial heterogeneity in antibody breadth, Fc-effector function, and cross-variant reactivity. Parallel advances in T-cell immunology reveal that SARS-CoV-2–specific $CD4^+$ and $CD8^+$ responses including activation markers, TCR repertoire patterns, and cytokine signatures may serve as durable biomarkers of prior infection, and protective immunity. An integrated immune-screening approach is needed to map population-level exposure and guide diagnostic and surveillance strategies. We developed a discovery pipeline combining multiplex antigen-specific serology, functional antibody assays, and T-cell biomarker profiling. Plasma samples were screened for IgG/IgA binding against flavivirus and coronavirus panels, followed by neutralization, ADCP, and Fc-effector analyses. Parallel PBMC assays assessed SARS-CoV-2–specific T-cell responses using peptide megapools, AIM (activation-induced marker) assays, and cytokine profiling. Bioinformatic clustering integrated antibody and T-cell features into shared immune signatures. Broad antibody screening revealed 20–30% cross-reactivity across flaviviruses and SARS-CoV-2 variants, with preserved Fc-effector activity despite reduced neutralization. T-cell profiling identified consistent SARS-CoV-2 biomarkers $OX40^+CD137^+$ $CD4^+$ T cells, $CD69^+CD137^+$ $CD8^+$ T cells, and distinct cytokine clusters capable of distinguishing naïve and previously infected individuals. Integrated serology–T-cell signatures improved classification accuracy and identified conserved epitopes suitable for diagnostic assay development. Combined antibody and T-cell immune discovery provides a powerful framework for identifying cross-reactive biomarkers of exposure and disease trajectory across emerging RNA viruses. These insights support the design of next-generation diagnostics that incorporate both humoral and cellular markers, offering a scalable approach for outbreak surveillance and clinical triage in resource-limited settings.

Keywords: cross-reactive immunity, T-cell biomarkers, Fc-effector antibody functions,multiplex serological screening, RNA virus diagnostics

Conference Track: *Human Health*

Invited Speaker 02

Dr. Martina Vidmar

Quadram Institute Bioscience, Norwich, United Kingdom

Martina holds a degree in Medical and Pharmaceutical Biotechnology and completed her PhD in Molecular Biology in April 2024, through a joint programme between King's College London and the University of Trieste. During her doctoral studies, she worked on two main projects: investigating the role of oral and gut microbiota in pediatric autism spectrum disorder, and exploring the interactions between ACE2, TMEM16s, and the SARS-CoV-2 Spike protein. She is currently a postdoctoral researcher in Fred Warren's group, where she has returned to the field she is most passionate about. Her work, in collaboration with two different start-ups, focuses on in vitro digestion models and the effects of dietary fibres and probiotics on the microbiota, short-chain fatty acid production, and hormone regulation.

Fermented coconut: a tasty remedy for gut health

Martina Vidmar[1,*], James Lazenby[1], Catherine Booth[1], Alise Ponsero[1], Marie Laure Prevost[2], Fred Warren[1]

[1]Quadram Institute Bioscience, Norwich, United Kingdom

[2]Fermenti, London, United Kingdom

*martina.vidmar@quadram.ac.uk

Abstract

Fermenti, a London-based start-up, has developed a novel functional ingredient from freeze-dried, fermented coconut containing high levels of probiotic bacteria and dietary fibre in a naturally sweet format. This project investigates whether Lactobacilli from this ingredient can survive digestion, establish within the gut microbiota, and enhance microbial diversity and short-chain fatty acid (SCFA) production. We also aim to assess its impact on gut-derived hormone secretion. The overarching goal is to evaluate its potential as a palatable alternative to traditional fermented foods for supporting gut and metabolic health. The ingredient, alone or combined with fruit, was subjected to an in vitro digestion protocol (INFOGEST). Lactobacilli viability was assessed via CFU counts and qPCR, with further validation planned using flow cytometry and FISH. Post-digestion samples were used as substrates in a batch in vitro colonic fermentation model to measure SCFA production (NMR) and microbial community shifts (shotgun metagenomics). The SameSt pipeline was applied to identify overlapping strains between the original ingredient and the colon model. Colon-derived metabolites are applied to STC-1 enteroendocrine cells to evaluate GLP-1 and serotonin responses (ELISA). Statistical analyses were performed in R. The ingredient maintained viable lactic acid bacteria (10^8 to 10^7 CFU/mL) following the in vitro simulated gastric phase (pH 3), confirmed by qPCR and FISH. SCFA analysis showed significant increases in acetate, butyrate, isobutyrate, and isovalerate for both fermented and non-fermented coconut, with fermented coconut displaying higher baseline acetate and other fermentation-related metabolites. PERMANOVA indicated significant variance explained by fibre treatment. Community clustering (dbRDA) revealed clear separation of samples by fibre type, and MaasLin2 identified lactic acid bacteria (mainly Leuconostoc and Lactobacillus genera) driving differences between fermented and non-fermented coconut—strains that remained viable post-digestion and matched the original culture

via SameSt. STC-1 hormone assays are ongoing. Freeze-dried fermented coconut is a promising functional ingredient that, despite containing fewer probiotics than traditional fermented foods, delivers a concentrated, fibre-rich, low-sugar matrix with measurable prebiotic and probiotic effects. The observed SCFA increases and microbial shifts support its potential role in modulating gut microbiota and contributing to gut and metabolic health. Ongoing work will clarify its influence on gut hormone secretion, further informing its application as a health-promoting snack component.

Keywords: fermented food, fermented coconut, lactic acid bacteria, gut health, microbiota, microbiome, short chain fatty acids

Conference Track: *Human Health*

Invited Speaker 03

Dr. Sakhila Ghimire

University Hospital Regensburg, Regensburg, Germany

Dr. Sakhila Ghimire is an immunologist whose research has significantly advanced understanding of gut microbiome–immune interactions in allogeneic stem cell transplantation. She has produced high-impact evidence linking intestinal cytokine pathways and microbiome-regulated immune receptors to graft-versus-host disease severity and transplant-related mortality. Her work integrates human tissue immunology, immune phenotyping, and translational microbiome science to elucidate mechanisms of immune dysregulation. Through international collaborations across leading European institutions, she has contributed to shaping microbiome-informed immunotherapeutic strategies. Her research provides a strong mechanistic foundation for microbiome-targeted interventions to restore immune homeostasis in clinical settings.

Interplay between gut microbiome and immune cells in health and disease

Sakhila Ghimire
University Hospital Regensburg, Regensburg, Germany
sakhila.ghimire@klinik.uni-regensburg.de

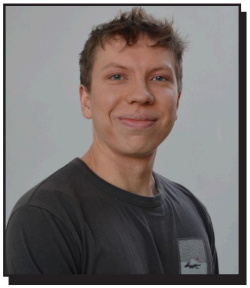
Abstract

The human gastrointestinal tract harbors a complex and dynamic community of microorganisms that plays a pivotal role in shaping host immunity. Microbiota–immune interactions begin early in life and are fundamental for the education and maturation of both innate and adaptive immune cells. Commensal bacteria influence immune homeostasis through microbial metabolites, pattern-associated molecular signals, and modulation of barrier integrity, directing the differentiation and function of T cell subsets, regulatory B cells, innate lymphoid cells (ILCs), and antigen-presenting cells. Disruptions in microbiome composition—termed dysbiosis—can perturb immune regulation, leading to chronic inflammation, autoimmune disorders, metabolic dysfunction, and compromised host defense. Mechanistically, microbial products such as short-chain fatty acids and bile acids shape cytokine profiles, support regulatory cell development, and influence systemic immune responses beyond the gut. Conversely, immune cell signals maintain microbial community structure through antimicrobial peptides, IgA secretion, and mucosal barrier maintenance. This bidirectional dialogue underscores the importance of a balanced gut ecosystem for health and highlights emerging therapeutic avenues—including probiotics, dietary modulation, and microbiome-targeted interventions—to restore immune equilibrium in disease states. Harnessing these interactions offers promising strategies for preventing and treating infectious, inflammatory, and immune-mediated diseases across the lifespan.

Keywords: gut microbiome, immune regulation, host–microbe interactions, dysbiosis, immunomodulation, health and disease

Conference Track: *Human Health*

Invited Speaker 04



Stefan Harper

Quadram Institute Bioscience, Norwich, United Kingdom

Stefan is a CTP PhD student working at Quadram Institute Biosciences and with Campden BRI as his industry partner. He is looking at the impact of fibre and nutrient bio-accessibility on the gut microbiota. He will be using in vitro models of human digestion including INFOGEST and colon models combined with metabolomics and metagenomics to study the impact of processing fibre on gut microbiota composition and microbial accessibility.

The impact of wheat arabinoxylan fermentation in the gut microbiota

Stephan Harper
Quadram Institute Bioscience, Norwich, United Kingdom
stefan.harper@quadram.ac.uk

Abstract

The human gut microbiome comprises the collective genomes of all the microbiota within the gastrointestinal tract with the largest quantity predominantly in the large intestine. Fibres are non-digestible carbohydrates, resistant to human enzymatic breakdown, providing an important nutrient source to the gut microbiota. The interaction of fibre within gut microbiota can produce beneficial responses to the host's physiology, mainly known through short chain fatty acids (SCFA). However, not all fibres behave in the same way or are fermented in the colon equally and so it is important in finding each fibres' role in shaping the microbial community and SCFA production. Arabinoxylan (AX) is the main fibre present in wheat's starchy endosperm and is common in our diets. Wheat breeding programmes have developed wheat lines with ranges of AX content and solubility. Isolated AX has been shown to be beneficial via production of SCFA and microbial composition, but little is known about its digestion within bread flour. We have developed and used a higher throughput digestion and colon model to stimulate AX flour digestion with a focus on the gut microbiota response in healthy people. Here I show that these wheat lines with increasing water extractable AX have an impact on the gut microbiome response with evidence of increasing butyrate production, a key SCFA. Individual responses are also seen, with one microbiome community responding particularly well in terms of SCFA's to the AX flour treatment with specific strain differences. This confirms a potential positive impact AX can have on our health and as a potential prebiotic within wheat flour as well as utilising bacteria strain differences for development of future foods.

Keywords: gut microbiome, fibre, arabinoxylan, short chain fatty acids

Conference Track: *Human Health*

Invited Speaker 05

Gopiram Syangtan

Amrit Campus, Kathmandu, Nepal

Gopiram is a Medical Microbiologist and faculty member at the Department of Microbiology at Amrit Campus, Tribhuvan University, Nepal (Former Research Associate/ Lab Manager at Department of Infection and Immunology, KRIBS). His research interests focus on infectious diseases, tropical diseases, and immunology, with particular emphasis on host–pathogen interactions and emerging viral infections. He has extensive research experience on the Dengue virus, HIV, SARS-CoV-2, and antimicrobial resistance in WHO priority pathogens. Engaging this research, his team investigated seroprevalence, genetic diversity, and immune mechanisms and developed the Enzyme-Linked Immunospot (ELISpot) Assay and the Focus Reduction Neutralization Test (FRNT) Assay. Currently, he is working on "One Health" approach to strengthen evidence-based strategies for the prevention and control of emerging infectious diseases in resource limited setting.

Development of Data Transfer Ethics Framework (daTEF): a participatory approach to delivering evidence-based guidelines for healthcare data transfer

Gopiram Syangtan*, Sauhardra Manandhar, Manjula Bhattarai, Minu Singh, Binod Rayamajhee, Anurag Adhikari
Kathmandu Research Institute for Biological Sciences, Lalitpur, Nepal
*syangtangopiram1@gmail.com

Abstract

In Nepal, insufficient healthcare infrastructure and limited funding contribute to unmet public healthcare needs and reduced quality of care. While foreign health researchers have stepped in to support local research initiatives, their involvement has sparked ethical concerns regarding the sharing and ownership of data. This study aims to develop a locally governed framework for ethical healthcare data exchange, establish an evidence base to understand local challenges in data transfer, and to identify potential solutions for data sharing with international research teams. This cross-sectional qualitative study was conducted in Kathmandu, Nepal, using 11 multiple-choice and 12 open-ended questionnaire models. We conducted a pre-structured questionnaire survey to best identify local ethics issues related to international data transfer and proposed solutions for these challenges. The key representatives identified from the non-governmental and not-for-profit research institute (n = 14) and the life sciences society (n = 7) were invited to one-to-one blind interviews, and their recorded transcripts were coded using the QDA Miner Lite software (version 3.0) for analysis. The ratio of female to male participants was 2:3, while the ratio of junior-level staff to senior staff (≥3 years of experience in the sector) was 1:9. Approximately 42.86% of participants shared both raw and analytical data, while <5% shared no data with collaborators. Concerning knowledge, attitudes, and practices, most (38.46%) preferred open-access storage, while approximately 23.1% had limited knowledge, and 15.38% opted for confidentiality. Additionally, < 10% were in the learning process and sought training in data transfer procedures. Within this group of key representatives, participants faced main challenges in the data transfer process from four key categories: (i) (i) the lack of standardized guidelines from government or institutes for data transfer, (ii) inadequate awareness and training in data sharing, (iii) problems related to data sharing, and (iv)

problems related to biological sample transfer. In summary, this study emphasizes the importance of a standardized data-sharing platform, focusing on protecting intellectual property rights and establishing a centralized data repository in Nepal. It also recommends educational reforms, legal measures, well-defined agreements, and dedicated oversight to ensure data integrity and security, while streamlining sample transfer processes to enhance transparency and scientific progress in Nepal's research landscape.

Keywords: health-care data sharing, ethical data transfer, daTEF, Nepal

Conference Track: *Environmental Health*

Invited Speaker 06

Krishna Hari GC

SNV, Lalitpur, Nepal

Mr. Krishna Hari GC is a senior WASH professional with more than 15 years of experience working with national and international organizations to improve public health through water, sanitation, and hygiene (WASH) interventions in Nepal. He holds a Master's degree in Development Studies from Kathmandu University. He has contributed to the design and implementation of rural, urban, and systems-strengthening WASH programmes across different tiers of government. His experience includes supporting planning, financing, and management of WASH services. Krishna has worked for integrated WASH interventions involving behaviour change communication (BCC), governance, service delivery, and inclusive approaches, including occupational health and safety for WASH workers.

