XVIII[th] RENCONTRES DU VIETNAM
Gặp gỡ Việt Nam lần thứ 18

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International Centre for Genetic Engineering and Biotechnology

ABSTRACTS BOOK

2nd Rencontres de Quy Nhon

INTERNATIONAL WORKSHOP ON MOLECULAR DIAGNOSTICS IN MICROBIOLOGY AND DISEASES

December 10 - 15, 2023

ICISE Quy Nhon, Vietnam

The second Rencontres de Quy Nhon International Workshop on Molecular Diagnostics in Microbiology and Diseases

ICISE, Quy Nhon City, Binh Dinh province, Vietnam
11-14 December, 2023

PROGRAMME

Two days: 11rd - 12th December, 2023		
Two-day training course on molecular diagnostics of foodborne microbes		
Wednesday, *13th December, 2023*		
8:00 – 8:30	Moving to ICISE from Seagull Hotel by Shuttle Buses	
8:00 – 16:00	Opening registration and poster hanging	*ICISE, Quy Nhon City*
Chair: Assoc. Prof. Nguyen Bao Quoc		
8:30 – 9:00	Welcome address Opening remarks	**Assoc. Prof. Dr. Nguyen Bao Quoc** Chair of Organizing Committee, MDMD2022 **Assoc. Prof. Dr. Nguyen Tat Toan** Vice-President, Nong Lam University **Assoc. Prof. Dr. Nguyen Thi Thu Hoai** Vice Director of RCID, International University, VNU-HCMC **Dr. Tran Thanh Son** ICISE, Quy Nhon City
Plenary talks – Main Hall		
Chair: Assoc.Prof.Dr. Rajesh Pandey		
9:00 – 9:40	**Plenary lecture 1 (PO-01)** **Title of talk: *Stitching together an abode for itself by Mycobacterium tuberculosis***	**Dr. Dhiraj Kumar** Cellular Immunology, ICGEB New Delhi, India
9:40 – 10:20	**Plenary lecture 2 (PO-02)** **Title of talk: *Multi-locus sequence analysis (MLSA) system for plant bacterial pathogen diagnosis and a case study with Xanthomonas***	**Prof.Dr. Seong Hwan Kim** Department of Microbiology Dankook University Republic of Korea
10:20 – 11:00	**Group photo** Tea break and poster visiting	
Keynote talks – Main Hall		
Chair: Dr. Dhiraj Kumar		
11:00 – 11:30	***Keynote 1:*** **Title of talk: *Can Transcriptionally Active Microbes (TAMs) be used for Disease Severity Prediction?***	**Prof. Rajesh Pandey** Institute of Genomics and Integrative Biology, New Delhi, India
11:30 – 12:00	***Keynote 2:*** **Title of talk*: *Development of diverse diagnostic tools to understand poultry diseases***	**Assoc.Prof.Dr. Thi Thu Hao Van** RMIT University, Australia
12:00 – 13:30	Lunch break	*ICISE, Quy Nhon City*
13:30 – 14:00	Poster presentation	

Keynote talks – Main Hall			
Chair: Assoc.Prof.Dr. Thi Thu Hao Van			
14:00 - 14:30	***Keynote 3:*** **Title of talk*: Translating the uses of molecular techniques into routine diagnostics***		**Dr. Ngo Tat Trung** Centre for Genetics Counsulation and Cancer Screening Viet-German Medical Research Center (VGCARE) 108 Military Central Hospital Hanoi, Vietnam
Concurrent sessions			
	Infectious diseases and pathology - Main Hall	**Plant and Animal Diseases – Meeting Room 1**	**New technologies and microbial Genomics – Meeting Room 2**
	Chair: Dr. Ngo Tat Trung	**Chair: Assoc.Prof.Dr. Tran Van Hieu**	**Chair: Dr. Vu Minh Thiet**
14:45 – 15:05	**Invited speaker (IO-01):** *Selective Detection of HBV Pre-Genomic RNA in Chronic Hepatitis B Patients Using a Novel RT-PCR Assay* **Dr. Ho Huu Tho** Vietnam Military Medical University Hanoi, Vietnam	**Invited speaker 5 (IO-05):** *Identification and Characterization of Microbial Pathogens in Agriculture Through High Throughput Sequencing* **Prof.Dr. Kumar Pankaj** Sardar Vallabh Bhai Patel University of Agriculture & Technology, Meerut, UP, India	**Invited speaker 9 (IO-09):** *A pilot exploration of gut microbiota diversity in colorectal cancer patients using 16S rRNA sequencing* **Dr. Tran Thi Thanh Tam** University of Science and Technology Hanoi (USTH), Hanoi, Vietnam
15:05 – 15:25	**Invited speaker (IO-02)** *The potential of F12 as a biomarker for early diagnosis, prognosis, and development of treatment strategies for patients with hepatocellular carcinoma* **Dr. Nguyen Minh Nam** School of Medicine, VNU-HCMC Ho Chi Minh City, Vietnam	**Invited speaker 6 (IO-06):** *Fast and reliable method for molecular identification of Bos Gaurus, an example of applying animal forensic for wildlife conservation* **Dr. Le Minh Thong** International University, Vietnam National University – Ho Chi Minh City, Vietnam	**Invited speaker 10 (IO-10):** *Investigating the circulation of AMR between animals, humans and their environment using (meta)genomics approaches* **Dr. Juliette Hayer** Infectious Diseases: Vector, Control, Genetic, Ecology and Evolution Centre IRD de Montpellier France
	Chair: Dr. Ho Huu Tho	**Chair: Dr. Nguyen Minh Nam**	**Chair: Dr. Duong Vu**
15:25 -15:45	**Invited speaker 3 (IO-03):** *Amplification efficiency comparison of different polymerases and application in real-time PCR reaction for the rapid detection of Clostridium botulinum serotypes A and B* **Dr. Pham Bao Yen** University of Science, VNU-Hanoi Hanoi, Vietnam	**Invited speaker 7 (IO-07):** *Immunosensor development: antibody conjugation matters* **Assoc.Prof.Dr. Hieu Tran Van** University of Science, VNU-HCMC Ho Chi Minh City, Vietnam	**Invited speaker 11 (IO-11):** *Optimizing Electrode Surfaces in Electrowetting-on-Dielectric-Based Digital Microfluidic Platforms for Automated Molecular Biology Assays* **Dr. Huynh Chan Khon** International University, VNU-HCMC Ho Chi Minh City, Vietnam
15:45 – 16:05	**Invited speaker 4 (IO-04)** *Application of the Peptide Nucleic Acid Blocker to Improve the Sensitivity of Real-Time PCR for Quantitating JAK2 V617F Mutation* **Dr. Nguyen Tuan Anh** Molecular Biomedical Center University Medical Center Ho Chi Minh City, Vietnam	***Invited speaker 8 (IO-08):*** *Molecular Identification of 16SrIX group of Phytoplasma associated with Ash gourd in Eastern Uttar Pradesh in India* **Assist.Prof.Dr. Smriti Mall** Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, India	**Invited speaker 12 (IO-12):** *Genomic sequencing and a novel mouse-adapted Helicobacter pylori* model for hpEastAsia genotype **Dr. Vu Minh Thiet** NTT Hi-Tech Institute Ho Chi Minh City, Vietnam
16:05 – 16:30	**Tea break and poster visiting**		
	Chair: Assoc.Prof.Dr. Nguyen Thi Thu Hoai **Dr. Nguyen Tuan Anh**	**Chair: Prof. Dr. Kumar Pankaj** **Dr. Bui Phu Nam Anh**	**Chair: Dr. Tran Thanh Tam** **Dr. Juliette Hayer**

16:30 – 16:50	**Oral talk 1 (OP-01)** *A novel way to reduce brucella shedding and its reoccurrence in bovines to overcome human brucellosis* **Prof.Dr. Kumar Amit** Sardar Vallabh Bhai Patel University of Agriculture & Technology, Meerut, UP, India	**Oral talk 6 (OP-06)** *Isolation and identification of Escherichia coli and other bacterial species from the lambs affected with diarrhea and evaluation of their antimicrobial resistance* **Dr. Ganesh Gangaram Sonawane** ICAR-Central Sheep and Wool Research Institute, Avikanagar, India	**Oral talk 10 (OP-10)** *Uncovering Genetic Determinants of Antibiotic Resistance in Helicobacter pylori through Next-Generation Sequencing and Genome-Wide Association Study* **Dr. Bui Hoang Phuc** Van Lang University, Ho Chi Minh City, Vietnam
16:50 – 17:10	**Oral talk 2 (OP-02)** *Transcriptionally active nasopharyngeal commensals and opportunistic microbial dynamics define mild symptoms in the COVID 19 vaccination breakthroughs* **Ms. Priti Devi** CSIR-Institute of Genomics and Integrative Biology	**Oral talk 7 (OP-07)** *Isolation, characterization and molecular confirmation of multidrug resistance Staphylococcus aureus from mastitis in sheep of semi-arid Rajasthan* **Dr. Dushyant Kumar Sharma** ICAR-Central Sheep and Wool Research Institute, Avikanagar, India	**Oral talk 16 (OP-11)** *The first draft genome of Bordetella bronchiseptica strain isolated from symptomatic dog in Vietnam* **Ms. Van Ngoc Dung** University of Sciences, VNU-HCMC, Vietnam
17:10 – 17:30	**Oral talk 3 (OP-03)** *Monitoring the distribution of molecular markers of antimalarial drug resistance in the Highland region of Vietnam* **Ms. Nguyen Minh Trinh** Institute of Malariology, Parasitology and Entomology Quy Nhon, Vietnam	**Oral talk 8 (OP-8)** Discovery of a Novel Alphaendornavirus in *Plantago ovata* Using Transcriptome Data Analysis **Mr. Malyaj Rajeev Prajapati** Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, India	**Oral talk 17 (OP-12)** *Study of genetic diversity of acne-associated bacterial isolates in Thailand using the multi-locus sequence typing (MLST) method* **Ms. Khemrutai Sripath** Kasetsart University, Bangkok, Thailand
17:30 – 17:50	**Oral talk 4 (OP-04)** *Bacterial Isolates from Clinical Samples of Dogs and Cats in Thailand* **Ms. Supanida Dechawongse** Kasetsart University, Bangkok, Thailand	**Oral talk 9 (OP-9)** *Whole genome analysis on a novel mutant Vibrio strain causing Acute Hepatopancreatic Necrosis Disease (AHPND) on shrimp* **Ms. Bui Nguyen Tram Anh** University of Science, VNU-HCMC, Ho Chi Minh City, Vietnam	**Oral talk 18 (OP-13)** *Genomic characterization and diversity of Vibrio parahaemolyticus causing acute hepatopancreatic necrosis disease in Vietnam* **Mr. Huynh Tuan Binh** University of Sciences, VNU-HCMC, Ho Chi Minh City, Vietnam
17:50 – 18:10			**Oral talk 19 (OP-14)** *Low-cost microfluidic-based devices for biological cells monitoring and biomarker detection* **Dr. Nguyen Tien Anh** Le Quy Don Technical University, Hanoi, Vietnam
18:30 – 19:00	Cocktail banquet		
19:00 – 21:00	GALA dinner		
21:00 ~	Returning to Seagull Hotel by shutter Buses		
Thursday, 14th December, 2023			
8:15 – 8:30	Moving to ICISE from Seagull Hotel by shuttle Buses		