His work emphasises area-wide approaches and WASH systems strengthening. He has supported local governments to adopt improved sanitation service delivery models, including policy formulation, development of costed and evidence-based plans, and faecal sludge management (FSM) in collaboration with government and private sector partners. Krishna has also engaged in nclusive WASH research and advisory roles to mainstream inclusion and strengthen WASH programmes.

In his current role as WASH Advisor at SNV Nepal, he supports WASH systems strengthening to promote inclusive, climate-resilient, and safely managed WASH services, with a focus on improving public health outcomes for poor and marginalized communities and reducing death of children under five in the long term.

Area-wide approach to improving environmental health

Nadira Khawaja*, Krishna Hari GC
SNV, Lalitpur, Nepal
*nkhawaja@snv.org

Abstract

The Constitution of Nepal (2015) and Human Rights resolutions guarantee a clean and safe living environment for all people in Nepal, ultimately contributing to improved health outcomes. At the core of the human rights principles is the obligation of duty bearers, i.e. the State, to incrementally make provisions for fundamental well-being. In Nepal's federal system of governance, the State comprises three autonomous tiers of government with exclusive and concurrent powers. Broadly, the responsibility for providing basic services that improve environmental health, i.e. drinking water supply, sanitation and wastewater management, solid waste management, air and water quality control, lies with the local government. The federal government provides guidance through legislation and policy, the provincial government supports an enabling environment for up-scaling, and all three tiers have jurisdiction over infrastructure development (depending on the size and complexity of projects). SNV works with the three tiers of government as per their respective authorities, private sector, and civil society to strengthen systems that contribute to progress on environmental health. Through an area-wide approach, SNV strengthens the capacities of local governments for inclusive planning and investment for basic services, implements behaviour change campaigns to create demand and encourage behaviours for proper use and maintenance of facilities, establishes linkages to supply chains in the local markets for appropriate technologies, and supports professionalisation of service providers, while paying attention to the most vulnerable communities and people. With the increasing vulnerability of the country to impacts of climate change, SNV is also integrating climate risk assessments and adaptation strategies in its programming. As a result, in the recent years, SNV has supported: communities across 19 districts to stop defecating in the open; 93,750 people in urban areas to have access to safely managed sanitation; reduced indoor air pollution in 22,500 households through the use of clean cookstoves; and supported progress on other aspects of environmental health including water supply, hygiene, and clean energy.

Keywords: environmental health, human rights, area-wide approach

Conference Track: *Environmental Health*

Invited Speaker 07

Lokesh Sapkota

Soil, Water and Air Testing Laboratories Pvt. Ltd., Kathmandu, Nepal

Lokesh Sapkota is currently holding the position of Managing Director at SWAT Labs. He holds a Master's degree in Environmental Management. Currently, he is a PhD Scholar in Environmental Engineering at Kathmandu University. Lokesh Sapkota is an environmental consultant and laboratory professional with expertise in water, wastewater, soil, and environmental quality assessment. He has extensive experience working with government agencies, development partners, and local institutions in areas such as laboratory strengthening, environmental monitoring, landfill leachate studies, climate and disaster risk reduction, and public health–linked WASH interventions. Lokesh is actively engaged in applied research, capacity building, and policy-relevant environmental solutions in Nepal.

Environmental monitoring and environmental health: a private laboratory perspective

Lokesh Sapkota
Soil, Water and Air Testing Laboratories Pvt. Ltd., Kathmandu, Nepal
swatlab2017@gmail.com

Abstract

Environmental health outcomes are directly influenced by the quality of environmental media, including drinking water, wastewater, soil, and ambient environments. Systematic environmental monitoring provides the scientific foundation for identifying exposure pathways, assessing health risks, and informing preventive public health actions. In this context, environmental laboratories, particularly private laboratories play a critical yet often underutilized role in translating environmental data into health-protective decisions. This presentation explores the contribution of private environmental laboratories to environmental health from both technical and policy perspectives. It highlights how routine and targeted monitoring of physicochemical, microbial, and emerging contaminants supports early risk detection, regulatory compliance, and evidence-based interventions at the monitored site. Reliable laboratory data are essential for understanding contamination trends, supporting disease surveillance systems, and strengthening preparedness for environmental and climate-related health risks. Drawing on practical experience from Nepal, the presentation discusses the operational role of private laboratories in supporting drinking water safety plans, wastewater surveillance, landfill leachate monitoring, industrial effluent assessment, ambient air quality and noise level monitoring. Emphasis is placed on laboratory quality assurance and quality control (QA/QC), standard operating procedures, and data integrity as critical components for ensuring credible environmental health evidence. The integration of laboratory-generated data with public health, WASH, and environmental regulatory frameworks is examined as a key pathway for maximizing health impact. The presentation also addresses policy-relevant challenges faced by private laboratories, including regulatory harmonization, data reporting mechanisms, coordination with government institutions, and capacity constraints. Opportunities for strengthening public–private collaboration, digital environmental surveillance platforms, and laboratory accreditation systems are

highlighted as strategic approaches to improving environmental health governance. The keynote concludes by positioning private environmental laboratories as essential partners in achieving Sustainable Development Goal 6 (Clean Water and Sanitation) and strengthening national environmental health systems. Integrating robust environmental monitoring into public health decision-making is critical for reducing exposure to environmental hazards, preventing disease, and promoting resilient and healthy communities.

Keywords: environmental monitoring, environmental health, private laboratories, water quality, wastewater surveillance, public health, SDG 6, policy integration

Conference Track: *Environmental Health*

Invited Speaker 08

Sadikshya Dahal

Phutung Research Institute, Kathmandu, Nepal

Sadikshya Dahal is a Microbiology graduate from Tribhuvan University, Nepal. She is currently working as a Junior Research Assistant at the Phutung Research Institute, Kathmandu, where she performs daily drinking-water surveillance.

Real-time fluorometric quantification of residual chlorine at sub-PPM levels using the WAS device

Sadikshya Dahal[1,*], Rajin Pradhan[1], Rijan Maharjan[1], Thomas F Krauss[2], Anusa Thapa[1], Ashim Dhakal[1]

[1]Phutung Research Institute, Kathmandu, Nepal

[2]School of Physics, Engineering and Technology, University of York, York, UK

*sadikshyadahal.pri@gmail.com

Abstract

Nearly 85% of Nepalis lack safe drinking water, leading to over 3500 deaths due to diarrheal diseases alone. Chlorination is an effective and widely used water treatment method; however, monitoring residual chlorine is crucial due to the undesirable taste and odor, as well as potential health hazards associated with over-chlorination. Therefore, chlorine levels must be monitored accurately and routinely. The World Health Organization (WHO) has set the permissible limit for residual chlorine at 0.2-0.5 ppm. Chlorine detection techniques available today employ colorimetry, electrochemical sensors, photoionization detectors, and spectroscopic (UV-Vis absorption) approaches. These techniques require skilled personnel, proper laboratory setup, and multiple reagents, which contribute to high costs and operational complexity. Moreover, when chlorine levels reach sub-ppm levels, these methods become inaccurate and imprecise, limiting their effectiveness and necessitating a benchmark method. To address these limitations, we present a fluorometric approach for real-time chlorine quantification using the water assessment (WAS) device, which PRI has successfully developed to detect fecal coliforms in drinking water, and is affordable and portable. In this technique, we use a low-cost 275 nm UV LED to excite a sample and measure the fluorescence emitted by it. The fluorescence, at ~365 nm, is collected with a low-cost silicon photodiode and a custom trans impedance amplifier. The entire system is controlled with an STM32 microcontroller, powered by commercially available lithium-ion cells. The small size (1.5 kg, 15x16x19 cm^3) and battery operation make it a highly portable device. The chlorine-specific method includes the addition of a ready-to-use buffered fluorophore to water samples under study. The calibrated system then automatically leverages the quenching property of the fluorophore with chlorine, allowing detection at concentrations as low as 0.06 ppm OCl- within three minutes.

This analyte-induced "off-switch," i.e., inactivation, forms the basis of our method, which is not only rapid and sensitive at low concentrations, but also cost-effective and field-deployable, making it suitable for routine monitoring of residual chlorine in water supplies. The results are delivered in real-time in both numerical as well as color-coded forms, improving the system's usability and accessibility for non-expert users. By combining sensitivity, speed, portability, and intuitiveness, this approach overcomes the key challenges of existing chlorine detection methods and also provides a practical solution for improving drinking water safety with its multi-parameter capability to detect fecal coliforms and turbidity as well.

Keywords: residual chlorine, fluorometric, quenching, buffered fluorophore, multi-parameter capability

Conference Track: *Environmental Health*

Invited Speaker 09

Dr. Nabin Aryal

University of South Eastern Norway, Notodden, Norway

Nabin Aryal is an Associate Professor at the University of South-Eastern Norway (USN) in the Department of Process, Energy and Environmental Technology. His research focuses on renewable energy systems, bioprocess engineering, and sustainable wastewater treatment technologies. He has contributed extensively to projects on biofilm-based reactors, anaerobic digestion optimization, and electroactive microbial systems for carbon capture and resource recovery. Dr. Aryal has received multiple research grants, including projects on energy-efficient wastewater treatment, biogas optimization, and renewable energy education. He also serves as an Associate Editor for the International Journal of Environmental Science and Technology (Springer Nature). His academic background includes an Erasmus Mundus MSc Fellowship and active participation in international collaborations on bioenergy and environmental sustainability.

Biofilm based technologies for chemical synthesis and environmental remediation

Nabin Aryal
University of South Eastern Norway, Notodden, Norway
nabin.aryal@usn.no

Abstract

Biofilmbased systems represent a promising platform for sustainable bioprocessing due to their structural stability, metabolic robustness, and ability to facilitate efficient microbial–material interactions. These properties make biofilms attractive for applications in carbon utilization, chemical synthesis, and environmental remediation, supporting circular economy and climate mitigation strategies. Biofilms were developed through selective microbial enrichment and surface attachment, including the incorporation of electrochemically active biomaterials using electrochemical techniques. Biofilm development and functionality were characterized using scanning electron microscopy (SEM), confocal laser scanning microscopy (CLSM), and electrochemical analyses to understand structure–function relationships relevant to synthesis and remediation processes. The biofilm matrix enabled enhanced microbial activity and electron transfer, facilitating the bioconversion of CO_2 into value-added products such as methane and short to medium chain organic compounds via redox-driven processes. Methanogenic and electroactive microbial consortia showed increased stability compared to planktonic systems. Characterization results demonstrated well-developed biofilm architecture and thickness, directly correlating with improved functional performance. Beyond chemical synthesis, biofilms demonstrated strong potential for pollutant degradation, metal immobilization, and nutrient recovery under diverse operational conditions.

Keywords: biofilms, carbon dioxide utilization, chemical synthesis, environmental remediation, electroactive microorganisms

Conference Track: *Environmental Health*

Invited Speaker 10

Prof. Thomas F. Krauss

Professor of Physics,
University of York,
York, United Kingdom

Thomas F. Krauss is a Professor of Photonics at the University of York. He completed his first degree in Optical Engineering at Cologne, Germany in 1992, followed by a PhD in Electrical Engineering in Glasgow, UK, in 1992. He held EPSRC and Royal Society Fellowships at Glasgow before becoming Chair of Optoelectronics at St Andrews in 2000. His pioneering research in photonic crystals (Nature 1996) was initially directed towards datacomms applications, where he led 2 EU grants and several large EPSRC awards. He moved to the University of York in 2012 where he redirected his activity towards optical biosensors and spun out a company, Phorest Diagnostics, in 2022. Thomas was awarded the Thomas Young Medal of the Institute of Physics in 2022.

Technologies for detecting bacterial contamination in water: a critical review

Thomas F. Krauss
University of York, York, United Kingdom
thomas.krauss@york.ac.uk

Abstract

The problem of drinking water assessment and monitoring in developing countries is well understood, as are the related morbidity and mortality implications. Accordingly, UNICEF has defined a Target Product Profile for a rapid water quality detection test, which stipulates a Sensitivity and Specificity of >85%, that the test be easy to use, low-cost, rapid and portable. So far, no test has been able to reach these demanding requirements. Because such a test is not available, agencies instead recommend the culturing and enumeration of faecal indicator organisms as a reference method to detect bacterial contamination in water. However, culturing typically takes 18-48 hours of incubation and it requires reagents and skilled personnel. Culturing techniques are thus impractical in many developing countries and, as a consequence, are rarely used. Several methods have been developed to address these issues. The most obvious approaches are also based on culturing, as it is the accepted method, and they aim to make the method simpler and faster. For example, Aquatest and the Fujifilm Wako Aquatest add a selective growth medium to the water sample, then culture approx. 24h and assess the water quality by observing the presence or absence of a colour change. These methods indeed simplify the readout, but the 24h timescale is still impractical for most users, as is the requirement to incubate at 37°, since normal citizens do not have an incubator to provide these conditions, and they want to know the outcome in seconds or minutes, not in days. The WaterScope goes a step further by offering a more comprehensive and automated culture test, using a microscope to take a time-lapse image of the membrane, i.e., a “Lab-in-a-box”. Nevertheless, the test still takes at least 8h. More recently, fluorescence-based methods have been developed, mainly based on the detection of tryptophan. Tryptophan is produced by the metabolic activity of bacteria and offers a rapid assessment, as the fluorescence can be measured in seconds. Nevertheless, the specificity is typically too low for a reliable assessment, as tryptophan is produced both by benign and harmful bacteria.

In a recent breakthrough, researchers at Phutung Research Institute, Kathmandu, have developed a more sophisticated method that analyses the emission lines of multiple fluorophores and is able to provide a much more comprehensive picture. In fact, they were able to reach the stipulated 85%/85% requirement for Sensitivity and Specificity without compromising the simplicity, rapidity and low cost of the test. This test is now being commercialised with the goal of a widespread roll-out across Nepal and other developing countries in the near future. A very different approach is being pursued by Phorest Diagnostics, a spin-out from the University of York, UK. Their approach is based on the detection of biofilms, which are formed by bacteria as a protection mechanism to ensure survival. Biofilms provide an indirect indication of bacterial presence and they are currently developed for industrial applications, but may also be useful for the monitoring of water storage tanks and water treatment plants. Most importantly, they can be installed in-situ in the given water system, so they can be automated and do not need user intervention. Overall, the important problem of drinking water monitoring provides a rich field of innovation and a number of methods are being developed. Amongst these, the advanced fluorescence method appears to be the most promising solution, as it is the only method meeting all of the UNICEF TPP requirements.

Keywords: optical sensor, water monitoring, bacterial contamination

Conference Track: *Plant Health*

Invited Speaker 11

Dr. Pablo D. Cárdenas

Assistant Professor – Novo Nordisk Foundation Emerging Investigator

Department of Plant and Environmental Sciences, University of Copenhagen, Denmark

Dr. Cárdenas' group aims to advance our understanding on how local wild plants can be domesticated into future food crops that improve lives and contribute to a more sustainable society, while also uncovering fundamental aspects of plant biology. The research group approaches this challenge from both the lab and the field, driven by the vision that the next generation of climate-resilient and nutritious crops may come not from improving current staples but from directly domesticating local wild species. Emerging tools such as plant omics, artificial intelligence, gene editing, and speed breeding now make this vision actionable. By integrating these technologies with knowledge of antinutritional compounds and agronomic constraints, the research group outlines a roadmap for transforming wild plants into viable crops. Their current proof of concept focuses on the neglected wild plant Chenopodium album, which they are developing to demonstrate the potential of domestication in local wild species. Through this work, Dr. Cárdenas' and his team aim to rethink the origins of crops and contribute to a more diverse and sustainable food future.

From wild to tamed: reimagining novel crops through omics and local plant diversity

Pablo D. Cárdenas
University of Copenhagen, Copenhagen, Denmark
pdcardenas@plen.ku.dk

Abstract

Wild plant species, long excluded from mainstream agriculture, hold untapped potential for building resilient and diverse food systems. Today's agrifood landscape relies on a narrow selection of high-input, genetically uniform crops, reinforcing biodiversity loss, environmental degradation, and vulnerability to climate change. Expanding beyond this limited genetic base is essential and requires us to rethink what future crops can be and where they originate. Through our research, we propose that the next generation of climate-resilient and nutritious crops may come not from improving current staples but from directly domesticating local wild species. Emerging tools in plant omics, artificial intelligence, gene editing, and speed breeding now make rapid domestication a realistic strategy. By integrating these technologies with knowledge of antinutritional compounds and agronomic constraints, we outline a practical roadmap linking molecular insights with the development of new crops. Our current work focuses on *Chenopodium album*, a promising Amaranthaceae species due to its nutritional value and adaptation to marginal environments. By bridging advanced technologies with neglected local biodiversity, we argue that the future of sustainable agriculture lies not in incremental gains to current crops, but in reimagining the wild plants we have long overlooked.

Keywords: plant bioengineering, wild species domestication, plant specialized metabolites

Conference Track: *Plant Health*

Invited Speaker 12

Ashok Limbu

Temperate Horticulture Development Centre, Mustang, Nepal

Ashok holds a Bachelor's degree in B.Tech in Biotechnology and has been working as a biotechnologist at the Temperate Horticulture Development Centre, Mustang for the past four years. His work focuses on developing efficient in vitro italicize protocols for temperate fruit species and scaling them for commercial production. He has successfully applied plant tissue culture technology to produce essential apple rootstocks required for high-density plantation systems.

Enhancing high-density apple plantations in Mustang through tissue culture production of M9 dwarf rootstock

Ashok Limbu
Temperate Horticulture Development Center, Mustang, Nepal
ashoklimbuas@gmail.com

Abstract

Apple cultivation in Nepal, particularly in the Mustang region, is undergoing a transformative shift with the rapid adoption of high-density plantation (HDP) systems. These modern planting systems have demonstrated significantly enhanced production efficiency, improved fruit quality, and greater economic returns compared to traditional orcharding. Encouraged by these promising outcomes, federal, provincial, and local governments are actively promoting HDP through policy support, subsidies, and technical interventions. Despite this momentum, the expansion of high-density apple orchards is critically constrained by the inadequate availability of clonally propagated dwarf rootstocks, especially the globally preferred M9 rootstock. M9 rootstock plays an indispensable role in the success of HDP systems due to its exceptional agronomic attributes. It exhibits wide environmental adaptability, induces a dwarf and manageable canopy architecture, and promotes early fruiting and higher productivity. Furthermore, M9 ensures uniform tree performance and contributes to the production of superior-quality fruit—traits that make it the rootstock of choice for commercial high-density orchards worldwide. However, the conventional propagation of M9 is slow, inconsistent, and insufficient to meet the growing demand in Nepal. To overcome this limitation, plant tissue culture emerges as a vital technology capable of producing disease-free, genetically uniform, and true-to-type rootstocks on a commercial scale. Recognizing this need, the Temperate Horticulture Development Centre (THDC) has initiated pioneering research to develop an efficient micropropagation protocol for M9 apple rootstock for the first time in Nepal. Through systematic experimentation across initiation, multiplication, rooting, and acclimatization stages, THDC has successfully established a reliable and scalable tissue culture protocol suited for commercial production. The optimized protocol ensures high multiplication rates, stable plantlet development, and robust acclimatization success under Mustang's temperate agro-climatic conditions. This breakthrough marks a significant advancement in Nepal's

apple sector, positioning the country to reduce dependency on imported rootstocks and enabling timely and sufficient supply for expanding HDP orchards. The successful development of a commercial-scale tissue culture protocol for M9 rootstock represents a milestone in strengthening Nepal's apple value chain. It supports government initiatives, enhances farmers' access to quality planting material, and ultimately contributes to increasing productivity and sustainability in the Mustang apple industry. This presentation highlights the methodology, key findings, and practical implications of the developed protocol, with a focus on its role in accelerating the adoption of high-density apple plantation systems in Nepal.

Keywords: apple, high-density plantations, tissue culture, M9, rootstocks, acclimatization

Conference Track: *Plant Health*

Invited Speaker 13

Prasodhan Niraula

Apex Biotech and Agroforestry Research Center, Jhapa, Nepal

Prasodhan Niraula is a biotechnology professional with a Master's degree from Kathmandu University. He is currently pursuing a PhD, specializing in the optimization of potato microtuber production through advanced plant tissue culture techniques. He is also the founder and director of Apex Biotech and Agroforestry Research Center, where he leads a team in developing and commercializing tissue-cultured planting materials to enhance agricultural sustainability and productivity.

Plant tissue culture, quality seed, and yield: a strategic imperative for Nepal's potato sector

Prasodhan Niraula[1,*], Dhurva Prasad Gauchan[2]
[1]Apex Biotech and Agroforestry Research Center Pvt. Ltd., Jhapa, Nepal
[2]Kathmandu University, Dhulikhel, Nepal
*prasodhan@gmail.com

Abstract

Potato (*Solanum tuberosum*) is a critical staple and cash crop in Nepal. However, agricultural productivity remains inhibited by the limited availability of high quality, disease free seed tubers. To address this, the present research develops and evaluates a consolidated in vitro-ex vitro production module integrating three sequential biotechnological platforms to optimize the supply chain for high grade potato seed. The module initiates with the aseptic establishment and micropropagation of virus-indexed plantlets from apical meristem culture on Murashige and Skoog (MS) medium, ensuring a disease free foundation. To reduce the unit cost and in vitro stage, these plantlets are transitioned to an *ex vivo* Apical Rooted Cutting (ARC) system. Here, nodal segments from in vitro derived shoots are treated with a rooting hormone and rooted under high-humidity, low-light mist conditions. Finally, ARC derived plants are transferred to a closed loop aeroponic system for microtuber induction. Key efficacy metrics including multiplication coefficient (ARC stage), root induction percentage, microtuber number per plant, mean microtuber mass (>5g target), tuber uniformity, and production cycle duration are quantified against conventional solid medium and soil based controls. Preliminary data indicate the ARC stage yields a 10-15 times propagule increase per in vitro plantlet with >90% survival

Keywords: pre basic seed (PBS), in vitro micropropagation, ex vitro rooting, apical rotted cutting (ARC), tuber induction, technology scaling, sustainable agriculture

Conference Track: *Plant Health*

Invited Speaker 14

Dr. Bhupal Govinda Shrestha

Kathmandu University
Dhulikhel, Nepal

Dr. Bhupal Govinda Shrestha, is a Professor at Department of Biotechnology at Kathmandu University, Nepal. He did my Masters in Nutritional Biochemistry and PhD in Cancer Biology from Tokyo University of Agriculture, Japan. He has also done Post doc from University of British Colombia, Vancouver, Canada, German Cancer Research Center, University of Heidelberg, Germany and Department of Chemistry, Mahidol University. Also, he was Visiting Scientists at Tianjin Institute Industrial Biotechnology/ Chinese Academy of Sciences, China. He has over twenty years of research experience in medicinal plants and its anti-cancer activity. He has about 40 publications in National and International journals and serves as editor of many National and International Journals. He has also presented his research in many National and International conferences as an Invited Speaker.

Merger of ayurveda and biotechnology for study of anti cancer activity of medicinal plants of Nepal

Basanta Lamichhane, Pritish Shrestha, Sandeep Adhikari, Jaya Bhandari and Bhupal Govinda Shrestha*
Kathmandu University, Dhulikhel, Nepal
*bgs@ku.edu.np

Abstract

In the last twenty-five years, approximately half of all newly registered chemotherapeutics have been developed from natural products isolated from plants, fungi or microorganism. Nepal because of her geographical biodiversity, is home to flora and fauna of tropical, sub tropical and alpine origin. These herbs has been used since ancient time to treat numerous diseases. The present study was undertaken so as to find the phytochemical presence, antioxidant and antimicrobial activity and anticancer activity of methanol extract of Nepalese medicinal plants. Phytochemical screening of extracts revealed presence of various phytochemicals like alkaloids, flavonoids, terpenoids, coumarin, saponin, reducing sugar, glycosides, tannin, and steroid. The plant extract also showed antioxidant assay namely DPPH (Diphenyl-2-picrylhydrazyl) free radical scavenging activity. Antimicrobial screening showed sensitivity against *C. albicans, S. typhii*, *P. aeruginosa*, *Klebsiella pneumonia*, *Staphylococcus aureus*, and *E. coli* by the plants. We also looked at anti cancer activity in human normal and cancer cell lines and we see cytotoxic effect of the extracts against cancer cells lines as seen by MTT assay and CV staining and also looked at their target proteins through Western Blotting.

Keywords: antioxidant, ZOI (Zone of Inhibition), phytochemicals, cancer, cell lines

Conference Track: *Human Health*

Lightning Talk 01

Dipak Paudel

Prithvi Narayan Campus, Pokhara, Nepal

Dipak Paudel is a Ph.D. Scholar in the Department of Chemistry, specializing in the research of Natural Products and their metabolites. His research focuses on evaluating anticancer properties using a comprehensive approach that spans *in silico*, *in vitro*, and *in vivo* models. Mr. Paudel is proficient in advanced analytical techniques, including HPLC, GC-MS, LC-MS, and NMR. Additionally, he also possesses experience in cell culture.

Time and altitude variation of cinnamaldehyde and anticancer potential of Cinnamomum tamala from different locations of Nepal

Dipak Paudel[1, 2, 3,*], Santosh Koirala[3], Prayan Pokharel[3], Pranit Hemant Bagde[4], Nfor Gael Njini[4], Hem Chandra Jha[4], Megh Raj Pokhrel[1], Achyut Adhikari[1], Dhaka Ram Bhandari[3]
[1] Central Department of Chemistry, Tribhuvan University, Kirtipur, Nepal
[2]Prithvi Narayan Campus, Tribhuvan University, Kirtipur, Nepal
[3] Center for Environmental and Sustainable Agriculture Research, Pokhara, Nepal
[4]Indian Institute of Technology, Indore, India.
*dipak.795703@iost.tu.edu.np

Abstract

Cinnamomum tamala (Tejpat, तेजपात) serves as both a culinary ingredient and a traditional remedy in South Asia. However, researchers still lack precise data on how its primary bioactive compound, E-cinnamaldehyde, changes after harvest or how these changes influence its anticancer activity. No previous study has investigated the combined effects of altitude, storage duration, and metabolite degradation on its biological activity. This gap limits the development of reliable quality standards for herbal, nutraceutical, and functional food products. Gastric cancer remains a significant global health issue, and interest in plant-based therapeutic agents continues to increase. These factors motivated us to examine how altitude and time alter the phytochemical profile and cytotoxic activity of *C. tamala*. Our goal was to establish whether changes in chemical stability translate into measurable changes in anticancer potential. We collected fresh leaves from three altitudes in Nepal at 420 m, 816 m, and 1540 m. We analyzed their chemical composition and monitored cinnamaldehyde levels for one year of storage at room temperature. We used Gas Chromatography Mass Spectrometry and Proton Nuclear Magnetic Resonance spectroscopy to characterize volatile and non-volatile metabolites. We quantified E-cinnamaldehyde using Reverse-Phase High-Performance Liquid Chromatography at 1, 6, and 12 months. We evaluated cytotoxicity with the MTT assay and measured apoptotic and oncogenic protein expression through Western blot analysis. The 816 m sample had the highest cinnamaldehyde concentration, and all samples showed a substantial decline during storage, with reductions up to 77% within 1 year. Fresh extracts reduced AGS cell

viability more effectively than older extracts. They also activated caspase-mediated apoptosis and suppressed c-Myc and β-catenin. Twelve-month extracts showed weak activity because their cinnamaldehyde levels dropped sharply. These findings show that altitude and storage conditions strongly influence the chemical integrity and anticancer strength of *C. tamala*. The results support the need for marker-based quality control and proper post-harvest handling to preserve the therapeutic and commercial value of *C. tamala*.

Keywords: *Cinnamomum tamala*, तेजपात, E-cinnamaldehyde, HPLC, GC-MS, anticancer activity

Conference Track: *Environmental Health*

Lightning Talk 02

Asim Maharjan

Phutung Research Institute, Kathmandu, Nepal

Asim is an Electronics Engineer currently working as a Research Assistant at Phutung Research Institute. His research is primarily based on developing effective and low-cost techniques for drinking water monitoring using the realtimeWAS device. He has also conducted research to optimize optics for fluorometric systems in order to improve their performance, portability and cost-effectiveness.