Plenary/keynote talks – Main Hall		
Chair: Prof.Dr. Seong Hwan Kim **Prof.Dr. Jitender Singh**		
9:00 – 9:30	***Keynote 4:*** **Title of talk: *Organoid based drug discovery and development; from Science to Industry***	**Assoc.Prof. Jongman Yoo** Department of Microbiology CHA university School of Medicine Republic of Korea
9:30 – 10:00	***Keynote 5:*** **Title of talk: *Development of LAMP based assays for detection of microbial pathogens***	**Assoc. Prof. Dr. Nguyen Bao Quoc** Faculty of Biological Sciences Nong Lam University Ho Chi Minh City Vietnam
10:00 – 10:30	***Keynote 6*:** **Title of talk: *Exploring Cutting-Edge Approaches for Detecting Antimicrobial Resistance***	**Assoc.Prof.Dr. Nguyen Thi Thu Hoai** Research Center for Infectious Diseases International University, VNU-HCMC Vietnam
10:30 -11:00	Coffee break and poster visiting	
Chair: Dr. Duong Vu		
11:00 – 11:30	***Keynote 7:*** **Title of talk: *Bacterial Genetics and Omics Exploration to Unveil Molecular Basis of Animal and Human Infectious Diseases***	**Assist.Prof.Dr. Teerasak E-kobon** Faculty of Science Kasesart University Bangkok, Thailand
11:30 – 12:00	***Keynote 8:*** **Title of talk: *Unveiling the Viral Diversity in Indian Garlic Cultivation: A Comprehensive Genomic Study using High-Throughput Sequencing***	**Prof. Dr. Jitender Singh** Ch.Charan Singh University Meerut, UP, India
12:00 – 12:30	***Keynote 9:*** **Title of talk: Clinical Genomics and Epigeneomics Testing**	**Dr. Loi Luu** Grant and Innovation Center, UMP Ho Chi Minh City, Vietnam
12:30 – 13:30	Lunch break	*ICISE, Quy Nhon City*
13:30 – 14:00	Poster presentation	
Keynote talks – Main Hall (cont.)		
Chair: Assist.Prof.Dr. Teerasak E-koborn		
14:00 – 14:30	***Keynote 10:*** **Title of talk: *Enhancing fungal identification in environemental and clinical samples***	**Dr. Duong Vu** The Westerdijk Fungal Biodiversity Institute (WI), Netherlands
14:30 – 14:50	**Oral talk 7 (OP-05):** *Development of Hepatitis C virus quantification assay using the chip-based digital PCR and evaluation its application*	**Dr. Nguyen Thi Le Thuy** Biotechnology Center, Ho Chi Minh City, Vietnam
14:50 – 15:30	Round Discussion (Network and Future Direction of MDMD in Asia and Worldwide)	
Closing ceremony – Main Hall		
Chair: Assoc.Prof.Dr. Nguyen Bao Quoc **Co-chair: Assoc.Prof.Dr. Nguyen Thi Thu Hoai**		
15:30 – 16:00	**Closing ceremony – Main Hall** + Best oral and poster prize for students	
16:00 ~	Returning to Seagull Hotel by shutter Buses	

Organizing Committee

No	Fullname	Address/Institution
1	**Chairman**: Assoc.Prof. Nguyen Bao Quoc	Nong Lam University HCMC – Vietnam
2	**Co-Chairman**: Assoc.Prof.Dr. Nguyen Phuong Thao	Research Center of Infectious Diseases, International University, VNU-HCMC
3	Assoc.Prof.Dr. Nguyen Vu Phong	Nong Lam University, HCMC, Vietnam
4	Dr. Nguyen Van Phuong	University of Science and Technology Hanoi, Vietnam
5	Dr. Bui Phu Nam Anh	Ho Chi Minh City Open University, HCMC, Vietnam
6	Dr. Huynh Vinh Khang	Nong Lam University, HCMC, Vietnam
7	Dr. Huynh Chan Khon	International University, Vietnam National University, HCMC, Vietnam.
8	Dr. Tran Thanh Son	ICISE, Quy Nhon, Binh Dinh, Vietnam
9	Dr. Pham Bao Yen	University of Sciences, VNU Hanoi, Vietnam
10	Dr. Phung Van Canh	Poultry Research Centre , Hanoi, Vietnam
11	Ms. Nguyen Thi Loi	ICISE, Quy Nhon, Vietnam
12	Ms. Tran Pham Quynh Nhu	ICISE, Quy Nhon, Vietnam
13	Mr. Nguyen Trong Nhan	ICISE, Quy Nhon, Vietnam
14	Mr. Nguyen Mai Nghiep	Nong Lam University, HCMC, Vietnam

Scientific Advisory Committee

No	Fullname	Academic Title	Address/Institution
1	Nguyen Tat Toan	Assoc. Prof.	Nong Lam University HCMC – Vietnam
2	Trinh Xuan Hoat	Assoc.Prof.Dr.	Vietnam Institute of Plant Protection, Hanoi - Vietnam
3	Ngo Thi Hoa	Assoc.Prof.	Oxford University Clinical Research Unit (OUCRU) – HCMC- Vietnam
4	Hemant Gautam	Prof.Dr.	CSIR-Institute of Genomes and Integrative Biology New Delhi, India
5	Woubit Abebe	Prof.Dr.	University of Tuskegee, Alabama, USA
6	Jitender SINGH	Prof.Dr.	Ch. Charan Singh University Campus, Meerut, UP, India
7	Dilip Kumar Ghosh	Dr.	ICAR – Central Citrus Research Institute India
8	Dhiraj Kumar	Dr.	Cellular Immunology, ICGEB, New Delhi, India

Program Committee

No	Fullname	Address/Institution
1	Assoc.Prof. Nguyen Bao Quoc	Nong Lam University,HCMC – Vietnam
2	Assoc.Prof. Nguyen Vu Phong	Nong Lam University,HCMC – Vietnam
3	Assoc.Prof. Nguyen Duc Hoang	University of Sciences VNU-HCMC Vietnam
4	Assoc.Prof. Nguyen Thi Thu Hoai	International University, VNU-HCMC – Vietnam
5	Assoc.Prof.Dr. Do Tien Duy	Nong Lam University, HCMC,Vietnam
6	Dr. Dinh Xuan Phat	Nong Lam University, HCMC,Vietnam
7	Dr. Nguyen Ngoc Bao Chau	Ho Chi Minh City Open University, HCMC, Vietnam
8	Dr. Vu Minh Thiet	Nguyen Tat Thanh University, HCMC, Vietnam
9	Dr. Ngo Ba Duy	Nong Lam University, HCMC, Vietnam
10	Dr. Nguyen Minh Nam	School of Medicine, Vietnam National University Ho Chi Minh City, Vietnam
11	Dr. Huynh Chan Khon	International University, VNU-HCMC, Vietnam
12	Dr. Nguyen Cuong	LOBI, VAST, Vietnam
13	Dr. Nguyen Van Phuong	University of Science and Technology Hanoi,Vietnam

Supporting Teams

No	Fullname	Institution
1	Huynh Thuc Quyen	RCID Core Team - International University, VNU-HCMC, Vietnam
2	Tran Doan Hong Ngoc	RCID Core Team - International University, VNU-HCMC, Vietnam
3	Mai Bao Tran	Volunteer of RCID Core Team - International University, VNU-HCMC, Vietnam
4	Ly Nguyen Hoang Trinh	Volunteer of RCID Core Team - International University, VNU-HCMC, Vietnam

PLENARY LECTURES
(Main Hall)

[PO-01] Stitching together an abode for itself by *Mycobacterium tuberculosis*

Tuberculosis (TB), caused by the pathogen *Mycobacterium tuberculosis* (*Mtb*) is a global health challenge. The pathogen is known to alter diverse host physiological processes in order to establish infection and cause pathology. We earlier showed that *Mtb* could alter the pattern of RNA splicing in the host macrophages upon infection[1,2]. Surprisingly, the alteration of host RNA splicing appeared both targeted and global in nature, suggesting a pervasive mechanism for the same. Using a high-throughput screening and a combination of molecular, biochemical, cell biological and microbiological assays, we now establish that select Mtb secreted proteins[3] can alter a key step during the RNA splicing event, which renders the RNA splicing event inefficient causing widespread host RNA-splicing alterations. Interestingly, monocyte transcriptomes from TB patients show severely altered RNA splicing, pointing towards a potential strategy to stratify individuals as sensitive or tolerant to TB upon exposure to the pathogen. Through these results, we establish RNA splicing as a key target of host-pathogen interactions during *Mtb* infections. These results now add to a growing list of pathogenic conditions, including both viral and bacterial infections, where host alternative splicing is targeted by the pathogen[4].