A multiparameter, low cost and portable fluorometer for drinking water monitoring

Asim Maharjan[1], Rajin Pradhan[1], Paru Hang Rai[1], Sadikshya Dahal[1], Sharad Timilsina[1], Thomas F Krauss[2], Rijan Maharjan[1], and Ashim Dhakal[1,*]

[1]Phutung Research Institute, Kathmandu, Nepal

[2]School of Physics, Engineering and Technology, University of York, York, United Kingdom

*ad@pinstitute.org

Abstract

Recent studies have shown UV-based fluorimeters to be effective in monitoring different parameters of water such as level of fecal contamination, Biological Oxygen Demand (BOD) and Dissolved Organic Carbon (DOC) by measuring the Tryptophan-like Fluorescence (TLF) and Humic-like Fluorescence (HLF). While effective, such fluorometers use expensive optical components (such as filters) and are usually limited to monitoring a single parameter. This becomes highly uneconomical when multiple parameters have to be measured which would require multiple such devices. Here, we present a filterless, single sample chamber fluorometer that can accurately measure TLF, HLF and Turbidity from a single water sample. The fluorometer does not employ any optical filters and uses a single detector which allows for reduction in the overall size of the system while also minimizing the cost. To correct for the interferences occurring from a lack of filters, we use the excitation from three different sources to correct for interferences and accurately estimate the parameter concentrations. By using a linear decomposition method, we report average errors of 29%, 27% and 3.2% when estimating concentrations of TLF, HLF, and Turbidity respectively from lab prepared samples containing a mixture of all three parameters over a range of concentrations (<50ppb TLF, <30ppb HLF, <5 NTU Turbidity). Compared to existing corrections models, our model performs three times better when predicting low concentrations of TLF at low turbidity levels (<5 NTU). This can be invaluable as a first screening tool for drinking water, especially in rural settings where sophisticated testing is unavailable.

Keywords: drinking water assessment, fluorescence spectroscopy, fluorometers

Conference Track: *Human Health*

Lightning Talk 03

Monima Karmacharya

Research Institute for Bioscience and Biotechnology (RIBB), Kathmandu, Nepal

Monima Karmacharya is a biotechnology graduate from Kantipur Valley College. Currently working as a Research Assistant at the Research Institute for Bioscience and Biotechnology (RIBB). Her work revolves around fermentation science, food microbiology, and food safety. She is deeply interested in advancing food science for sustainable development and contributing to a healthier planet.

Enterococcus detection and microbial safety assessment of vegetable- and legume-based fermented foods from Nepal

Monima Karmacharya[1], Utsav Dahal[1], Suvechhya Bastola[1], Durga Karki[1], Raunak Shrestha[2], Remco Kort[3], Prajwal Rajbhandari[1,*]

[1]Research Institute for Bioscience and Biotechnology, Kathmandu, Nepal

[2]Nepal Applied Mathematics & Informatics Institute for Research, Lalitpur, Nepal

[3]Vrije Universiteit Amsterdam, Amsterdam, The Netherlands

*prajjwalrajbhandari@ribb.org.np

Abstract

Enterococcus spp. are members of the Lactic Acid Bacteria (LAB) group found in fermented foods which can survive in extreme conditions such as high salinity, different temperatures and pH levels. Although some strains are used as probiotics, the genus lacks Generally Recognized as Safe (GRAS) and Qualified Presumption of Safety (QPS) status due to their dual role as beneficial and opportunistic pathogens. Nepal's rich culture is reflected in its traditional fermented foods, including gundruk, masaura, arikanchan, sinki and achar. Fermented foods are regularly consumed in Nepal; however, their microbiological safety has not been well studied. This research aims to assess the prevalence of the *Enterococcus* genus, along with selected foodborne pathogens and hygiene indicator bacteria, in fermented foods collected from various regions of Nepal. A total of 29 samples comprising five fermented foods (*gundruk*, *masaura*, *arikanchan*, *sinki* and *achar*) were collected from 17 districts across altitudes ranging from 80 m to 3660 m. Preliminary identification of *Enterococcus* spp. was performed on Bile Esculin Azide Agar (BEAA), followed by DNA extraction, PCR amplification and 16s rRNA Sanger sequencing. Sequencing data were analyzed using R-packages (isolateR and SangerseqR) to determine the taxonomic classification at the genus level. Detection of potential pathogens and hygiene indicators was conducted using Polymyxin Pyruvate Egg yolk Mannitol Bromothymol Blue Agar (PEMBA) for Bacillus cereus and Violet Red Bile Glucose Agar (VRBGA) for Enterobacteriaceae. Out of 165 isolates from 29 samples, 66 (40%) were preliminarily identified as *Enterococcus* through the BEAA test, and Sanger sequencing confirmed 44 (27% of total isolates) as *Enterococcus*. This study demonstrates that Enterococcus spp. were detected in vegetable- and legume-based fermented foods in Nepal. According to the Food Safety Authority of Ireland (FSAI)

guidelines, *Bacillus cereus* was found in a few samples at borderline levels. At the same time, Enterobacteriaceae were commonly detected in short-duration, non-airtight fermented legume-based foods. These results provide insights into the microbial food safety and contribute to the scientific understanding of traditional fermented foods in Nepal. Concluding, most traditional fermented foods tested were microbiologically safe for these tests, though other food pathogens should also be assessed.

Keywords: traditional fermentation, lactic acid bacteria, food safety, food-borne pathogens, hygiene indicator bacteria

Conference Track: *Human Health*

Lightning Talk 04

Jamie Tuibeo

La Trobe University, Melbourne, Australia

Tuibeo is a second year PhD candidate at La Trobe University in Australia, supervised by Dist. Prof. Stephanie Gras and co-supervised by Dr. Anurag Adhikari. Her work focuses on viral immunology, specifically T cells in the context of viral infections by HIV and SARS-CoV-2.

Investigating the mechanism of viral control in HIV-infected individuals

Jamie Tuibeo[1*], Daisy Awale[2], Monika Chaudhary[2], Anurag Adhikari[1,2], Demetra Chatzileontiadou[1], Stephanie Gras[1]

[1]Department of Biochemistry & Chemistry, School of Agriculture, Biomedicine and Environment, La Trobe University, Melbourne, Australia

[2]Department of Infection and Immunology, Kathmandu Research Institute for Biological Sciences, Nepal

*21049499@students.latrobe.edu.au

Abstract

Human Immunodeficiency Virus (HIV) remains a major global health burden, affecting millions worldwide. While antiretroviral therapies (ARTs) can suppress viral replication to undetectable and untransmittable levels, they do not eliminate the virus due to persistent latent reservoirs. As a result, lifelong treatment and monitoring is required. A rare subset of individuals, known as HIV controllers, maintain low to undetectable viral loads (<50–2,000 RNA copies/mL) without ART. Though they make up less than 1% of people living with HIV, controllers provide valuable insight into natural viral suppression. In this study, we aim to characterise the CD4+ and CD8+ T cell profiles and responses in an understudied cohort of HIV-positive individuals from Nepal, where HIV still remains a major public health issue. Peripheral blood mononuclear cells (PBMC) were isolated from venous blood collected from a cohort of 190 HIV-positive individuals in Nepal. In this cohort, ~5% (n=10) are controllers and the rest are typical progressors or non-controllers. Absolute counting of T cell subsets (CD4+ and CD8+) was conducted on the PBMCs using BD Trucount tubes. Ex vivo intracellular cytokine staining (ICS) assay was used to measure the responses of CD4+ and CD8+ T cells to a HIV Gag peptide pool. CD4+ T cell count in controllers was found to be trending higher (222-1124 cells/µL) compared to non-controllers (11-2658 cells/µL), CD8+ T cell count was trending lower in controllers (203-3596 cells/µL) compared to non-controllers (19-4839 cells/µL), and the CD4/CD8 ratio was significantly higher ($p<0.05$) in controllers (0.1894-2.191) compared to non-controllers (0.03720-3.117). Preliminary results from ex vivo ICS of HIV-positive PBMCs show positive IFNγ, TNF, and CD107 response to the HIV Gag peptide pool. The difference between CD4/CD8 ratio between controllers and non-controllers were found to be statistically significant, aligning with known characteristics of controllers from previous literature. Further investigation into the immune response and phenotype profiles of the T cells will provide a better insight into the link between T cells and protection to HIV.

Keywords: T cells, HIV, adaptive Immunity

Conference Track: *Human Health*

Lightning Talk 05

Kriti Rajbhandari

Kathmandu University, Dhulikhel, Nepal

Research Institute for Bioscience and Biotechnology, Kathmandu, Nepal

Kriti Rajbhandari is a recent graduate of B.Tech in Biotechnology from Kathmandu University. She completed her undergraduate thesis on "Circulating miR-1246 as a Diagnostic and Prognostic Biomarker in Dengue Infection: A Case–Control Study from Nepal." Currently she is working at the Research Institute for Bioscience and Biotechnology (RIBB) as a Research Assistant and has a strong interest in molecular biology and infectious diseases.

Circulating miR-1246 as a diagnostic and prognostic biomarker in dengue infection: a case–control study

Kriti Rajbhandari[1,2], Vishesh Rajbhandari[1,†], Rasika Ghulu[1,2], Frienson Pradhan[1,†], Ashna Dhakal[1], Amol Dahal[1,*]

[1]Kathmandu University, Dhulikhel, Nepal

[2]Research Institute for Bioscience and Biotechnology, Kathmandu, Nepal

[*]amol.dahal@ku.edu.np

[†]These authors contributed equally to this work.

Abstract

Dengue is a growing mosquito-borne viral infection of global concern. It remains a major public health challenge in Nepal, where reliable biomarkers for disease staging and prognosis are lacking. In this study, we investigated circulating microRNA-1246 (miR-1246) as a potential diagnostic and prognostic marker in dengue infection. Serum samples from 21 dengue-positive patients and 20 healthy controls were analyzed by quantitative Reverse Transcription Polymerase Chain Reaction (RTqPCR), with RNU6 as an internal control. Dengue patients showed markedly elevated miR-1246 levels, with a mean 47-fold increase compared to controls ($p = 0.001$). Expression varied by disease stage, peaking in IgM-positive cases, declining in weakly positive IgM patients, and reaching the lowest levels in IgG-positive convalescent cases, a pattern consistent with clinical parameters such as platelet recovery. Receiver Operating Characteristic (ROC) analysis further highlighted the diagnostic potential, yielding an Area Under the Curve (AUC) of 0.79, sensitivity of 95.24%, and specificity of 60.00%. These findings imply that miR-1246 is drastically dysregulated during dengue infection and could be a useful biomarker for tracking the intensity and course of the illness.

Keywords: dengue, microRNA, miR-1246, biomarker, quantitative reverse transcription polymerase chain reaction, ROC analysis

Conference Track: *Animal Health*

Invited Speaker 15

Wen-Chi Hsu

National Pingtung University of Science and Technology, Pingtung, Taiwan

Wen-Chi Hsu is a specialist in Animal Science with a Master's degree from the Department of Animal Science at National Pingtung University of Science and Technology (NPUST), Taiwan. Currently pursuing a Ph.D. in the Graduate Institute of Bioresources at NPUST, she specializes in reproductive physiology, nutritional physiology, and molecular biology of economic animals. Notably, Wen-Chi's previous research focused on optimizing the post-thaw quality of frozen semen in indigenous Taiwanese black pigs by supplementary natural plant extracts. Wen-Chi possesses a broad spectrum of research expertise. Her background also extends to animal stem cell technology, in vitro embryo production (IVP), and embryonic gene editing.

Fecal RNA-based profiling as a non-invasive alternative for characterizing active gut microbiota in cattle

Wen-Chi Hsu*, His-Ping Yang, Shao-Yu Peng
National Pingtung University of Science and Technology, Pingtung County, Taiwan
*op263399@gmail.com

Abstract

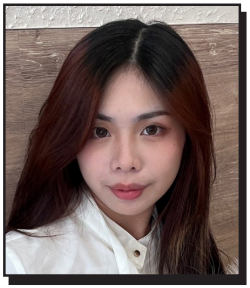
The gut microbiota plays a pivotal role in ruminant nutrition, immune regulation, and metabolic health. Traditional studies largely rely on invasive rumen sampling to characterize microbial communities, which raises animal welfare concerns. This study aims to evaluate whether RNA-based microbial profiling of fecal samples, with Dutch cattle serving as a representative model for determining if this method can act as a non-invasive proxy for active gut microbiota. Particular focus on functionally relevant, fiber-degrading and short-chain fatty acid (SCFA)–producing bacteria. Rectal fecal samples were collected from Dutch cattle (n=10 per trial) maintained under identical management conditions and fed a total mixed ration. Two independent sampling trials were conducted with an interval of approximately ten months. Total RNA was extracted from fecal suspensions to target transcriptionally active bacterial populations, followed by DNase treatment and reverse transcription to generate cDNA. The bacterial 16S rRNA gene (V6–V8 region) was amplified using primers 968F and 1391R, and amplicons were sequenced on the Illumina MiSeq platform. High-quality reads were clustered into operational taxonomic units (OTUs) at 97% sequence similarity, followed by taxonomic assignment and diversity analyses. Relative abundance data were statistically analyzed using SAS 9.4 (PROC GLM), with significance defined at $P < 0.05$. RNA-based microbiome analysis has been increasingly adopted in recent years to better reflect metabolically active microbial communities rather than total DNA-based presence. The results showed that Firmicutes and Bacteroidetes dominated the active fecal microbiota. Several functionally important families—including *Rikenellaceae, Lachnospiraceae, Clostridiaceae, Prevotellaceae, Ruminococcaceae, Victivallaceae,* and members of *Bacteroidales*—were consistently detected across trials. These taxa are well known for their roles in fiber degradation and short-chain fatty acid production, contributing to energy supply and intestinal health in cattle. While partial overlap with rumen-associated microbiota was observed at the family level, notable differences remained

at finer taxonomic resolution. In conclusion, fecal RNA-based profiling provides a practical and animal-friendly tool for assessing active gut microbiota in cattle. Although it cannot fully substitute for rumen sampling, this approach offers valuable insights into hindgut fermentation and its potential contributions to nutrient utilization, supporting applications in herd health monitoring, nutritional management, and longitudinal microbiome studies.