References

1) Kalam, H., Fontana, M.F. and **Kumar, D.*** (2017) Alternate splicing of tranåscripts shape macrophage response to Mycobacterium tuberculosis infection. ***PLoS Pathogens***, **13**, e1006236.

2) Kalam, H., Singh, K., Chauhan, K., Fontana, M.F. and **Kumar, D.*** (2018) Alternate splicing of transcripts upon Mycobacterium tuberculosis infection impacts the expression of functional protein domains. ***IUBMB Life***, **70**, 845-854.

3) Malakar, B, Chauhan, K., Sanyal, P., Naaz, S., Kalam, H., Vivek-Ananth, RP, Singh, LV, Samal, A., **Kumar, D***., and Nandicoori, V.* **(2023)** Phosphorylation of CFP10 modulates Mycobacterium tuberculosis virulence, ***In Press, mBio.*** **(*Co-corresponding).**

4) Chauhan, K., Kalam, H., Dutt, R. and **Kumar, D.*** (2019) RNA Splicing: A New Paradigm in Host-Pathogen Interactions. ***J Mol Biol***. 431 (8), 1565-1575

Speaker: Dhiraj Kumar

Email: dhiraj@icgeb.res.in; dhiraj.kumar@icgeb.org

Position: Group Leader

Affiliation: ICGEB, New Delhi



Biography:

- 2007 PhD, International Centre for Genetic Engineering and Biotechnology, New Delhi
- 2007-2010 Postdoctoral researcher, International Centre for Genetic Engineering and Biotechnology, New Delhi
- 2010-2015 Staff Research Scientist, International Centre for Genetic Engineering and Biotechnology, New Delhi
- 2016- Group Leader, Cellular Immunology Group, International Centre for Genetic Engineering and Biotechnology, New Delhi

[PO-02] Multi-locus sequence analysis (MLSA) system for plant bacterial pathogen diagnosis and a case study with Xanthomonas

MLSA-based approaches are increasingly being applied for the re-evaluation of some plant pathogenic bacterial species[1]. In MLSA analysis, partial sequences of genes coding for proteins with conserved functions ('housekeeping genes') are used to generate phylogenetic trees and subsequently deduce phylogenies[2]. Several molecular marker genes were tested for their amplification ability with Xanthomonas species. This example was chosen because of the importance of Xanthomonas which causes severe disease in many plants and economic loss[3]. And some species of Xanthomonas contain many pathovars that are difficult to diagnose. A DNA database for Xanthomonas species identification by MLSA analysis is developed. This case study reports the technological advances and the methodologies used to classify and identify Xanthomonas bacterial species. Pathogenic safety data sheet (PSDS)[4] for plant pathogenic bacteria, virus, and fungi which is under the development in Korea will be presented.

References

1) Visnovsky, S.B. et al. Using multilocus sequence analysis to distinguish pathogenic from saprotrophic strains of Pseudomonas from stone fruit and kiwifruit. *Eur J Plant Pathol* **155**, 643–658 (2019).

2) Almeida. N. F. PAMDB, a Multilocus Sequence Typing and Analysis database and website for plant-associated microbes *Phytopathology* **100**:208-215 (2010).

1) Mansfield, J. Top 10 plant pathogenic bacteria in molecular plant pathology. *Mol Plant Pathol* **13**:614-629 (2012).

3) Pathogen Safety Data Sheets. https://www.canada.ca/en/public-health/services/laboratory-biosafety-biosecurity/pathogen-safety-data-sheets-risk-assessment.html

Speaker: Seong Hwan Kim

Email: piceae@dankook.ac.kr

Position: Professor

Affiliation: Dankook University



Biography:

- 1997 PhD, University of British Columbia, Canada
- 1998-2000 Postdoctoral Research Fellow, University of British Columbia, Canada
- 2001-2003 Research Associate, University of British Columbia, Canada
- 2003-Present Professor, Dept. of Microbiology, Dankook University, South Korea
- 2008-2010 Chairman of the Industry-Academic Cooperation Committee, Korean Society of Plant Pathology
- 2006-Present Advisory Committee Member for Pest Risk Assessment, Animal and Plant Quarantine Agency, South Korea
- 2019-Present Editor-in-Chief, Journal of Odor and Indoor Environment
- 2022 President, Korean Society of Mycology
- 2023-Present President, Korean Society of Mushroom Science

KEYNOTE TALKS
(Main Hall)

[Keynote 1]

Can Transcriptionally Active Microbes (TAMs) be used for Disease Severity prediction?

Intracellular microorganisms, like viruses, bacteria, and fungi, pose challenges in detection due to their non-culturable forms. Transcriptomic analysis at cellular level enables exploration of distributions and the impact of these microorganisms on host cells, a domain that remains underexplored because of methodological limitations. Single-cell technology shows promise in addressing this by capturing polyadenine-tailed transcripts, since recent studies confirmed polyadenylation in microbial transcriptomes. We utilized single-cell RNA-seq from PBMCs to probe intracellular microbes in Healthy, SARS-CoV-2 positive, and recovered individuals. Amongst 76 bacterial species detected, 16 showed significant abundance differences. *Buchnera aphidicola*, *Streptomyces clavuligerus*, and *Ehrlichia canis* emerged significantly in Memory-B, Naïve-T, and Treg cells. *Staphylococcus aureus*, *Mycoplasma mycoides*, *Leptospira interrogans*, and others displayed elevated levels in SARS-CoV-2 positive patients, suggesting possible disease association. This highlights the strength of single-cell technology in revealing potential microorganism's cell-specific functions. Further research is essential for functional understanding of their cell-specific abundance across physiological states.

References

1) Mehta P, Chattopadhyay P, Ravi V, Tarai B, Budhiraja S, Pandey R*. SARS-CoV-2 infection severity and mortality is modulated by repeat-mediated regulation of alternative splicing. Microbiology Spectrum, 2023. doi.org/10.1128/spectrum.01351-23.
2) Yadav S, Mehta P, Soni J, Chattopadhyay P, Devi P, Habyarimana T, Tardalkar K, Joshi M, Pandey R*. Single-cell RNA-Seq reveals intracellular microbial diversity within Immune cells during SARS-CoV-2 Infection and Recovery. iScience, 2023.
3) Devi P, Kumari P, Yadav A, Tarai B, Budhiraja S, Shamim U, Pandey R*. Longitudinal study across SARS-CoV-2 variants identifies Transcriptionally Active Microbes (TAMs) associated with Delta severity. iScience, 2023. doi.org/10.1016/j.isci.2023.107779.
4) Devi P, Kumari P, Yadav A, Tarai B, Budhiraja S, Shamim U, Pandey R*. Transcriptionally active nasopharyngeal commensals and opportunistic microbial dynamics define mild symptoms in the COVID 19 vaccination breakthroughs. PLOS Pathogens, 2023. doi: 10.1371/journal.ppat.1011160.

Speaker: Rajesh Pandey, PhD

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Position: Professor

Affiliation: CSIR-Institute of Genomics & Integrative Biology



Biography:

- 2020 onwards, Principal Scientist at CSIR-IGIB, Delhi, India.
- 2019-2020, Scientist Fellow at CSIR-IGIB, Delhi, India.
- 2016-2019, Research Scientist at MRC Harwell Institute, Oxfordshire, UK.
- 2012-2016, Project Scientist at CSIR Unit-TRISUTRA, Delhi, India.
- 2012, Visiting Scientist at Johns Hopkins University, Maryland, USA.
- 2011, PhD from CSIR-IGIB, Delhi, India.

[Keynote 2]
Development of diverse diagnostic tools to understand poultry diseases.

Spotty Liver Disease (SLD) currently poses significant challenges for the Australian poultry industry and many others, compromising hen welfare and leading to increased mortalities and egg production losses (10-25%). The cost of SLD can be up to 95 million dollars for the Australian poultry industry each year and at least 16 billion dollars for the 33 billion chickens used for egg production globally. Although the disease was first reported in the USA during the 1950s, the causative organism was only recently identified as a novel *Campylobacter* species, *Campylobacter hepaticus*. Additionally, a new species, *C. bilis*, has been found to be the cause of the disease, revealing the complexity of SLD.

This talk will describe the development of various diagnostic tools to understand this significant disease in poultry, including the use of whole-genome sequencing data to develop different types of PCRs to detect *C. hepaticus* DNA (for the detection of current infection) and differentiate it from common *Campylobacter* spp. in poultry. Furthermore, the development of two Enzyme-Linked Immunosorbent Assays for detecting *C. hepaticus* antibodies, hence for the detection of current and past infection, will be discussed, along with 16S rRNA metagenomic sequencing to study how SLD affects chicken gut microbiota. The tools aid in understanding the epidemiology of the disease, developing treatment, and have been globally utilized in studying this significant poultry disease.

References

1) Tudor, D.C. (1954). A liver degeneration of unknown origin in chickens. Journal of the American Veterinary Medical Association, 125, 219–220.
2) Van TTH et al. (2016). Campylobacter hepaticus sp. nov., isolated from chickens with spotty liver diseas. *Int J Syst Evol Microbiol, 66*, 4518-4524. https://doi.org/10.1099/ijsem.0.001383
3) Phung et al. (2022). Int J Syst Evol Microbiol. 72(4). doi: 10.1099/ijsem.0.005314
4) Van TTH et al (2022). Campylobacter bilis, the second novel Campylobacter species isolated from chickens with Spotty Liver Disease, can cause the disease. Vet Microbiol, 276:109603. doi: 10.1016/j.vetmic.2022.109603.