Keywords: feces, gut microbiota, Holstein cow, short-chain fatty acids, fiber degradation

Conference Track: *Animal Health*

Invited Speaker 16



Zi-Chen Hsu

National Pingtung University of Science and Technology, Pingtung, Taiwan

Zi-Chen Hsu is currently studying in the Department of Animal Science and Animal Husbandry at National Pingtung University of Science and Technology. In the Reproductive Technology Laboratory, she focuses her research in areas such as in vitro culture of porcine oocytes, stem cell culture, and extracellular vesicle extraction, and also on the nutritional physiology of chickens and pigs. These experiments have not only taught her many professional techniques but also sparked strong interest in scientific research. She is particularly interested in the application of sambar deer antler stem cells, and have published articles such as "Effects of Formosan Sambar Deer Antler Stem Cell Secretome and Extracted Extracellular Vesicles on the In Vitro Culture of White Pig Embryos" (2025) and "Effect of different concentrations of ginger powder added to diet on diarrhea and egg production rate of laying hens."

Effects of dietary tannic acid supplementation on the active gut microbiota of pigs

Zi-Chen Hsu*, His-Ping Yang, Shao-Yu Peng
National Pingtung University of Science and Technology, Pingtung County, Taiwan
*hsumi920616@gmail.com

Abstract

This study evaluated the effects of dietary tannic acid (TA) supplementation on the metabolically active gut microbiota of pigs and assessed its potential as an alternative to in-feed antibiotics. Crossbred pigs (Landrace × Yorkshire × Duroc) raised under commercial conditions were assigned to either a control diet or a diet supplemented with 0.1% tannic acid. At approximately 130 days of age, fecal samples were collected from healthy pigs. Total RNA was extracted to profile transcriptionally active microbial populations, followed by DNase treatment, reverse transcription, 16S rRNA gene amplification, and next-generation sequencing using the Illumina MiSeq platform. Microbial communities were analyzed based on operational taxonomic units (OTUs) clustered at 97% sequence similarity. Supplementation with 0.1% tannic acid did not affect growth performance but significantly altered the structure of the active gut microbiota. Tannic acid reduced taxa associated with mucosal stress and inflammation, including *Prevotellaceae* (Bacteroidota) and *Epsilonbacteraeota* (currently classified within Campylobacterota), which include genera such as *Helicobacter* and *Campylobacter*. This reduction suggests decreased intestinal irritation and inflammatory risk. Conversely, tannic acid increased the relative abundance of beneficial Gram-negative bacterial families, including *Bacteroidaceae, Barnesiellaceae,* and *Marinifilaceae* (Bacteroidota), which ferment complex polysaccharides and produce short-chain fatty acids (SCFAs). Enrichment of butyrate-producing bacteria supports intestinal epithelial energy supply, tight junction integrity, and anti-inflammatory responses. *Succinivibrionaceae* (Proteobacteria) also increased, potentially enhancing microbial cross-feeding via succinate production. Some Proteobacteria, such as *Desulfovibrionales* and *Campylobacterales*, were elevated, though their functional roles require further investigation. In conclusion, dietary supplementation with 0.1% tannic acid modulates the active gut microbiota of pigs by suppressing inflammation-associated taxa while promoting microbial groups involved in polysaccharide fermentation, SCFA production, and mucosal protection. These findings suggest that tannic acid may improve intestinal health and represents a promising candidate for reducing reliance on antibiotic growth promoters.

Keywords: tannic acid feces feed additive gut microbiota RNA extraction

Conference Track: *Animal Health*

Invited Speaker 17

Prof. Neil Mabbott

University of Edinburgh, Edinburgh, United Kingdom

Prof. Mabbott research aims to understand the pathogenesis of infectious diseases within the immune system. Particular interests include understanding host-pathogen interactions within the mucosal immune system, especially prion diseases and other gastrointestinal pathogens such as Salmonella and nematodes. Studies are also focused on the effects of host age on the function of the immune system and how this influences susceptibility to gastrointestinal pathogens. A systems biology approach is also being used to compare the transcriptomic profiles of distinct immune cell populations in the steady-state, and also during ageing. This research benefits greatly from the availability of precisely defined mouse prion pathogenesis models, unique transgenic and immunodeficient mice and state-of-the-art bio-imaging and bioinformatics expertise.

The impact of gastrointestinal helminths on susceptibility to co-infection with other parasite infections

Neil Mabbott*, Temitayo Ademolue, Liam Morrison
University of Edinburgh, Edinburgh, United Kingdom
*neil.mabbott@roslin.ed.ac.uk

Abstract

In endemic areas, pathogen co-infections within the same host are a common occurrence, and may affect a third of people and the majority of livestock in some low and middle income countries. Parasites have evolved many mechanisms to evade the mammalian host's immune system in order to establish chronic infections. Thus, co-infections with different parasites may alter susceptibility to other pathogens, and/or influence vaccine efficacy through effects on host immune responsiveness. Co-infections may also hinder accurate diagnosis of other diseases. Despite their prevalence and potential impact across the globe, co-infections are poorly studied. For example, infections with gastrointestinal helminths and African trypanosomes occur across large areas of sub-Saharan Africa. Each of these parasites has evolved mechanisms that enable them to manipulate the mammalian host's immune system in order to be able to establish chronic infections. African trypanosomes, for example, are extracellular protozoan parasites that establish chronic infections in the mammalian bloodstream, causing significant morbidity in animals in endemic regions. Although livestock species such cattle and buffalo are regularly exposed to gastrointestinal helminth parasites, nothing is known of how co-infection with these parasites may affect susceptibility to African trypanosomes. I will present data on how infections with a gastrointestinal helminth parasite can influence disease pathogenesis following infection with African trypanosomes within the same host. A greater understanding of how infectious disease susceptibility and pathogenesis can be influenced by parasite co-infections will enhance disease diagnosis and the design of novel vaccines or therapeutics to more effectively control the spread of certain infectious diseases.

Keywords: Animal health, parasite infections, disease susceptibility, pathogenesis, co-infections, immunology

Conference Track: *Animal Health*

Poster No. 01

The effects of tannic acid as feed additive on fecal flora of chicken

Hsiu-An Tang*, His-Ping Yang, Shao-Yu Peng
National Pingtung University of Science and Technology, Pingtung County, Taiwan
*showan0906660275@gmail.com

Abstract

The gut microbiota plays a crucial role in intestinal integrity, immune regulation, and nutrient utilization in broiler chickens. With increasing restrictions on the use of antibiotic growth promoters, plant-derived compounds such as tannic acid have gained attention as potential alternatives. This study aimed to investigate the effects of low-dose dietary tannic acid supplementation on the active gut microbiota of broiler chickens, with particular emphasis on microbial groups associated with mucosal health and metabolic function. Broiler chickens were fed a control diet or diets supplemented with 0.05% or 0.1% tannic acid. Fecal samples were collected to profile metabolically active microbial communities using RNA-based analysis. Total RNA was extracted, reverse transcribed, and subjected to 16S rRNA gene sequencing using next-generation sequencing. Microbial community composition and relative abundance were compared among dietary treatments to evaluate the modulatory effects of tannic acid. At the phylum level, broilers receiving tannic acid supplementation exhibited distinct microbial profiles compared with the control group. Supplemented groups showed increased microbial diversity and the emergence of non-dominant bacterial lineages. In particular, Verrucomicrobia increased exclusively in the 0.05% tannic acid group, primarily driven by Akkermansia, a mucin-degrading genus known to enhance intestinal epithelial barrier function and modulate host immune responses ($P < 0.05$). Minor populations of Cyanobacteria and Actinobacteria were also detected only in the low-dose group. In contrast, the control group was dominated by Firmicutes and Epsilonbacteraeota, with a significant enrichment of *Peptostreptococcaceae* and Clostridium_sensu_stricto_1, taxa associated with protein fermentation, mucosal irritation, and the production of potentially harmful metabolites ($P < 0.05$). Tannic acid supplementation increased the relative abundance of several functionally beneficial taxa, including *Bacteroidaceae,*

Barnesiellaceae, Marinifilaceae, Bacillales, and *Desulfovibrionales*. These microbial groups are involved in polysaccharide degradation, short-chain fatty acid production, antimicrobial activity, and redox balance, collectively supporting intestinal homeostasis and metabolic stability. In conclusion, low-dose tannic acid supplementation modulated the active gut microbiota of broiler chickens by suppressing microbial groups associated with intestinal stress while promoting taxa linked to mucosal protection and beneficial metabolic functions. These findings suggest that tannic acid has potential as a feed additive for improving intestinal health in broiler production systems

Keywords: bacterial microbiota, feces, feed additives, RNA extraction, tannic acid

Conference Track: *Animal Health*

Poster No. 02

Effects of black pig seminal plasma supplementation on the quality of frozen–thawed black pig sperm

Shao-Yu Peng*, Shen Perng-Chih, Tam Wai-Sze
National Pingtung University of Science and Technology, Pingtung County, Taiwan
*sypeng@mail.npust.edu.tw

Abstract

Semen cryopreservation is a critical tool for the conservation of swine genetic resources, as it enables long-term preservation of valuable traits and mitigates the risk of genetic loss during disease outbreaks or population declines. However, boar spermatozoa—particularly those of black pig breeds—are highly sensitive to low temperatures and are prone to cold shock and ice crystal–induced damage during freezing and thawing. These vulnerabilities often result in compromised post-thaw sperm quality and limit the effectiveness of cryopreservation protocols. During routine cryopreservation, seminal plasma is typically removed by centrifugation to reduce its potential inhibitory effects during freezing. Nevertheless, seminal plasma contains numerous bioactive components that may exert protective effects on sperm function after thawing. Based on this premise, the present study investigated whether supplementation of seminal plasma after thawing could improve the quality of frozen–thawed black pig semen. To establish an optimized cryopreservation baseline, we first evaluated the effects of varying concentrations of glycerol and low-density lipoprotein (LDL) in the freezing extender. The results demonstrated that an extender containing 4% glycerol and 9% LDL significantly improved post-thaw sperm survival compared with other formulations ($p < 0.05$). This optimized extender was therefore selected for subsequent experiments. Using this formulation, we assessed the effects of different concentrations of seminal plasma supplementation in the post-thaw medium. Among the tested treatments, supplementation with 50% seminal plasma resulted in the highest sperm survival rate (65.1 ± 4.0%), which was significantly greater than that observed in the 75% and 100% supplementation groups ($p < 0.05$). These findings indicate that moderate, rather than excessive, levels of seminal plasma confer protective benefits

to spermatozoa following cryopreservation. In conclusion, post-thaw supplementation with an appropriate concentration of seminal plasma represents an effective strategy for enhancing the viability of frozen–thawed black pig semen. This approach has the potential to improve fertility outcomes and strengthen genetic conservation efforts for indigenous pig breeds. Future studies will focus on identifying the specific functional components within seminal plasma that contribute to these protective effects, with the goal of further refining and optimizing boar semen cryopreservation protocols.

Keywords: black pig, cryopreservation, semen

Conference Track: *Environmental Health*

Poster No. 03

Building in-house Laser Tweezer Raman Spectroscopy for rapid identification of microorganisms

Ashish Regmi[1,*], Rijan Maharjan[1], Utsav Dahal[2], Monima Karmacharya[2], Prajwal Rajbhandari[2], and Ashim Dhakal[1]

[1]Phutung Research Institute, Kathmandu, Nepal

[2]Research Institute for Bioscience and Biotechnology, Lalitpur, Nepal

[*]ashish.regmi@pinstitute.org

Abstract

South Asia is estimated to have 44% of the overall global disease burden. Health outcomes are greatly impacted by delayed diagnosis, which raises morbidity and mortality from infectious diseases and uncommon conditions. For example, a bacterial infection like melioidosis is frequently underdiagnosed due to its symptoms resembling other diseases, and the bacteria are often misidentified in laboratories. Building a rapid and accurate system for the detection of harmful microorganisms is imperative for public health safety. Laser Tweezer Raman Spectroscopy (LTRS) is a non-invasive, non-destructive, single-cell/particle analysis technique capable of rapidly identifying biochemical information of trapped microparticles within a minute. An in-house Laser Tweezer Raman Spectroscopy was built to trap different particles present in the sample, one at a time, and acquire their Raman spectrum within a few minutes. A laser source of 785 nm was used to trap and excite the microorganism and acquire its Raman signal, while the backscattered Raman light was filtered and detected using a high-resolution spectrometer. The trapping capability of the system was first validated using cornstarch particles and polystyrene beads, whose characteristic Raman signals were successfully obtained. Samples (yeast, *E. coli*, *E. faecalis*) were prepared following standard laboratory procedures. Each cell was individually trapped, and its Raman spectrum was recorded within 100 seconds, followed by background subtraction and baseline correction. The obtained spectra showed the biomolecular features associated with mitochondrial activity, DNA, tyrosine, phenylalanine, amide groups,

and lipids, consistent with literature-reported Raman peak assignments. Each cell type showed unique Raman signatures, providing distinct biochemical information. This setup enables stable trapping of single cells and real-time biochemical identification without causing cellular destruction. This system can reduce detection times compared to traditional techniques such as culturing, PCR, etc., which may take from 4 to 72 hours. This system can also be used to generate a comprehensive spectral database of microorganisms and, combined with machine learning, has strong potential for rapid detection of harmful microorganisms in real-world samples.

Keywords: laser tweezer raman spectroscopy, microorganism, biochemical information, PCR, machine learning

Conference Track: *Human Health*

Poster No. 04

Real-time and reagentless detection of Urinary Tract Infection (UTI) Using fluorescence analysis

Bigysha Dhakal[1,*], Paru Hang Rai[1], Sadikshya Dahal[1], Asim Maharjan[1], Rajin Pradhan[1], Anusa Thapa[1], Rijan Maharjan[1], Thomas Krauss[2], and Ashim Dhakal[1]

[1]Phutung Research Institute, Kathmandu, Nepal

[2]School of Physics, Engineering and Technology, University of York, York, UK

*bigysha.dhakal@phutung.org.np

Abstract

Urinary Tract Infection (UTI) is one of the most prevalent infectious diseases, caused by *Escherichia coli (E. coli)*, Proteus mirabilis, and Enterococcus faecalis bacteria, accounting for >95% of the cases. Current diagnostic methods for UTI rely on culture-based approaches that require 12-24 hours for results, delaying treatment. With the real-time, reagent-less fluorescence technology we have developed for detecting fecal coliforms in drinking water, we aim to overcome these challenges in urine as well. This study characterizes urinary fluorescence signatures of causative bacteria that have fecal origin and evaluates their diagnostic potential for UTI detection. We systematically analyze the intrinsic emission characteristics of key urinary metabolites, such as uric acid, creatinine, and tryptophan, for UTI screening. Firstly, we establish baseline fluorescence profiles for the dominant fluorescence properties of urinary components like urea, uric acid, and creatinine. Next, we characterize fluorescence patterns in artificially synthesized urine to validate spectral reproducibility. The comparative analysis of excitation and emission spectra across different matrices and derived spectral features enables decomposition of total urine fluorescence into contributions from individual urinary components, bacteriuria, and their interactions. This complementary analysis of artificial urine matrices is expected to establish quantitative fluorescence thresholds for UTI diagnosis. By establishing these spectral baselines and diagnostic thresholds, this research could potentially provide a foundation for rapid, noninvasive, label-free detection of urinary tract infections that significantly reduces diagnostic turnaround time and improves clinical outcomes. In our preliminary experiments with artificial

urine samples, we found that the fluorescence intensity of the samples at ~350 nm (with an excitation wavelength of 275 nm) has a baseline of 86 (counts/s)/(mg/dl creatinine). This intensity increases by approximately 6% for every part per billion (ppb) of tryptophan present in the sample. An elevated level of tryptophan (Trp) more than 21 ppb Trp/(mg creatinine) in urine is known to indicate urinary tract infections (UTIs). Our results suggest that our setup can measure this threshold, corresponding to an increase of 108 (counts/s)/(mg/dl creatinine) from the baseline.

Keywords: urine tract infection, metabolites, Bacteriuria, real-time, reagent-less, fluorescence technology

Conference Track: *Environmental Health*

Poster No. 05

Detection of microplastics in water using time-based fluorescence spectroscopy: a low-cost optical approach

Hritika Pratap, Asim Maharjan, Rijan Maharjan, and Ashim Dhakal*
Phutung Research Institute, Kathmandu, Nepal
*ashim.dhakal@pinstitute.org

Abstract

Microplastic contaminants in drinking water is a new global public health risk that has deleterious effects across multiple organ systems. The existing methods of detection utilize expensive and sophisticated equipment like Fourier Transform Infrared (FTIR), Raman spectroscopy, Scanning Electron Microscopy (SEM) and Pyrolysis-gas chromatography, and are costly, time-intensive, and demand specialized expertise, therefore limiting usability for field detection. This study proposes a cost-effective novel method for the detection and size determination of microplastic particles in real-time from aqueous solutions through optics-based analysis using time-resolved fluorescence spectroscopy. We observe that the random motion of microplastics causes fluctuations in the intrinsic fluorescence intensity of a water sample which is collected in the 445-490 nm range using a 365nm excitation source. Such fluctuations occur in the form of temporal signal peaks which are then extracted and analyzed using Python. Diffusion coefficients were determined from full width half maxima of the detected fluorescence peaks and converted to particle sizes using the Stokes-Einstein equation, assuming spherical morphology and known solution viscosity at a validated temperature of 20 ± 0.5°C. We were able to detect polylactic acid (PLA) and determine its size ranging 0.5 - 8 µm through their dynamics. While the fluorescence intensity peaks are not entirely specific to microplastics, further classification can be done using the obtained size information. The approach offers significant advantages over traditional methods: continuous monitoring capability, low-cost instrumentation, field portability, and non-destructive analysis. Further development is needed to distinguish more commonly used polymeric classes, such as polyethylene, polystyrene, and polypropylene.

Keywords: microplastic, LED (Light Emitting Diode), polylactic acid, fluorescence, temporal fluctuations

Conference Track: Environmental Health

Poster No. 06

Differentiating gram-positive and gram-negative and bacteria using machine learning assisted Raman spectroscopy

Iswori Prasad Paudel[1,2], Ashish Regmi[1], Utsav Dahal[3], Monima Karmacharya[3], Anusa Thapa[1], Prajwal Rajbhandari[3], Suresh Manandhar[2], Rijan Maharjan[1,2], Ashim Dhakal[1,*]

[1]Phutung Research Institute, Kathmandu, Nepal

[2]Madan Bhandari University of Science and Technology, Makwanpur, Nepal

[3]Research Institute for Bioscience and Biotechnology, Kathmandu, Nepal

*ashim.dhakal@pinstitute.org

Abstract

Millions of people die every year from bacterial infections due to delayed or inaccurate identification of bacteria, which subsequently lead to the inappropriate use of antibiotics. This leads to the misuse or overuse of antibiotics, which accelerates one of the most pressing global threats, antimicrobial resistance (AMR). The use of antibiotics can be significantly narrowed down if the bacteria is classified into Gram-positive and Gram-negative immediately upon sample acquisition, which would allow more targeted prescription. The widespread classification methods are Gram staining and polymerase chain reaction (PCR), but have several limitations, as these methods require longer processing time, specific reagents, professional health workers, and advanced laboratory infrastructure. In this study, we developed a rapid, reliable, and non-invasive alternative diagnostic system that integrates Raman spectroscopy with a machine learning technique for the classification of bacteria into Gram-positive and Gram-negative. Raman spectroscopy uses light to identify the chemical composition and structural characteristics of molecules by measuring the vibrational modes of its chemical bonds. Since Gram-positive and Gram-negative bacteria have differences in the chemical compounds present in their cell wall, they exhibit subtle differences in their Raman spectrum. In order to capture these differences between spectra and classify them into Gram-positive and Gram-negative, machine learning methods have to be used. This study is mainly focused on partial least squares discriminant analysis (PLS-DA) because it is able to work with complex high dimensional data with many

correlated variables like Raman spectra. The PLS-DA model is trained using a reference training set from Ho et al that has 56000 Raman datasets across 28 different bacterial strains. Performance of the model is evaluated using 5-fold cross validation and during the reference testing, the model is able to achieve a sensitivity of 90% and a specificity of 93%. The model was validated using an independent laboratory dataset of 147 spectra of pure cultures from *Escherichia coli* 25922 ATCC (Gram-negative bacteria), *Enterococcus faecalis* 19433 ATCC (Gram-positive bacteria), and *Enterococcus* spp. isolates from fermented foods of Nepal. By using preprocessing steps that included background correction, pixel correction, baseline subtraction, and normalization, the model achieved 85% sensitivity and 97% specificity. Also, the method can identify the most important parts of the spectrum that helps in differentiating the classes. The distinct components between the classes are found to be present in the Raman signal corresponding to vibrations associated with carbohydrates, which highlights the distinct cell wall composition of the two classes attributable to lipopolysaccharides and peptidoglycan. By using this approach, health workers would be able to classify and characterize the bacteria during point-of-care treatment. This would ultimately help in narrowing down the use of broad-spectrum of antibiotics, thereby mitigating AMR associated mortality.

Keywords: AMR, PCR, microbiology, raman spectroscopy, partial least squares discriminant analysis, american type culture collection (ATCC)

Conference Track: *Environmental Health*

Poster No. 07

Bio-geophysical feedback approach to track the effects of climate change in the Himalayas

Manjil Ghimire, Aasharya Bhandari, Rijan Maharjan, and Ashim Dhakal*
Phutung Research Institute, Kathmandu, Nepal
*ashim.dhakal@pinstitute.org

Abstract

Snow and ice surfaces in the Himalayas host active microbes that respond to environmental change and are sensitive indicators of climate variability. The Himalayan high-altitude ecosystem presents a varied surface environment, encompassing exposed bare ice in the ablation zone and firn in the accumulation area. This environment is conducive to the development of photosynthetic microbes and their associated ecosystems. These microorganisms, stored annually in firn and glacial layers, offer valuable insights into past climate changes. These permanent photosynthetic microbial communities have evolved a physiology that encourages melt close to their cell walls. Specifically, snow-dwelling microbes like snow algae and cyanobacteria reduce albedo by developing strongly light-absorbing pigments (e.g., carotenoids, chlorophylls, and phenolic compounds). The resulting increase in microbial activity can accelerate the melting of snow and ice in the Himalayas, producing meltwater more quickly. This enhanced melting, in turn, creates conditions even more favorable for microbial growth than ice. Furthermore, the accumulation of biologically active dark granular cryoconite on the surface of snow and glacier surfaces, comprising a mixture of mineral particles, black carbon, organic matter, and diverse microorganisms, plays a significant role in bio-geophysical feedback by introducing bioalbedo-driven reductions in surface reflectivity. The positive feedback loop between microbial activity and meltwater generation supports the hypothesis of a bio-geophysical feedback mechanism on glacial landscapes. This is an active, yet unexplored, area of research within the Himalayan regions. To investigate this, our study models a monitoring approach that rigorously accounts for the conservation of mass and energy. Critically, this approach allows the surface energy balance to change based on microbial growth via processes

like bioalbedo modification and nutrient release during melt. This framework is implemented as a mathematical model that simulates the evolution of the snow-ice surface under varying geophysical conditions. It explicitly captures the coupled feedback: microbial growth alters bioalbedo and the surface energy balance, which subsequently regulates surface temperature, snow-ice persistence, and melt dynamics. Our findings suggest that snow-dwelling microorganisms directly accelerate glacier melt by at least 2-fold through bio-geophysical feedback by lowering albedo and indirectly by exposing underlying low-albedo glacier ice.

Keywords: ablation zone, cryoconite holes, mineral dust, black carbon, bioalbedo

Conference Track: *Environmental Health*

Poster No. 08

Rapid identification of rotavirus via on-chip Raman: a pathway to detecting microbes in drinking water

Murli Jha, Chandrika Pun Magar, Sadikshya Dahal, Anusa Thapa, Rijan Maharjan, and Ashim Dhakal*

[1]Phutung Research Institute, Kathmandu, Nepal

*ashim.dhakal@pinstitute.org

Abstract

The timely identification of microorganisms is essential for various biomedical applications. An example application we consider here is detection of rotavirus. More than 100 million people are infected with rotavirus-induced gastroenteritis. The estimated diarrheal deaths of children under the age of 5 years are more than 578,000. Among these, 37% deaths are due to rotavirus. Currently, Polymerase Chain Reaction (PCR), is the gold standard method to detect viruses, and typically takes 1 to 3 days to completely identify and validate. It is also costly and requires trained personnel. In this work, we demonstrate the effectiveness of nanophotonic waveguide-enhanced Raman spectroscopy for the detection of rotavirus within 5 minutes, which in the future can be devised as a compact, label-free, portable, and cost-effective diagnostic method. By utilizing the enhanced light-matter interaction between optical modes between the waveguide and the sample, we obtained a 1000 times higher Raman signal than the conventional micro-Raman spectroscopy method. Early spectral measurements with the Rotarix oral vaccine were affected by considerable background noise originating from the waveguide itself. To overcome this issue and thoroughly evaluate the detection threshold of our nanophotonic chip, we selected Isopropyl alcohol (IPA) as a reference analyte because of its well-established spectral characteristics. We developed a novel signal processing approach that successfully detected IPA below 1%, allowing us to identify the system's background and noise profiles accurately. Utilizing this noise modeling on the data obtained from the Rotarix, we obtained molecular fingerprints of the viral nucleobases. The spectra that we obtained compared very well and the peaks of 446, 512, 604, 702, and 936 cm -1 matched with nanoplasmonic-based methods

reported in the literature. These results confirm that on-chip Raman spectroscopy serves as a reliable tool for the molecular identification of complex molecules, offering a promising pathway toward more sensitive, accurate, and portable diagnostic devices that can facilitate rapid virus detection through its capability to measure biomolecules of dimensions 200 nm.

Keywords: Nano-photonic chip, waveguides, Raman spectroscopy, rotarix vaccine, isopropyl alcohol, machine learning

Conference Track: *Environmental Health*

Poster No. 09

Imaging-based label-free optical setup for potential biosensing applications

Phadindra Raj Karki[1,*], Rijan Maharjan[1], Thomas F. Krauss[2], and Ashim Dhakal[1]
[1]Phutung Research Institute, Kathmandu, Nepal
[2]University of York, York, United Kingdom
*phadindraraj.karki@phutung.org.np

Abstract

Suspended matter in water can affect environmental and industrial systems, yet conventional detection methods are often complex or costly. We present a simple imaging-based setup using a chirped grating waveguide (CGW) biosensor to detect refractive index changes at the sensor surface. The CGW was illuminated with a 635 nm laser at a fixed angle, and the reflected light was recorded by a CMOS camera, producing a spatial resonance pattern. In preliminary demonstrations, the CGW surface was exposed to air, water, and ethanol, inducing measurable resonance shifts corresponding to the refractive index of the liquid at the surface. A reference image was first acquired in air. Adding water produced a measurable shift relative to the reference, and replacing water with ethanol caused an additional shift, consistent with the higher refractive index of ethanol. These shifts were quantified by calculating the difference in pixel-averaged intensity profiles, tracking the spatial position of the resonance along the surface. The results indicate that this setup can detect surface refractive index variations and may have potential for monitoring microbes or early-stage biofilm formation. Although the present work is limited to laboratory demonstrations, this approach provides a versatile foundation for bioscience and environmental sensing applications and, with further optimization and validation, could be developed into compact, portable systems for water quality monitoring.

Keywords: label-free imaging, chirped grating waveguide, guided-mode resonance, water quality assessment, biofilm monitoring, optical biosensing

Conference Track: *Environmental Health*

Poster No. 10

Real-time, low-cost fluorescence spectroscopy system for automated water quality monitoring

Rijan Bhandari[1,2], Vinam Kumar Shrestha[1,2], Asim Maharjan[1], Paru Hang Rai1, Rajin Pradhan[1], Sharad Timilsina[1], Baikuntha Kumar Acharya[2], Thomas F Krauss[3], Rijan Maharjan[1], and Ashim Dhakal[1,*]

[1]Phutung Research Institute, Kathmandu, Nepal

[2]Sagarmatha Engineering College, Tribhuvan University, Lalitpur, Nepal

[3]School of Physics, Engineering and Technology, University of York, York, United Kingdom

*ashim.dhakal@pinstitute.org

Abstract

Clean water is essential in many areas, from personal and public health to operating factories and science laboratories. Modern industries require continuous information of the quality of their water, to keep their systems running safely. However, traditional testing processes, such as culturing and Polymerase Chain Reaction (PCR), are batch processing-based and are not suitable for automation. Recently, fluorescence spectroscopy-based techniques have shown promising solutions offering a low-cost, realtime, and reagentless way to test water. By combining this technique with additional low-cost electronics, we developed a continuous monitoring and data logging system. The system has a detection limit of <1 ppb equivalent to tryptophan-like fluorescence (TLF) concentration, consistent with the performance of the validated manual device. To achieve the necessary stability, we implemented a passive bubble-trapping mechanism and integrated a Faraday cage for electromagnetic shielding while using analog-to-digital converter (ADC) oversampling to improve signal-to-noise ratio (SNR) on a smaller, low-cost STM32 microcontroller. The device yields quantitative results on a local display and is logged to the remote server. By eliminating manual sampling and providing automated and immediate drinking water assessment, our solution reduces the time for contamination events to preventive action from days to near real-time with very little to no human intervention. The device is compatible with conventional distribution systems with minimal modifications, allowing automation on many levels, remote monitoring, etc. This also opens up possibilities in automated decontamination with the implementation of these systems.