Speaker: A/Prof. Thi Thu Hao Van

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Position: Vice Chancellor's Principal Research Fellow

Affiliation: RMIT University, Australia



Biography:

- A/Prof. Thi Thu Hao Van obtained an undergraduate degree in Food Technology from Victoria University and a PhD in Molecular Microbiology from RMIT University, Australia. She is currently a Vice Chancellor's Principal Research Fellow at RMIT University. She has led impactful industry related research, gaining recognition nationally and internationally. Her areas of expertise include gut microbiota characterisation and manipulation, genomics, identification of bacterial pathogens and deciphering their biology, and developing intervention strategies to combat bacterial diseases and improve gut health, including development of probiotics, postbiotics, fermented food and vaccines.

[Keynote 3]
Translating the uses of molecular techniques into routine diagnostics

In recent years, in Vietnam, the incidence and mortality of hepatitis B (HBV) related hepatocellular carcinoma (HCC) rank second after lung cancer. Although HCC patients diagnosed at early stages or patients who are free of liver cirrhosis (LC) have a good chance of a successful curative operation, however, the 5-year overall survival for all HCC patients is still lower than 10% in Vietnam. The high mortality rate of HCC is due to the lack of suitable tools for early detection, inadequate understanding of the molecular features and genomic traits, and resistance to chemotherapy. Therefore, the implementation of effective and reliable strategies to survey the risk populations (HBV carriers) and to detect HCC at an early stage could improve the survival of patients with this disease. For this purpose, new biomarkers with better accuracy or with capabilities to complement hepatic imaging are desirable to improve early detection and surveillance of HCC. Recently, next generation sequencing (NGS) technologies have been used to identify the genomic landscape and key pathways that contribute to the aetiology of hepatocellular carcinoma. However, acquired changes within the cancer under therapy can alter the mutational spectrum and its responsiveness to therapies, which may require repeated tumor biopsies in the future to guide therapy. Biopsies are invasive and costly and only provide a snapshot of mutations present at a given time and location. To accurately monitor a patient's clinical presentation and properly drive the therapeutics regimens, it is essential that the patient's mutational profile is recorded in a kinetics manner during treatment. It is hypothesized that cell free DNA (cfDNA) can be used as a novel genetic biomarker to predict tumor load, early disease recurrence and therapeutic response in various cancer entities including HCC. So far only little is known about the role of cfDNA in treatment and follow-up of HCC. cfDNA has the advantages that it can be isolated from a simple blood sample and can be easily integrated in standard follow up procedures. Under the directionship of Dr Trung (he got dozen international peer-review papers and lots of national patented files in the field of molecular diagnostics), The Centre of Genetics Counsulation & Cancer Screening – (CGC) of the 108 Military Central Hospital will put the effort to analyze cell free DNA from Vietnamese patients with regards to 1) quantity – the amount of cfDNA will be measured and correlated to the clinical course and 2) quality – somatic mutations, identified by whole genome sequencing of the patient's tumor tissue and patients ctDNA, will be monitored during therapy and follow-up and to transfer of knowledge of advanced genomics technologies to the next generation of Vietnamese young researchers.

References

1) Trung, et al 2020, Clinical significance of combined circulating TERT promoter mutations and miR-122 expression for screening HBV-related hepatocellular carcinoma
2) Trung, et al 2018, Optimisation of quantitative miRNA panels to consolidate the diagnostic surveillance of HBV-related hepatocellular carcinoma

Speaker: Dr. Ngo Tat Trung
Email: tatrungngo@gmail.com
Position: Director
Affiliation: 108 Military Hospital, Hanoi, Vietnam



Biography:

- 1996-2001: Undergraduate in Biochemical Engineering Hanoi University of Technology
- 2004-2006 Master studies in Molecular Biology & Biochemistry, Bremen University, Germany
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- 2018 until now, Dr Ngo Tat Trung is the director of Centre for Genetics Counsulation and Cancer Screening, he is also a principal investigator in the scope of molecular genetics and molecular medicine, Dr Trung acquires the functions to establish molecular diagnostics methods for tracking various pathological conditions of infectious disease or cancer related genetics lesions.

[Keynote 4]
Organoid based drug discovery and development; From science to Industry

"Organoid," referring to 3D mini-organs produced from human tissues or stem cells, exhibits similarities in terms of cells, structures, and functions with actual organs. Organoids can replicate various organs, including the liver, intestines, brain, skin, and even tumors, achieving a high degree of similarity to the human body. By utilizing organoids, it is anticipated that the efficiency of drug development can be significantly improved by conducting accurate toxicity and efficacy evaluations in preclinical trials. Furthermore, organoids have recently found applications in validating the effectiveness of cosmetics and dietary supplements, expanding their influence across various industries. Additionally, when organoids are transplanted into damaged areas, they have a direct regenerative effect, garnering significant attention as regenerative therapies. In this lecture, we aim to cover the entire spectrum of organoids, from their fundamentals to their commercialization, given their increasing importance in various fields.

References

1) 1. Hahn S, Nam MO, Noh JH, Lee DH, Han HW, Kim DH, Hahm KB, Hong SP, Yoo JH, Yoo J, Organoid-based epithelial to mesenchymal transition (OEMT) model: from an intestinal fibrosis perspective, Scientific Reports, May 26 2017; 7:2435 (Correspondence)
2) 2. Koo JB, Nam MO, Jun Y, Yoo J, Kim DH, Kim G, Shin SJ, Lee KM, Hahm KB, Kim JW, Hong SP, Lee KJ, Yoo JH, Anti-fibrogenic effect of PPAR-γ agonists in human intestinal myofibroblast, BMC gastroenterology, Jun 7 2017; 17:73 (Co-author)
3) 3. Hahn S, Yoo J, Gastrointestinal Epithelial Organoid Cultures from Post-Surgical Tissues, Methods in Molecular Biology volume "Organoids: Stem Cells, Structure, and Function", Aug 17 2017; Epub (Correspondence)
4) 4. Nam MO, Hahn SJ, Jee JH, Hwang TS, Yoon H, Lee DH, Kwon MS, Yoo J, Effects of a small molecule R-spondin-1 substitute RS-246204 on a mouse intestinal organoid culture, Oncotarget, Dec 25 2017; Epub (Correspondence)
5) 5. Park MJ, Park HS, You MJ, Yoo J, Kim SH, Kwon MS, Dexamethasone induces a specific form of ramified dysfunctional microglia, Mol Neurobiol, Jun 2018; Epub (Co-author)
6) 6. ¬¬¬¬¬¬Han HW, Hahn S, Jeong HY, Jee JH, Nam MO, Kim HK, Lee DH, Lee SY, Choi DK, You JH, Min SH, Yoo J, LINCS L1000 dataset-based repositioning of CGP-60474 as a highly potent anti-endotoxemic agent, Scientific Reports, Oct 2018 (Correspondence)
7) 7. Hahn S, Kim MS, Jung SI, Jee JH, Nam MO, Kim HK, Jung SY, Shin H, Park JS, Yoo J, Leucine-rich repeat-containing G-protein coupled receptor 5 enriched organoids under chemically-defined growth conditions, BBRC, Jan 2019 (Correspondence)
8) 8. Jee JH, Ko J, Lee DH, Hahn S, Choi SY, Jeong S, Jeong SY, Kim HK, Cho HJ, Park E, Kwon MS, Yoo J, In vivo evaluation of scaffolds compatible for organoid engraftments onto injured mouse colon epithelium, FASEB, Jul 2019 (Correspondence)
9) 9. Jee JH, Ko J, Jeong SY, Kim HK, Yoo J, Development of Collagen Based 3D Matrix for Gastrointestinal Tract- Derived Organoid Culture, Stem Cell Int, Apr 2019 (Correspondence)
10) 10. Park E, Kim HK, Jee JH, Hahn S, Jeong S, Yoo J, Development of organoid-based drug metabolism model, Toxicol Appl Pharmacol, Nov 2019 (Correspondence)
11) 11. Park MJ, Park HS, You MJ, Yoo J, Kim SH, Kwon MS, Dexamethasone Induces a Specific Form of Ramified Dysfunctional Microglia, Molecular neurobiology, 2019 (Co-author)
12) 12. Kyungmin Ko, Chae Won Lee, Sangmin Nam, Song Vogue Ahn, Chi Yong Ban, Jungho Bae, Jongman Yoo, Jungmin Park, Hyun Wook Han, Epidemiological Characterization of a Directed and Weighted Disease Network: Network Analysis Using One Million Cohort Data, JMIR, Mar 2020 (Co-author)
13) 13. Kim. A, Lee SK, Parupudi T, Rahimi R, Song SH, Park MC, Islam S, Zhou J, Majumdar AK, Park JS, Yoo J, Ziaie B, An Ultrasonically Powered Implantable Microprobe for Electrolytic Ablation, Scientific reports, 2020 (Co-author)
14) 14. Kwon MS, You MJ, Park HS, Yang B, Jang B, Yoo J, Hwang DY, Kim MY, Kim B, Lee SH, , Human umbilical cord-derived mesenchymal stem cells alleviate schizophrenia-relevant behaviors in amphetamine-sensitized mice by inhibiting neuroinflammation, Translational psychiatry, 2020 (Co-author)
15) 15. Jeong SY, Lee S, Choi WH, Jee JH, Kim HR, Yoo J, Fabrication of Dentin-Pulp-Like Organoids Using Dental-Pulp Stem Cells, Cells, 2020 (Correspondence)