Keywords: fluorescent spectroscopy, tryptophan-like fluorescence (TLF), real-time water monitoring, ADC oversampling, bubble-trapping mechanism

Conference Track: *Environmental Health*

Poster No. 11

Low-cost optical technique to detect real-time, in-situ identification of microparticles in drinking water using DLS

Roshni Tamang, Anish Dahal, Rijan Maharjan, and Ashim Dhakal*
[1]Phutung Research Institute, Kathmandu, Nepal
*ashim.dhakal@pinstitute.org

Abstract

Providing access to clean, safe, and contaminant-free drinking water to everyone is a challenge worldwide. Detecting any and all impurities and contaminants in drinking water needs fast, reliable, and highly sensitive technologies, which will help protect the general public from waterborne pandemics. Traditional methods for detection of microorganisms include culturing, PCR, etc., which takes a significant amount of time, highly skilled personnel, and sophisticated laboratories. The infrastructure required to set up these laboratories are expensive and quite difficult to operate in the rural parts of the country. The subsequent delays in detection of these microorganisms lead to exacerbation of harm to public health. In this work, we introduce an alternative to these traditional methods: dynamic light scattering (DLS) for the detection and characterisation of microorganisms in water resources. DLS has emerged as one of the fastest, reagentless, and convenient methods for the detection of nano/microscale particles that enable real-time analysis of their diffusion behaviour. DLS is a technique used to identify the size and motion of the suspended particles by measuring the change in intensity of the scattering signal. The random motion in the suspended particles creates fluctuations in the scattered light i.e., smaller particles move faster than the larger one. We present a proof of concept to identify polystyrene microspheres, simulating bacterial and viral clusters in water. A 532 nm laser is used as the source, and the beam focused onto a sample of water using a planoconvex lens. If there are foreign particles in the sample, they scatter the excitation light, which is collected through two cleaved, SMF-28 single-mode optical fibers, which are placed symmetrically at 15 degrees from the optical axis. Depending on how the incident light is scattered by the particles in the sample, we can infer the size and motility patterns of the foreign particle, from which we identify the specific contaminants. We therefore show that simple and low-cost systems like DLS can be used to detect microparticles, which may lead to significant improvement in water quality monitoring and public health.

Keywords: diffusion, dynamic light scattering, low-cost, microparticles

Conference Track: *Human Health*

Poster No. 12

Expression of Dengue-1 recombinant antigens as a vaccine candidate

Archana Maharjan,[1,2,*] Smita Shrestha,[1] Rajindra Napit,[3] Roji Raut,[1] Tek Raj Joshi,[1] Pawan Bhatta,[1]
Dilip Chaurasiya,1 Ganesh K.C,1 Krishna Das Manandhar1
[1]Tribhuvan University, Kirtipur, Nepal
[2]Nepal Academy of Science and Technology, Lalitpur, Nepal
[3]Deakin University, Melbourne, Australia
*archanamaharjan953@gmail.com

Abstract

Dengue has been spreading rapidly and becoming an important global health threat. Millions of people get infected per annum as there is no promising vaccine available for dengue. Thus, the recombinant DNA technology is gaining an important role to develop vaccines in a short period of time. Recombinant dengue antigens are the proteins similar to those derived from dengue virus which elicits robust and balanced immunity against dengue virus. This study aims for expression of recombinant dengue -1 antigens in a mammalian cell line as a vaccine candidate. The membrane (M), pre membrane (prM) and envelope (E) genes coding for the respective dengue serotype-1 (DENV1) were inserted into the pCAGGS vector. The plasmid was constructed with a CAG promoter gene for mammalian expression which was synthesized by NovoPro Bioscience Inc. Transformation of DENV -1 plasmid was carried out by heat shock method followed by transfection in HeLa cell lines to express plasmid DNA by chemical method using lipofectamine. Trypan Blue staining was done to analyze the efficiency of transfection. The Reverse Transcriptase (RT – PCR) was carried out to detect the transient expression of mRNA in HeLa cell lines. The cloning of a full length of 6767bp recombinant plasmid with insert size of 2064 bp polyprotein containing prM, M and E proteins of DENV1 was transformed into E. coli DH5α. The plasmid was able to express in HeLa cell lines. The membrane of transfected HeLa cell lines stained with a blue color, and no staining was observed in control HeLa cells which was visualized through microscope. The CAG gene present in DENV1 plasmid was amplified from transfected cells, and the bands were observed at 300bp whereas there were no bands observed in control cells. Thus,

the result showed that there is a transient expression of mRNA in transfected HeLa cells and production of recombinant DENV1 antigen. The recombinant plasmid of DENV1 was able to express in HeLa cell line and produced DENV1 recombinant dengue antigens. Those in vitro mammalian cells expressed prM/M and E proteins could be used as potential vaccine candidates for dengue. These antigens could also be used for diagnostic assay protocol development which helps to develop diagnostic tools/kits in a Nepalese laboratory set up.

Keywords: dengue, recombinant DNA technology, transfection, recombinant antigens, HeLa cell line

Conference Track: *Human Health*

Poster No. 13

Biomarker identification of SCLC using bioinformatics tools

Aryan Pyakurel, Saksham Shakya, Niraj Krishna Pandit, Dikshant Regmi, Amrita Acharya*
Kathmandu University, Dhulikhel, Nepal
*amrita.acharya@ku.edu.np

Abstract

Small cell lung cancer (SCLC) is an aggressive disease known for its rapid spread and high death rate. Finding reliable biomarkers is therefore essential to improve diagnosis and treatment. In this study, we used a bioinformatics pipeline to uncover the molecular drivers behind SCLC. We analyzed a rat gene expression dataset (GSE69091) from the Gene Expression Omnibus, which included three tumor samples and three matched controls. Using the GEO2R tool, we identified genes with significant expression changes and mapped them into a protein-protein interaction network. Through Cytoscape analysis, we pinpointed eight central hub genes: Vegfc, Cxcr4, Cdh1, Ccnd1, Cd34, Dll1, Kdr, and Kit. We focused on these genes because their high connectivity suggests they act as master regulators in the network. Notably, most of these proteins were significantly downregulated, implying that key regulatory functions are suppressed in the tumor. Further analysis using DAVID (Database for Annotation, Visualization and Integrated Discovery) and KEGG (Kyoto Encyclopedia of Genes and Genomes) linked these genes to critical processes like cell growth and angiogenesis. A major finding was the downregulation of Dll1, a vital component of the Notch signaling pathway. This result aligns with established clinical research, such as the study by George et al. (2015), which noted that the Notch family genes is inactive in roughly 25% of human SCLC cases. Based on this, Dll1 and the other identified hub genes appear to be promising biomarker candidates, though they warrant further validation in human datasets.

Keywords: small cell lung cancer (SCLC), biomarkers, PPI network, notch signaling, DLL1, bioinformatics pipeline

Conference Track: *Human Health*

Poster No. 14

Genomic analysis of breast cancer dataset using the METABRIC cohort

Ghanashyam Parajuli, Jyoti Timalsina, Manish Adhikari, Lakshyata Shakya, Amrita Acharya, Durga Karki*

Kathmandu University, Dhulikhel, Nepal

*durga.karki@ku.edu.np

Abstract

Breast cancer remains a critical global health burden, accounting for approximately 2.3 million new cases and 670,000 fatalities in 2022 alone. This study investigates the intricate genomic profile of the disease by utilizing the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) dataset, which contains comprehensive genetic and clinical data from nearly 2,000 primary cases. Our main objectives were to classify somatic mutation patterns, pinpoint frequently mutated genes, correlate clinical and genomic characteristics, and measure tumor mutational burden (TMB), with a specific focus on single-nucleotide variations (SNVs). Clinically, invasive ductal carcinoma was the predominant subtype in the cohort, with most patients diagnosed at early to intermediate stages (I and II). Somatic mutation analysis revealed that PIK3CA and TP53 were the most frequently altered genes, showing 670 and 552 mutations, respectively. In addition to these major drivers, significant alterations were observed in genes such as AHNAK2, MUC16, and KMT2C, suggesting their potential involvement in disease progression. Regarding tumor mutational burden, the majority of samples fell within the low to moderate range (0-1.5 mutations/Mb), although a small subgroup demonstrated notably high TMB. Furthermore, genome wide copy number variation (CNV) analysis highlighted distinct amplification and deletion patterns linked to specific subtypes. For instance, HER2-enriched tumors were characterized by substantial amplification of the ERBB2 oncogene. We also detected recurrent deletions in tumor suppressors such as CDH1, alongside amplifications in FGFR1 and ZNF703. Data analysis and visualization were conducted using R programming, with key results validated through cBioPortal. This study sheds light on the recurrent genomic variations that drive breast cancer heterogeneity, providing critical insights to aid the development of precision oncology and personalized therapeutic strategies.

Keywords: breast cancer, METABRIC cohort, somatic mutations, tumor mutational burden, SNVS, CNVS, cancer gene census, precision oncology.

Conference Track: *Human Health*

Poster No. 16

Pan1: An affordable attachment for water tanks to eradicate *E. Coli*

Manan Chaturved[i*], Bebas Dhungana, Anusha Das
Seva, United States
*mananchat03@gmail.com

Abstract

In many regions of Nepal, contamination of drinking water by biological pathogens is a major contributor to preventable disease. To address this challenge, our team developed a user-friendly, low-cost water sanitation device, Pan1, designed to attach to the underside of a pre-existing water storage tank lid. The Pan1 delivers controlled doses of diluted sodium hypochlorite (NaOCl) to inactivate pathogens, achieving a dosing precision with an approximate standard deviation of 14 mL. Our system includes a bleach-compatible reservoir that is able to hold 2.48 liters of liquid. The reservoir is connected to a diaphragm pump that then leads to the water tank. The connections are made of flexible tubing. As for the circuitry within the Pan1, it is powered using an internal independent power source. The microcontroller within Pan1 delivers the requisite amount of NaOCl based on automated fluorometric readings (such as from the PRI RealtimeWAS device), or as per the user input. From there, a signal is sent to a diaphragm pump to power on for a set amount of time with respect to the integer to dispense NaOCl into the water tank. Another aspect worth noting is that the plastics used in our device - Polyethylene terephthalate glycol (PETG) and High Density Polyethylene (HDPE) - stand up to long-term Ultra Violet Radiation and weather exposure. We estimate the cost of our current implementation to be approximately $175 or 25253 Nepalese Rupee (NPR). The STM32 microcontroller can receive information about water contamination levels and adjust NaOCl dosing accordingly. NaOCl is well established as an effective disinfectant at concentrations of approximately 2-6 parts per million (ppm). In fact, we anticipate that with improvements such as reusing standard 12-13 volt car batteries, using smaller and cheaper diaphragm pumps available within Nepal, using cheaper plastic alternatives, and using a standardized Printed Circuit Board (PCB) in consideration of manufacturing, the cost can go as low as $100 or 14430 NPR. Our prototype demonstrates the potential to support communities in improving the microbiological safety of their drinking water.

Keywords: STM 32, water treatment technologies, *E. Coli,* sodium hypochlorite, local water treatment

Conference Track: *Human Health*

Poster No. 17

Dengue virus propagation in mammalian and mosquito-derived cell lines

Monika Chaudhary*, Daisy Awale, Anurag Adhikari
Kathmandu Research Institute for Biological Sciences, Lalitpur, Nepal
*chaudhary.m@kribs.org.np

Abstract

A variety of dengue research that involves neutralizing antibody, vaccine candidate and pathogenesis require live dengue virus. Dengue virus is commonly isolated and grown in mosquito derived cells (C6/36), mammalian kidney epithelial cells (Vero E6) and Baby Hamster Kidney fibroblast cells (BHK-21). This study aims to optimize the method of Dengue virus propagation on the basis of host selection and multiplicity of infection (MOI). Dengue virus propagation was performed in Vero E6 and C6/36 cells. For Vero E6, a million cells were infected with strain of DENV1-4 serotype at MOI of 0.2, 0.1, 0.1 and 0.1 respectively. In contrast, approximately 2.8 million C6/36 cells were infected with Dengue virus type 2 New Guinea C strain at MOI of 0.01. The infection progression was monitored by viral RNA quantification where mock infected media served as baseline. The virus inoculated culture media was collected at 48, 96, 144 and 192 hour post infection (hpi) for C6/36 whereas at a single timepoint i.e 72 hpi, for Vero E6. The qualitative confirmation of virus in extracellular milieu was assessed by reverse transcriptase polymerase chain reaction (RT-PCR) followed by gel electrophoresis in Vero E6 whereas the TaqMan probe-based RT-qPCR method was used for C6/36 culture. A standard curve was plotted to interpolate RNA concentration from cycle threshold (Ct) value. The microscopic observation of cells was inconclusive for virus infection due to absence of cytopathic effect. Among four serotypes, the RT-PCR result for Vero E6 cells displayed amplification bands for DENV2 strain only, indicating its propagation. In C6/36 cells, the viral RNA concentration was found to be 3.36 x 10^5 copies/µl at 48 hpi and 3.08 x 10^6 copies/µL at 192 hpi, depicting 9.16-fold change. These findings suggest the optimal propagation of DENV2 strain in both Vero E6 and C6/36 cells at MOI 0.1 and 0.01 respectively. The peaked RNA concentration supports infection progression although the infectious titer remains undetermined. Moreover, it is recommended to perform endpoint dilution assay to determine infectious titer.