16) 16. Han SI, Lee SW, Cho MG, Yoo JM, Oh MW, Jeong B, Kim D, Park OK, Kim J, Namkoong E, Jo J, Lee N, Lim C, Soh M, Sung YE, Yoo J, Park K, Hyeon T, Epitaxially Strained CeO2/Mn3O4 Nanocrystals as an Enhanced Antioxidant for Radioprotection, Advanced Materials, 2020 (Co-author)
17) 17. Jeong SY, Choi WH, Lee S, Park JM, Park M, Lee H, Lew H, Yoo J, Establishment of Functional Epithelial Organoid from Human Lacrimal Glands, Stem cell research & therapy, 2021 (Correspondence)
18) 18. Jee JH, Park JH, Im JH, Kim MS, Park E, Lim T, Kim JH, Ko JS, Jeong SY, Ko SY, Lee JI, Hwang DY, Kim WR, Jeon H, Seo JH, Shin HS, Yoo J, Functional recovery by colon organoid transplantation in a mouse model of radiation proctitis, Biomaterials, 2021 (Correspondence)
19) 19. Lee BE, Kim DK, Lee H, Yoon S, Park SH, Lee S, Yoo J, Recapitulation of First Pass Metabolism Using 3D Printed Microfluidic Chip and Organoid, Cells, 2021 (Correspondence)
20) 20. Kim HK, Kim H, Lee MK, Choi WH, Jan Y, Shin JS, Park JY, Bae DH, Hyun SI, Kim KH, Han HW, Lim B, Choi G, Kim M, Lim YC, Yoo J, Generation of human tonsil epithelial organoids as an ex vivo model for SARS-CoV-2 infection, Biomaterials, 2022 (Correspondence)
21) 21. Go YH, Choi WH, Bae WJ, Jung SI, Cho CH, Lee SA, Park JS, Ahn JM, Kim SW, Lee KJ, Lee D, Yoo J, Modeling pancreatic cancer with patient-derived organoids integrating cancer-associated fibroblasts, Cancers 2022 (Correspondence)
22) 22. Lee JA, Bae DH, Choi WH, Cho CH, Bang YS, Yoo J, Effects of Sevoflurane Exposure on Fetal Brain Development Using Cerebral Organoids, Journal of Molecular Neuroscience, 2022 (Correspondence)
23) 23. Choi WH, Bae DH, Yoo J, Current status and prospects of organoid-based regenerative medicine, BMB Report, 2022 (Correspondence)
24) 24. Joo L, Jeong HY, Bae DH, Jee JH, Choi WH, Kim HY, Kim S, Yang DH, Gee HY, Jeon SG, Roh YG, Yoo J, Prostaglandin F2a analogue, Bimatoprost ameliorates colistin-induced nephrotoxicity, Biomedicine&Pharmacotherapy, 2023 (Correspondence)



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- 2018~, R&D Advisor, CHA Group, Korea
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[Keynote 5]

Development of LAMP based assays for detection of microbial pathogens

Until now, many worldwide scientists have developed numerous techniques for the detection of microbial pathogens, in particularly the use of PCR and realtime PCR based methods, RFLP analysis, ELISA, sequencing and etc. However, those methods are nomally labour and time intensive and can only be undertaken in well-equipped labs. Therefore, an alternative approach known as Loop Mediated Isothermal amplification (LAMP) has been studied and developed so much in the world as a rapid, simple and low cost diagnostic tool for microbial pathogens within one hour of sampling in the field or on-site detection that is appropriate to the poor and developing countries. Herein, we developed LAMP based assays for in-field/on-site detection of microbial pathogens such as phytoplasmas, virus, fungi, and bacteria in plants, animals and human indicating their advantages of LAMP method in comparison with other conventional techniques. The results obtained in our studies will be helpful for practical application of LAMP based diagnostics for the detection and control of diseases in plant, animal and human as well as for the development of new and promising diagnostic system for on-site detection of microbial pathogens in Vietnam.

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- 2010 – 2019: Scientist at the Research Institute for Biotechnology and Environment, Nong Lam University, HCMC, Vietnam
- 2014: Visiting scientist at University of Nottingham, UK
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[Keynote 6]

Exploring Cutting-Edge Approaches for Detecting Antimicrobial Resistance

Antimicrobial resistance (AMR) presents a substantial threat to human health globally, emphasizing the critical need for rapid and accurate identification of resistance. Existing approaches in clinical microbiology for AMR diagnostics and Antimicrobial Susceptibility Testing (AST) are laborous and time-consuming, often leading to the prescription of empirical antimicrobial therapies. This practice contributes to the proliferation of AMR, resulting in elevated mortality rates and heightened healthcare costs. This talk explores the progression of state-of-the-art methods and technologies, organized by key research domains, designed to address the looming AMR crisis through recent advances in diagnostic tools. Traditional AMR detection, surveillance, and AST methods are outlined, followed by an exploration of unconventional approaches, such as whole genome sequencing (WGS), matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) spectrometry, Fourier transform infrared (FTIR) spectroscopy, and microfluidics technology. Additionally, commercially available diagnostic platforms for AST are spotlighted. The talk concludes by offering insights into emerging concepts in technologies and methodologies that have the potential to revolutionize AMR diagnostics.

References

1) Burnham, CA., Leeds, J., Nordmann, P. et al. Diagnosing antimicrobial resistance. Nat Rev Microbiol 15, 697–703 (2017). https://doi.org/10.1038/nrmicro.2017.103.
2) Ritu Banerjee, Robin Patel, Molecular diagnostics for genotypic detection of antibiotic resistance: current landscape and future directions, JAC-Antimicrobial Resistance, Volume 5, Issue 1, February 2023, dlad018, https://doi.org/10.1093/jacamr/dlad018.
3) Muntean, M.M., Muntean, A., Preda, M., Manolescu, L.S., Dragomirescu, C., Popa, M., & Popa, G.L. (2022). Phenotypic and genotypic detection methods for antimicrobial resistance in ESKAPE pathogens (Review). Experimental and Therapeutic Medicine, 24, 508. https://doi.org/10.3892/etm.2022.11435
4) Zakarya Al-Shaebi, Fatma Uysal Ciloglu, Mohammed Nasser, and Omer Aydin. Highly Accurate Identification of Bacteria's Antibiotic Resistance Based on Raman Spectroscopy and U-Net Deep Learning Algorithms. ACS Omega (2022) 7 (33), 29443-29451. https://doi.org/10.1021/acsomega.2c03856.

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- 2020- now: Associate Professor, School of Biotechnology, International University, Vietnam National University Ho Chi Minh City
- 2022- now: Vice Director, Research Center for Infectious Diseases, International University, Vietnam National University, Ho Chi Minh City.

[Keynote 7]
Bacterial Genetics and Omics Exploration to Unveil Molecular Basis of Animal and Human Infectious Diseases

Bacterial infectious diseases are global issues in human health and animal welfare. Antibiotics and antibacterial drugs are widely used and drive the bacterial resistance and virulence. Bacterial phylogenetics helps monitor genetic variation, diversity, and adaptation to different selective pressures. This talk demonstrates the use of genetic typing and sequence analysis methods to examine infectious bacterial diversity from domesticated animals, pets (cats and dogs), and human skin. The examination provides valuable information for infectious bacterial control and molecular manipulation. An example of bacterial co-culture suggests possible regulatory mechanisms to control the infectious bacteria from other bacteria in the community. Also, Omics technologies have astonishingly progressed our understanding of infectious bacteria. Bacterial genomes are fast and efficiently compared to gain insights into genomic differences and molecular components related to bacterial virulence and pathogenesis. Metagenomics offers a holistic view of the bacterial community residing together with the presence or absence of infectious bacteria. Transcriptome and proteome analysis of the bacteria under the co-culture condition indicate molecular candidates that control the growth of pathogenic bacteria. Thus, integrative Omics data and powerful bioinformatics computing will open more opportunities to control diseases caused by these infectious bacteria.

References

1) Hanchanachai, N., Chumnanpuen, P., E-kobon, T. 2022. Effect of conditioned media from *Aeromonas caviae* on the transcriptomic changes of the porcine isolates of *Pasteurella multocida*. BMC Microbiology. 22:272; http://dx.doi.org/10.1186/s12866-022-02683-y.
2) Hanchanachai, N., Chumnanpuen, P., E-kobon, T. 2021. Interaction study of *Pasteurella multocida* with culturable aerobic bacteria isolated from porcine respiratory tracts using coculture in conditioned media. BMC Microbiology. 21: 19. https://doi.org/10.1186/s12866-020-02071-4.
3) Azama, F.M., Zamri-Saadc, M., Rahima, R.A., Chumnanpoen, P., E-kobon, T., Othman, S. 2020. Antigenic outer membrane proteins prediction of *Pasteurella multocida* serotype B:2. Asia-Pacific Journal of Molecular Biology and Biotechnology. 28(4): 102-116.

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- 2007: M.Res (Bioinformatics & Computational Biology), University of Leeds, UK
- 2012: Ph.D. (Infection and Immunity), University of Glasgow, UK
- 2012-present: Assistant Professor, Department of Genetics, Faculty of Science, Kasetsart University, Thailand
- 2018- 2023: Director of the International Undergraduate Program in Bioscience and Technology, Faculty of Science, Kasetsart University, Thailand
- 2020- present: Associate Dean, the Graduate School of Kasetsart University, Kasetsart University, Thailand

[Keynote 8]

Unveiling the Viral Diversity in Indian Garlic Cultivation: A Comprehensive Genomic Study using High-Throughput Sequencing

Garlic (*Allium sativum* L.) is widely utilized as a spice and medicinal plant worldwide due to its rich nutritional and therapeutic attributes. While fungal and bacterial diseases pose significant threats, viral diseases are also of utmost concern in garlic cultivation due to its vegetative propagation method and the transmission of viruses, which result in reduced yields and quality deterioration. Garlic plants often succumb to mixed viral infections in field conditions. In this study, we present the first comprehensive analysis of multiple viruses infecting Yamuna Safed-3 (G282) garlic cultivars in India, approaching genome-level characterization. We employed RNA-sequencing (RNA-Seq) on an Illumina HiSeq 2000 platform, yielding a total of 34,873,376 and 31,497,569 paired-end sequence reads. De novo assembly of garlic transcriptomes produced 131,305 and 108,668 contigs from garlic cloves and leaves, respectively. Our blast analysis confirmed the near-complete genome sequences of several viruses, including Allexiviruses (Garlic Virus A [GarV-A], Garlic Virus B [GarV-B], Garlic Virus D [GarV-D], Garlic Virus E [GarV-E], and Garlic Virus X [GarV-X]), Carlavirus (Garlic Common Latent Virus [GCLV]), and Potyviruses (Onion Yellow Dwarf Virus [OYDV] and Leek Yellow Stripe Virus [LYSV]). We further validated the presence of these viruses in collected field samples using PCR-based methods. However, additional investigations are required to ascertain their roles in symptom development, their nationwide distribution, genetic diversity, and potential yield losses in Indian garlic cultivation. The evidence concerning the prevalence of garlic viruses holds significance for virus indexing to produce virus-free propagative materials and for breeding new garlic cultivars with resistance to the aforementioned viruses.

References

1) Prajapati, M. R., Manav, A., Singh, J., Kumar, P., Kumar, A., Kumar, R., & Baranwal, V. K. (2022). Identification and characterization of a garlic virus E genome in garlic (Allium sativum L.) using high-throughput sequencing from India. Plants, 11(2), 224.
2) Singh, J., Truong, T. N., An, D., Prajapati, M. R., Manav, A., Quoc, N. B., & Baranwal, V. K. (2020). Complete genome sequence and genetic organization of a Garlic virus D infecting garlic (Allium sativum) from northern India. *Acta Virol*, *64*(4), 427-432.
3) Entezari, A., Mehrvar, M., & Zakiaghl, M. (2021). Identification of garlic-infecting leek yellow stripe virus through deep-sequencing analyses from Iran. *VirusDisease*, *32*(3), 595-600.
4) Singh, J., Singh, M. K., Ranjan, K., Kumar, A., Kumar, P., Sirohi, A., & Baranwal, V. K. (2020). First complete genome sequence of garlic virus X infecting Allium sativum-G282 from India. *Genomics*, *112*(2), 1861-1865.

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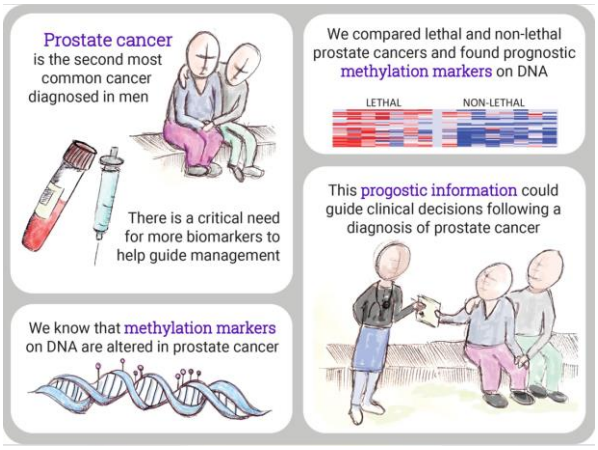
- Jitender Singh, Professor & Head, Department of Microbiology, Ch. Charan Singh University, Meerut, India, specializing in Plant Virology, Microbiology, Molecular Biology and Bioinformatics. His academic journey includes a PDF from University of Queensland, Australia; PhD in Botany [Plant Virology]; M.Sc in Botany; B.Sc in Biology from CCS University, Meerut, India.
- His research spans over two decades, focusing on Viruses and Phytoplasmas Diseases of Horticultural Crops in Western Uttar Pradesh. He holds expertise in various virus groups, including Allexiviruses, Geminivirus, tospoviruses, potyviruses, and carlaviruses. Singh has conducted extensive genomic and

proteomic studies on RNA viruses affecting horticultural crops, exploring molecular characterizations, gene structure-function relationships, and evolutionary studies.

- Singh has contributed significantly to the academic community through editorial roles. He serves as a Review Editor for Frontiers in Virology, a Topic Editor for Frontiers in Genome Editing, and a Guest Associate Editor for Front. Genet. - Plant Genomics. His editorial focus includes emerging genome editing techniques, plant bioinformatics, and cytokinin biology in crop biofortification for enhanced food security.

[Keynote 9]
Clinical Genomics and Epigenomics Testing

More and more genetic and genomic testing are developed and approved to be used in clinic after human genome project finished in 2001. With the emerging of NGS in 2005, the genetic and genomic testing is further advanced and plays an important role in clinical diagnosis and prognosis. Were born later, epigenetic and epigenomic testing are still unmature and in development phase. However, there are a few tests available for several cancers in oncology hospitals (2022). These tests are not only for pronosis and diagnosis but also for monitoring the treatments. In this presentation, Loi will share his own journey of development clinical epigenetic (DNA methylation) markers including tissue and liquid biopsy in some cancers and infection disease using short-read and long-read. In addition, Loi will also show some data of pharmaco-epigenomics in treatment of breast cancer using epigenetics drugs.



Credit: Dr. Kate Patterson

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Biography:

- Dr. Loi is currently an associate lecturer at University of Medicine & Pharmacy HCMC (UMP), Viet Nam. Before moving back Vietnam in 2022, Dr. Loi was a medical researcher at Garvan Institute of Medical Research, Sydney Australia since 2015. He has developed a long-term interest in clinical epigenetics and genomics using the next-generation sequencing (NGS) technologies since his Bioinformatics Master training at the Max Planck Institute for Informatics (2011) and doctoral at the Max Planck Institute for Molecular Biomedicine (2014), Germany. Based on the NGS, Loi has built multiple bioinformatics tools and wet-let protocols for a wide range of studies from mechanism studies to translational research. After moving to Garvan, Loi established his own research topic on translational studies including the roles of DNA methylation on gene expression regulation, pharmaco-epigenomics and epigenetics biomarker development for prognosis, diagnosis and disease progression monitoring in breast, prostate cancer, liver cancer, and rare genetic diseases.

[Keynote 10]
Enhancing Fungal Identification in Environmental and Clinical Samples

Fungi constitute the second-largest group of all organisms, with global estimates suggesting approximately 6 million predicted species. They play vital roles in ecosystems by contributing to nutrient cycling, symbiotic relationships, decomposition, and various other ecological processes. Fungi are essential for maintaining the health and stability of ecosystems. Some fungi are pathogenic and can cause severe diseases in plants, animals, and humans. Accurate and precise identification of fungi from environmental and clinical samples is crucial for gaining insights into the causes and consequences of environmental changes and for finding appropriate treatments for fungal diseases. Fungal identification can be challenging due to the lack of reference DNA sequences. In my talks, I will discuss several methods to enhance fungal identification from environmental and clinical samples, including the use of DNA barcodes and whole fungal genomes.

References

4) Vu, D., Groenewald, M., Szöke., S., et al. (2016). DNA barcoding analysis of more than 9000 yeast isolates contributes to quantitative thresholds for yeast species and genera delimitation. *Studies in Mycology* 85, 91-105.
5) Vu, D., Groenewald, M., de Vries, M., et al. (2019). Large-scale analysis of filamentous fungal DNA barcodes reveals thresholds for species and higher taxon delimitation. *Studies in Mycology* 92, 135-154.
6) Vu, D., Groenewald, M., Verkley, G. (2020). Convolutional neural networks improve fungal classification. *Scientific reports* 10 (1), 1-12.
7) Vu, D., Nilsson, H., Verkley, G. (2022). dnabarcoder: an open-source software package for analyzing and predicting DNA sequence similarity cut-offs for fungal sequence identification. *Molecular Ecology Resources* 22 (7).
8) Li, X., Muñoz, J.F., Gade, L., et al. (2023). Comparing genomic variant identification protocols for fungi. *Microbial Genomics* 9 (4).



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- 2007: PhD, Computer Science, University of Amsterdam, The Netherlands
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INVITED SPEAKERS

Infectious diseases and pathology

Main Hall

[IO-01] Selective Detection of HBV Pre-Genomic RNA in Chronic Hepatitis B Patients Using a Novel RT-PCR Assay

In the realm of chronic hepatitis B (CHB), the quantification of Hepatitis B Virus (HBV) pregenomic RNA (pgRNA) in plasma has emerged as a pivotal avenue for gaining profound insights into disease prognosis and assessing liver injury and histopathology. The complexity arises from the coexistence of HBV DNA within plasma samples, posing significant technical challenges for pgRNA detection.

Our research endeavors culminated in the successful development of a groundbreaking one-step RT-PCR assay, meticulously designed to facilitate the discerning quantification of HBV pgRNA. This comprehensive study engaged two distinct participant cohorts, each with its unique attributes: treatment-naïve CHB patients and HBeAg-positive CHB patients currently undergoing Tenofovir treatment. A subsequent 6-month monitoring phase was meticulously orchestrated to gauge the prognostic potential of baseline HBV RNA in facilitating HBeAg seroclearance. To bolster the robustness of our findings, we harnessed the power of statistical analysis using the sophisticated MedCalc version 20.019 software.

In the course of our investigation, the innovative one-step RT-PCR assay underwent rigorous validation, boasting an impressive limit of detection set at 100 copies/mL. Remarkably, this assay exhibited the capability to accurately and specifically measure HBV pgRNA levels, even in the presence of a formidable abundance of HBV rcDNA. Our observations within treatment-naïve CHB patients unveiled a noteworthy distinction: the levels of HBV pgRNA were notably lower than the concurrent concentration of HBV DNA. Furthermore, our findings unveiled a robust positive correlation between serum HBV DNA levels and the HBeAg status with the presence of HBV pgRNA. Particularly, the baseline serum HBV-RNA levels emerged as resilient predictors of subsequent HBeAg seroclearance after the six-month tenure of Tenofovir treatment.

In conclusion, our study introduces an innovative and robust RT-PCR assay that adeptly and accurately quantifies plasma HBV pgRNA in patients grappling with chronic hepatitis B, even when coexisting with a substantial load of HBV DNA. This remarkable selectivity represents a notable advancement, heralding the potential for pioneering discoveries in the realm of comprehending the clinical significance of HBV pgRNA.

References

1 Cloherty G, Butler E, Kuhns M. "Serum Hepatitis B Virus RNA as a Potential Diagnostic Biomarker During Chronic Hepatitis B Virus Infection." Clinical liver disease, 2019;13:90-92.

2 Wang J, Yu Y, Li G, Shen C, Meng Z, Zheng J, et al. "Relationship between serum HBV-RNA levels and intrahepatic viral as well as histologic activity markers in entecavir-treated patients." J Hepatol, 2017.