Keywords: dengue virus propagation, Vero E6, C6/36

Conference Track: *Human Health*

Poster No. 18

Comparative bioinformatics analysis of ribosomal RNA sequences in *Mycobacterium* species

Sayana Acharya, Anuska Poudel, Supriya Karki, Tisha Nyachhyon, Durga Karki
Kathmandu University, Dhulikhel, Nepal
*durga.karki@ku.edu.np

Abstract

The genus *Mycobacterium* includes some of the most dangerous bacteria in the world, such as *Mycobacterium tuberculosis*, which causes tuberculosis in humans. Because of this, it is very important to correctly identify these species and understand how they are related to one another. In this study, we performed a focused phylogenetic analysis using ribosomal RNA (rRNA) sequences to determine the evolutionary relationships among nine distinct *Mycobacterium* species. We retrieved gene sequences from the NCBI database for species including *M. smegmatis*, *M. avium*, *M. tuberculosis*, and *M. abscessus*. To ensure a robust analysis, we focused strictly on rRNA sequences. We aligned the sequences using the BioEdit tool, which resulted in a clean dataset of 133 genetic positions after removing unclear areas. Additionally, we observed a higher proportion of conserved regions compared to variable regions and gaps. We then constructed a phylogenetic tree using the Neighbor-Joining method in the MEGA12 software to visualize the genetic distance between the species. The resulting family tree clearly separated the species into distinct groups based on their genetic similarities. Specifically, we observed that *Mycobacterium tuberculosis* is evolutionarily much closer to *Mycobacterium marinum* than to *Mycobacterium smegmatis*.This supports why *M. marinum* is often used as a model organism for studying tuberculosis, whereas *M. smegmatis* is mainly used for genetic manipulation and lab studies due to its distant relationship. This grouping aligns with known biological classifications. Our analysis confirms that using rRNA sequences is a simple yet powerful way to identify and classify *Mycobacterium* species. Understanding these evolutionary links is useful for diagnostics and helps researchers track how these pathogens evolve.

Keywords: *Mycobacterium*, phylogenetic analysis, ribosomal RNA, MEGA12, evolutionary biology

Conference Track: *Human Health*

Poster No. 19

Development and validation of in house indirect IGG ELISA against hepatitis C virus among HIV infected patients on antiretroviral therapy

Shubhechchha Maharjan[1,2,*], Devaki Shrestha[1,2], Chandan Prasad Purbe[1,2], Monika Chaudhary[1], Daisy Awale[1], Anurag Adhikari[1], Prashanna Maharjan[2]
[1]Kathmandu Research Institute for Biological Sciences, Lalitpur, Nepal
[2]SANN International College, Kathmandu, Nepal
*mhrjn.shubhu@gmail.com

Abstract

HIV infected people coinfected with Hepatitis C virus (HCV) have become a global burden with increased risk of liver cirrhosis, hepatocellular carcinoma and non-AIDS related illness. Approximately 2.3 million people are living with HIV/HCV co-infection, who share a common route of transmission such as sharing needles, unsafe sexual contact. Coinfected people have low levels of anti-HCV antibodies as compared to HCV monoinfected individuals. Despite the availability of clinical diagnostic tests for detection of HCV, they show reduced sensitivity and reliability in immunocompromised individuals. So, this study aimed to develop and validate an inhouse ELISA, for the detection of anti-E2 HCV antibodies in HIV/HCV coinfected individuals. This study was conducted in the Department of Infection & Immunology at the Kathmandu Research Institute for Biological Sciences (KRIBS). Plasma samples from HIV infected patients that had been previously collected and processed in the laboratory were used in this study. Indirect ELISA was performed to detect and quantify the anti-HCV antibodies targeting E2 protein, enabling the identification of acute and historical HCV coinfections in HIV infected individuals. Optimization of the ELISA was performed using the HCV1 monoclonal antibody (mAb) to determine the optimal E2 antigen concentration. A total 27 plasma samples were analyzed, including 25 from HIV positive individuals and 2 from healthy donors. Among the HIV positive samples, 9 of them were identified as HCV coinfected, which included 4 acute cases and 5 historical cases, while remaining were HCV negative. The obtained results were verified with clinical reports of the patients, which validate our result. Hence, this assay successfully detected low levels of anti-E2

antibody in HIV/HCV coinfected patients. The developed in-house indirect ELISA assay was sensitive enough to work on as low as 8.1 µg/mL E2 and with at least 2.5 µg/mL anti-E2 HCV antibody. This allowed us to stratify the HIV patients coinfected with HCV based on their recent versus historical HCV exposure, indicating sensitivity and reliability of this assay in immunocompromised individuals. Furthermore, this assay can be considered for screening of HIV patients coinfected with HCV for epidemiological purposes. Similarly, it can also be useful for vaccine related studies in future.

Keywords: HIV/HCV Coinfection, diagnosis, antibody, antigen-antibody interaction, ELISA

Conference Track: *Human Health*

Poster No. 20

Exploring biochemical variation in *Enterococcus* spp. from traditional fermented foods of Nepal using Raman spectroscopy

Utsav Dahal[1], Monima Karmacharya[2], Durga Karki[1], Ashish Regmi[2], Roshni Tamang[2], Rijan Maharjan[2], Anusa Thapa[2], Ashim Dhakal[2], Remco Kort[3], Raunak Shrestha[4], Suvechhya Bastola[1], Prajwal Rajbhandari[1,*]

[1]Research Institute for Bioscience and Biotechnology, Kathmandu, Nepal

[2]Phutung Research Institute, Kathmandu, Nepal

[3]Vrije Universiteit Amsterdam, Amsterdam, The Netherlands

[4]Nepal Applied Mathematics & Informatics Institute for Research, Kathmandu, Nepal

*prajjwalrajbhandari@ribb.org.np

Abstract

Enterococcus, a genus of Lactic Acid Bacteria (LAB), is commonly found in the gut of animals and humans, as well as in various environments, including soil, water, and plants. *Enterococcus* play an important role in fermentation by producing organic acids, volatile compounds and bacteriocins which contributes to the flavour, aroma, texture and shelf life. Despite their importance, limited information on its biochemical composition (proteins, lipids, nucleic acids, and cell-wall structures) is known, especially in the strains isolated from fermented foods. The production of fermentation metabolites is closely linked with biochemical composition of cells. So, characterizing these components can explain how strains contribute to development of flavour and texture. Most studies focus on clinical samples, limiting our understanding of food-derived isolates. This study aims to characterize the biochemical composition of *Enterococcus* spp. isolated from traditional fermented foods using Raman spectroscopy. LAB were isolated from fermented foods (*gundruk*, *arikanchan*, *masaura*, and *achar*) using de Man-Rogosa-Sharpe (MRS) media, followed by the Bile Esculin Azide Agar (BEAA) test to presumptively identify Enterococcus. DNA extraction, PCR, and 16S rRNA gene sequencing using the Sanger sequencing method were performed, and data were analyzed using R-packages (isolateR and SangerseqR). An in-house Raman spectroscopy was used to obtain the Raman signals using a laser source of 785 nm. The Raman

spectra of *Enterococcus* spp. isolated from fermented foods showed characteristic peaks consistent with *Enterococcus faecalis* ATCC 19433. All samples showed Raman peaks at 785, 1247, 1339, 1485, and 1573 cm-1, representing molecular vibrations associated with nucleic acids and proteins. Cellular protein was identified by a sharp phenylalanine marker at 1004 cm-1, membrane lipids (CH2 bending) at 1452 cm-1, and Amide-I band at 1660 cm-1. Principal Component Analysis (PCA) of Raman spectra from *Enterococcus* isolates shows that the majority of variance (PC1: 61.7%) was due to intra-isolate heterogeneity present in cell clusters. The overlap between isolates DA4, LdG3, and the ATCC reference suggests high similarities in their biochemical core. BM9 and BRp3 showed distinct separation from other isolates along PC2 (12.2%), suggesting subtle differences in their biochemical compositions. This highlights the potential of Raman spectroscopy as a cost-efficient and non-destructive method for bacterial identification and detecting biochemical composition.

Keywords: lactic acid bacteria, raman spectroscopy, food microbiology, non-invasive, fermentation

Conference Track: *Human Health*

Poster No. 26

Diversity and functional potential of endomicrobiome associated with Taxus spp. From various geographical location of Nepal

Rojina Tandukar[1], Arpana Pandit[1], Dhurva prasad Gauchan[1], Rajeev Shrestha[1], Ramakanta Lamichhane[1], Namraj Dhami[2]
[1]Kathmandu University, Dhulikhel, Nepal
[2]Pokhara University, Kaski, Nepal
*rojeenatandukar143@gmail.com

Abstract

Taxus species are globally recognized for producing paclitaxel and for hosting metabolically versatile endophytes. While Taxus-associated endophytes have been widely investigated elsewhere, their functional diversity and antimicrobial potential from the unique Himalayan eco-geographical gradients of Nepal remain poorly explored. This study provides the first systematic evaluation of the endomicrobiome of *Taxus wallichiana* collected across distinct altitudinal regions of Nepal (Mustang & Kaski), with a specific focus on identifying endophytes capable of producing antimicrobial and antioxidant metabolites effective against multidrug-resistant (MDR) pathogens. By integrating biogeographic sampling, bioactivity screening, and chemical profiling, this work adds new insight into how Himalayan environments shape the functional potential of Taxus-associated endophytes. Endophytic fungi were isolated from surface-sterilized leaf and bark tissues and identified using Internal Transcribed Spacer (ITS) sequencing. Ethyl acetate extracts were screened for antimicrobial activity using disc diffusion and broth microdilution assays against reference strains and clinically relevant MDR bacteria, including methicillin-resistant *Staphylococcus aureus* and carbapenem-resistant Klebsiella spp. Antioxidant potential was assessed by DPPH assay, and metabolite diversity was evaluated using thin-layer chromatography. A total of 23 fungal endophytes belonging to diverse genera were identified. Several isolates exhibited pronounced antimicrobial activity, with *Cladosporium tenuissimum* showing the strongest inhibition against Gram-positive MDR pathogens and a minimum inhibitory concentration of 4 mg/L against S. aureus ATCC 43300. *Penicillium mallochii*

demonstrated the highest antioxidant activity (IC_{50} = 12 µg/ml), suggesting a link between redox-active metabolites and antimicrobial efficacy. TLC profiling revealed chemically diverse metabolites, including phenolics, flavonoids, and paclitaxel-like compounds. Overall, this study highlights Nepalese Taxus endophytes as an underexplored reservoir of bioactive metabolites and provides a foundation for future drug discovery targeting multidrug-resistant infections.

Keywords: *Taxus wallichiana*; endophytic fungi; multidrug-resistant bacteria; antimicrobial metabolites; Himalayan biodiversity; paclitaxel-associated endophytes

Jointly Organized by:

RESEARCH INSTITUTE FOR BIOSCIENCE AND BIOTECHNOLOGY

Co-organized by:

Engage Nepal With Science

KRIBS

Phutung Research Institute

Supported by:

ORGANIZATION FOR WOMEN IN SCIENCE FOR THE DEVELOPING WORLD

crimson Tech

NEPAL WINE-RY ACADEMY

talkbiotech FORUM

OPTICA NEPAL SECTION

KUBiC

Nepal Research Alliance

Sponsors:

Praramva Biotech Technology for Nature

HERVEDA® BOTANICALS Stories of Nature

SHIKHAR BIOTECH

Rajshree Scientific Suppliers Pvt. Ltd. Kathmandu, Nepal

APEX BIOTECH

Beverage Partners:

HIMALAYAN BREWERY PRIVATE LIMITED

HIMALAYAN PREMIUM LAGER BEER

RUSLAN PREMIUM VODKA

Gift Partners:

Gresmetic

MM MODERN MITHILA

Drinks Partners:

Fermentica

सर्वगुण SARVAGUNA FOODS & KITCHEN

Stationery Partner:

jamarko

Hospitality Partner:

ATITHI RESORT & SPA POKHARA

Agency Partner:

Pure Sound Advertising

Media Partner:

छाप्रोमा

Gear Partner:

DOLPO

Organizing Committee

Mr. Prajwal Rajbhandari

Co-chair

President, Research Institute for Bioscience and Biotechnology (RIBB), Nepal

Prof. Dr. Dhurva P. Gauchan

Co-chair

Head of Department, Department of Biotechnology, Kathmandu University, Nepal

Prof. Dr. Sangita Shakya

Member

Professor, Department of Biotechnology, Kathmandu University, Nepal

Dr. Amol Dahal

Member

Assistant Professor, Department of Biotechnology, Kathmandu University, Nepal

Dr. Sunita Gautam Ghimire

Member

Principal Investigator, RIBB, Nepal

Dr. Ashim Dhakal

Member

Co-founder and Chief Scientist, Phutung Research Institute, Nepal

Dr. Sunil Pokhrel

Member

Principal, Kathford International College of Engineering and Management, Nepal

Ms. Rojlina Manandhar

Member

Chair, Department of Natural Products and Green Chemistry, RIBB, Nepal

Ms. Suvechhya Bastola

Scretary

Chair, Department of Applied Microbiology and Food Technology, RIBB, Nepal

Abstract Selection Committee

Dr. Neha Shrestha
Chair
Research Institute for Bioscience and Biotechnology (RIBB), Nepal

Dr. Hitesh K. Bhattarai
Member
Assistant Professor, Department of Biotechnology, Kathmandu University, Nepal

Dr. Bishnu Maya K.C.
Member
Assistant Professor, Department of Biotechnology, Kathmandu University, Nepal

Dr. Anurag Adhikari
Member
Co-Founder/Head of Research/Group Leader, Department of Infection and Immunology, Kathmandu Research Institute for Biological Sciences, Nepal

Dr. Anusha Balla
Member
Assistant Professor at CiST College, Nepal

Dr. Rijan Maharjan
Member
Research Fellow, Phutung Research Institute, Nepal

Dr. Prayan Pokharel
Member
Center for Environmental and Sustainable Agricultural Research (CESAR), Pokhara, Nepal

Mr. Nishan Katuwal
Member
In-charge, Molecular and Genome Sequencing Research Lab and Project Manager, Dhulikhel Hospital, Kathmandu University Hospital, Nepal

Creative Heads

Aagat Awasti

Rebecca Pitkin

A DECADE OF
ADVOCATING

Conference Secretariat
Research Institute for Bioscience and Biotechnology (RIBB)
Biomedicum Research Campus Building
Saptakhel-9, Balkumari, Lalitpur, Nepal.
Phone: +977 9841600889 (Suvechhya), +977 9841804369 (Prajwal)
Email: info@icbb.com.np, info@ribb.org.np

www.icbb.com.np