3 van Bommel F, Bartens A, Mysickova A, Hofmann J, Kruger DH, Berg T, et al. "Serum hepatitis B virus RNA levels as an early predictor of hepatitis B envelope antigen seroconversion during treatment with polymerase inhibitors." Hepatology, 2015;61:66-76.

4 Wang J, Shen T, Huang X, Kumar GR, Chen X, Zeng Z, et al. "Serum hepatitis B virus RNA is encapsidated pregenome RNA that may be associated with the persistence of viral infection and rebound." J Hepatol, 2016.

5 Shi Liu, Juan D. Valdes, and Jian Sun. "Serum HBV RNA: A New Potential Biomarker for Chronic Hepatitis B Virus Infection." Hepatology, 2019;69:1365-1848.

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[IO-02] Unveiling F12 as a Pioneer Biomarker for Early Detection, Prognosis, and Personalized Treatment in Hepatocellular Carcinoma

Hepatocellular carcinoma (HCC), a global health challenge, demands a paradigm shift in biomarker exploration for improved early diagnosis, prognosis, and precision treatments. This presentation navigates the uncharted realm of the F12 gene's potential as a revolutionary HCC biomarker. Utilizing extensive datasets from GEO and TCGA databases, validated with diverse Vietnamese patient samples, the study provides nuanced insights into F12's efficacy in reshaping HCC diagnostics and patient care. The talk illuminates F12's diagnostic superiority over traditional markers, showcasing lower expression in cancerous tissues and robust accuracy in identifying HCC at very-early and early stages. Validated across diverse demographics, F12 emerges as a universally applicable biomarker. Moving beyond diagnosis, the presentation explores F12's untapped potential in prognostic insights and treatment response predictions. High prognostic indices correlate with enhanced overall and relapse-free survival, underscoring F12's pivotal role in guiding tailored treatment strategies. The speaker unravels F12's nuanced dynamics in predicting optimal responses to specific therapies, providing clinicians invaluable tools for personalized treatment decisions. Join us in deciphering the genetic code of F12, unlocking a new frontier in precision medicine for hepatocellular carcinoma.

References

1) Bertaccini A 2003. http://www.ipwgnet.org/doc/phyto_collection/ collection-august2010.pdf [accessed 20.03.2014].
2) Harrison NA, Rao GP and Marcone C 2008. Characterization, Diagnosis and Management of Phytoplasmas. (Harrison NA, Rao GP, Marcone C, Eds) Studium Press LLC, U.S.A. pp. 1-399.
3) Malembic-Maher S, Salar P, Filippin L, Carle P, Angelini E and Foissac X 2010. Genetic diversity of European phytoplasmas of the 16SrV taxonomic group and proposal of 'Candidatus Phytoplasma rubi'. International Journal of Systematic and Evolutionary Microbiology, DOI 10.1099/ijs.0.025411-0, in press

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- Nov 2006 – Mar 2010: Lecturer, Nong Lam University Ho Chi Minh City, Viet Nam.

[IO-03] Amplification efficiency comparison of different polymerases and application in real-time PCR reaction for the rapid detection of *Clostridium botulinum* serotypes A and B

Botulinum neurotoxins (BoNTs) is considered one of the most potent biological toxins known that can lead to death even in tiny amounts [1]. Soil, water, animal intestines, and food, particularly canned foods have been found to contain the toxin-producing Clostridium strains in both vegetative and sporulated forms. These bacteria produce seven types of toxins, labeled from A to G [2], four of which (serotypes A, B, E, F) are known to cause the high mortality human botulism disease [3, 4, 5]. In Vietnam, *Clostridium botulinum* serotypes A and B have been identified. However, individuals poisoned by the toxin often exhibit unclear symptoms or those similar to other neurological disorders, making diagnosis and treatment very challenging. The method of detecting *Clostridium botulinum* by real-time PCR reaction has high sensitivity and specificity, but the reaction time depends on the amplification rate present in the reaction. Compare 7 polymerases in the real-time PCR reaction to amplify BoNT/A- and BoNT/B encoding genes for the detection of *Clostridium botulinum* serotypes A and B. The fastest reaction completed in less than 45 minutes with the mastermix containing Vazyme's Taqpro polymerase. This could be employed for other targets, especially the acute infectious pathogens advised to acquire prescribed therapies within one hour of medical examination.

References

1) Münchau, A, and K P Bhatia. "Uses of botulinum toxin injection in medicine today." BMJ (Clinical research ed.) vol. 320,7228 (2000): 161-5.
2) Ruoff, K. L. "Streptococcus, Manual of Clinical Microbiology." American Society for Microbiology (2003): 405-421.
3) Arnon, S S et al. "Botulinum toxin as a biological weapon: medical and public health management." JAMA vol. 285,8 (2001): 1059-70.
4) Montecucco, Cesare, and Maria Berica Rasotto. "On botulinum neurotoxin variability." mBio vol. 6,1 e02131-14. 6 Jan. 2015,
5) Montal, Mauricio. "Botulinum neurotoxin: a marvel of protein design." Annual review of biochemistry vol. 79 (2010): 591-617.

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- 2011-current, Lecturer, Vietnam National University, University of Science, Hanoi, Vietnam
- 08-12/2013, USDA Borlaug Fellow, Louisiana State University at Baton Rouge, United States
- 08-09/2015, Visiting Research Scholar, San Diego State University, United States

[IO-04] Application of the Peptide Nucleic Acid Blocker to Improve the Sensitivity of Real-Time PCR for Quantitating JAK2 V617F Mutation

Myeloproliferative neoplasms are a heterogeneous group of diseases characterized by excessive production of blood cells by hematopoietic precursors, typically encompassing four types: polycythemia vera, essential thrombocythemia, myelofibrosis, and chronic myeloid leukemia. The cause of this disorder is genetic mutations in hematopoietic stem cells, including the V617F somatic point mutation in the JAK2 gene. This mutation accounts for about 94.7 – 98% of polycythemia vera, about 50 – 74% of essential thrombocythemia, and 50% of myelofibrosis.

According to WHO 2016, in addition to changes in hematological indicators, detection, and quantification of JAK2 V617F mutations is an important criterion in the prognosis and treatment of myeloproliferative disorders. Techniques being used to detect mutations include allele-specific polymerase chain reaction, allele-specific oligonucleotide polymerase chain reaction, amplification refractory mutation system polymerase chain reaction, and restriction fragment length polymorphism.

To quantify mutations, real-time PCR reactions are used. However, the limitation of accurately detecting and quantifying mutations is the high prevalence of wild genotypes in the sample, which reduces the sensitivity of the reaction.

This research applies a pyrrolidinyl peptide nucleic acid (PNA) blocker to increase the sensitivity of the real-time PCR method to quantify mutations JAK2 V617F. The PNA blocker sequence was designed to complement the wild-type gene and was added to the real-time PCR reaction with different concentrations, from 1, 2, and 3 µM per reaction, to block wild-type amplification.

The results showed that with two µM blockers, the sensitivity was increased significantly, about 100 times at different combinations of wild-type and mutant genotype amplicons.

In conclusion, we developed a highly sensitive JAK2V617F detection and quantification real-time PCR assay by inhibiting amplification of the JAK2 wild-type allele by means of a pyrrolidinyl PNA wild-type blocking oligonucleotide. The blocker could be used to increase the sensitivity of the real-time PCR assay substantially and reliably.

References

1) Boontha, B., Nakkuntod, J., Hirankarn, N., Chaumpluk, P., & Vilaivan, T. 2008. Multiplex mass spectrometric genotyping of single nucleotide polymorphisms employing pyrrolidinyl peptide nucleic acid in combination with ion-exchange capture. Anal Chem, 80(21), 8178-8186. doi:10.1021/ac801336q
2) Charoenpakdee, C., & Vilaivan, T. 2020. Quenching of fluorescently labeled pyrrolidinyl peptide nucleic acid by oligodeoxyguanosine and its application in DNA sensing. Org Biomol Chem, 18(30), 5951-5962. doi:10.1039/d0ob01299h
3) Huijsmans, C. J., Poodt, J., Savelkoul, P. H., & Hermans, M. H. 2011. Sensitive detection and quantification of the JAK2V617F allele by real-time PCR blocking wild-type amplification by using a peptide nucleic acid oligonucleotide. J Mol Diagn, 13(5), 558-564. doi:10.1016/j.jmoldx.2011.04.002
4) McLornan, D., Percy, M., & McMullin, M. F. 2006. JAK2 V617F: a single mutation in the myeloproliferative group of disorders. Ulster Med J, 75(2), 112-119. Retrieved from https://www.ncbi.nlm.nih.gov/pubmed/16755940
5) Percy, M. J., & McMullin, M. F. 2005. The V617F JAK2 mutation and the myeloproliferative disorders. Hematol Oncol, 23(3-4), 91-93. doi:10.1002/hon.761

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INVITED SPEAKERS

Plant and Animal Diseases

Meeting Room 1

[IO-05] Identification and Characterization of Microbial Pathogens in Agriculture Through High Throughput Sequencing

Agriculture, the cornerstone of food production, faces a relentless challenge from microbial pathogens that threaten crop yields, food security, and environmental sustainability. Effective identification and characterization of these agricultural pathogens are essential for implementing targeted disease management strategies. High throughput sequencing (HTS) has emerged as a powerful tool to unravel the complexity of microbial communities within agricultural ecosystems, aiding in the identification, characterization, and monitoring of pathogens. HTS, including next-generation sequencing (NGS) and third-generation platforms, has revolutionized agricultural microbiology. It enables comprehensive assessments of genetic diversity and microbial population dynamics affecting crops, soil, and the agroecosystem. This knowledge empowers researchers to identify known pathogenic species, discover novel threats, and gain insights into virulence mechanisms, host interactions, and environmental factors influencing pathogen dynamics. Applications of HTS in agricultural pathogen identification span viruses, bacteria, fungi, nematodes, and other biotic stressors. Addressing challenges in HTS data analysis, such as data management, quality control, and multi-omics dataset integration, is crucial for informed decision-making for farmers and agronomists. Furthermore, HTS supports sustainable agriculture by enabling precision disease management, reducing pesticide usage, and facilitating disease-resistant crop development. It offers the potential for rapid detection and early warning systems in agricultural settings.

References

1) Villamor, D.E.V., Ho, T., Al Rwahnih, M., Martin, R.R. and Tzanetakis, I.E., 2019. High throughput sequencing for plant virus detection and discovery. *Phytopathology*, *109*(5), pp.716-725.
2) Massart, S., Adams, I., Al Rwahnih, M., Baeyen, S., Bilodeau, G.J., Blouin, A.G., Boonham, N., Candresse, T., Chandellier, A., De Jonghe, K. and Fox, A., 2022. Guidelines for the reliable use of high throughput sequencing technologies to detect plant pathogens and pests. *Peer Community Journal*, *2*.
3) Prajapati, M.R., Manav, A., Singh, J., Kumar, P., Kumar, A., Kumar, R., Prakash, S. and Baranwal, V.K., 2022. Identification and characterization of a garlic virus E genome in garlic (Allium sativum L.) using high-throughput sequencing from India. *Plants*, *11*(2), p.224.
4) Prajapati, M.R., Singh, J., Kumar, P., Kumar, R. and Baranwal, V.K., 2023. Identification of a novel member of the alphaendornavirus genus in Plantago ovata through transcriptome dataset mining. *South African Journal of Botany*, *157*, pp.135-137.

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[IO-06] Fast and reliable method for molecular identification of *Bos Gaurus*, an example of applying animal forensics for wildlife conservation

Gaur is the largest wild animal in the bovine family and one of the largest land animals. The gaur has historically been widely distributed in South and Southeast Asia, but its population has been seriously reduced and is listed as vulnerable in the IUCN Red List. Recorded threats include shrinking habitat due to urbanization, the extent of farming, and, most seriously, poaching due to the high commercial value by rarity. Although gaur has been legally protected by local and international law, forensic science methods, especially modern molecular techniques, have played a key role in research, management, and conservation by high reliability and scientificity for species identification, providing substantial proof for legal actions. Technically, one of the biggest challenges is the specimen's decay when found in the natural scene, which requires intensive analysis effort. In this study, we analyzed 32 whole mitochondrial genomes, including five *Gaurus*, one *Hubacki*, three *Frontalis*, three *Javanicus*, five *Grunniens*, four *Mutus*, two *Primigenius*, five *Taurus*, and five *Indicus* genomes, to find the conserved genetic variants that distinguish the gaur species from other *Bos* species. Then, we designed a multiplex PCR that generate the gaur recognition amplicon and a mitochondrial universal amplicon, serving as an amplification control. We optimized and validated our design by direct PCR on tissue lysates from samples obtained with various degrees of degradation. This method successfully identified gaur from other bovine samples without DNA extraction. Furthermore, we enhance the method's portability by combining portable mini PCR, a handful device, and fluorescent dye-mediated monitoring of amplification products, allowing for the convenient deployment of gaur identification in the field. We hope this method can be applied broadly to contribute to the research, management, and conservation of the gaur by enabling quick and reliable identification.

References

1) Ahrestani, F.S., 2018. Bos frontalis and Bos gaurus (Artiodactyla: Bovidae). Mammalian Species 50, 34–50. https://doi.org/10.1093/mspecies/sey004
2) Duckworth, J.W., Sankar, K., Williams, A.C., Samba Kumar, N. & Timmins, R.J. 2016. Bos gaurus. The IUCN Red List of Threatened Species 2016: e.T2891A46363646. https://dx.doi.org/10.2305/IUCN.UK.2016-2.RLTS.T2891A46363646.en.

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- 2010-2015, PhD, Konkuk University, Seoul, Korea

[IO-07] Immunosensor development: antibody conjugation matters

Antibody immobilization is an important step in developing immunosensors. To achieve high sensitivity and low detection limits, antibodies need to be immobilized in a stable and oriented manner. The ideal orientation of antibodies should allow the fragment antigen-binding region of antibodies to be exposed, thus the fragment crystallizable (Fc) region is often chemically modified, which is complicated, costly, and can potentially affect the structure of antibodies. A simpler way to orientate antibodies is by utilizing staphylococcal protein A since it is capable of binding to the Fc region of immunoglobulins, especially IgGs. Furthermore, to increase the binding capability with sensor surfaces, protein A can be fused with different material-binding proteins/peptides resulting in a two-headed linker protein for simple and effective antibody immobilization. Protein A was fused with a nitrocellulose-binding anchor protein 3-Helix - a protein that has a high affinity for nitrocellulose membrane to form protein A-3-Helix; protein A was also fused with a gold-binding peptide - a peptide with a high affinity for the gold surface to form proAx1-Au-binding. The two novel proteins were cloned and expressed in Escherichia coli strains. The binding characteristics of these two proteins were evaluated and compared with protein A alone. The results showed the potential application of protein A-3-Helix in the immobilizing antibody on the test strip while proAx1-Au-binding had a higher affinity for AuNPs than protein A alone, thereby enhancing antibody immobilization onto gold nanoparticles. This laid the groundwork for facilely preparing any target-specific antibody.

References

1) Tran-Nguyen, T. S., Ngo-Luong, D. T., Nguyen-Phuoc, K. H., Tran, T. L., & Tran-Van, H. (2021). Simultaneously targeting nitrocellulose and antibody by a dual-headed protein. Protein Expression and Purification, 177, 105764.

2) Doan-Tran T. D., Nguyen T. T., and Tran-Van H. (2023). Generation and evaluation of gold-binding peptide fused protein A. Jordan J. Biol. Sci., 16(4).

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- Field of research: Biosensors, NGS, Oral vaccine, Structural biology

[IO-08] Molecular Identification of 16SrIX group of Phytoplasma associated with Ash gourd in Eastern Uttar Pradesh in India

The Cucurbitaceae family member *Benincasa hispida* (Thunb), sometimes known as ash gourd or wax gourd, is widely cultivated in tropical and subtropical regions of the world. Ash gourd plants are widely cultivated in Asian nations for their edible fruits, which are also valued for their therapeutic and dietary benefits. The aim of this work was to identify and characterize phytoplasma utilizing PCR assay, in vitro RFLP analysis and phylogenetic study in symptomatic ash gourd vegetable crop from Eastern Uttar Pradesh state of India. Ash gourd plants revealed phytoplasma suspected indications of witches broom during a survey in the month of July 2020 at eastern Uttar Pradesh, India, and witches' broom was gathered. For a genetic study, four asymptomatic and four symptomatic samples were processed. The CTAB approach was applied to the leaf midrib to extract DNA (Ahrens and Seemuller 1992). PCR amplification was carried out using phytoplasma-specific primer pairs P1/P7 (Deng and Hiruki 1991; Schneider et al. 1995). Following nested PCR utilizing R16F2n/R2 primers (Gundersen and Lee 1996) the amplified PCR product were electrophoresed for 1 hour in 1% agarose gel in Tris-borate-EDTA buffer and the gel was examined in a transilluminator (HI-UVTMMAX, Himedia). The phytoplasmas associated with ash Gourd witches' broom (AGW) had their 16S rRNA gene products amplified.

Using various bioinformatics tools (Bioedit, Clustal W, and MEGA X), the resulting sequence were aligned with ribosomal group/subgroup of phytoplasmas that are accessible in GenBank. The software MEGA 10 was used to create a phylogenetic tree using the maximum likelihood (ML) technique (Kumar et al. 2018). Underwent virtual RFLP analysis of 16S rRNA sequence using iPhyClassifier tool (Zhao et al. 2009). Witches'-broom (AGW) symptoms in ash gourd plants were seen in 2020 at the Eastern Uttar Pradesh, India, with a disease incidence of 5%. Through PCR amplification of approximately 1.2 kb products in nested PCR experiments with primers R16F2n/R2, the presence of phytoplasma was verified in all three symptomatic ash gourd samples.

The 16S rRNA sequences of the phytoplasma isolate from ash gourd witches broom were compared pairwise with phytoplasmas from various groups that were found in the NCBI database, and the results revealed that the AGW strains had 99–100% similarity with strains related to "Candidatus Phytoplasma phoenicium." The relationship between the 16SrIX group and the AGW isolate was verified by a phylogenetic tree. In contrast to the patterns of all previously recognized 16Sr groups and subgroups, the virtual RFLP pattern produced from the query 16S rDNA F2nR2 fragment. greatest similarity (0.97 similarity coefficient) with the reference pattern of 16Sr group IX, subgroup J , The ash gourd is a popular vegetable crop and a significant medicinal plant in the world. The recording of phytoplasma disease establishment on this crop unquestionably adds depth to the investigation of the variety of phytoplasmas. To comprehend the epidemiology of the illness, more research is required, and appropriate management should be devised.

References

1) Ahrens U, Seemüller E (1992) Detection of DNA of plant pathogenic mycoplasma like organisms by a polymerase chain reaction that amplifes a sequence of the 16S rRNA gene. Phytopathology 82:828–832
2) Deng S, Hiruki C (1991) Amplifcation of 16S rRNA genes from culturable and non-culturable mollicutes. J Microbiol Methods 14:53–61
3) Gundersen DE, Lee IM (1996) Ultrasensitive detection of phytoplas mas by nested PCR assays using two universal primer pairs. Phy topathol Mediterr 35:144–151
4) Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGAX: Molecular Evolutionary Genetic Analysis acrossComputing Platforms. Molecular biology and evolution,35(6):1547–1549

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INVITED SPEAKERS

New technologies and microbial Genomics

Meeting Room 2

[IO-09] A pilot exploration of gut microbiota diversity in colorectal cancer patients using 16s rRNA sequencing

Approximately 100 trillion microorganisms belonging to 1000 bacterial species resided in adult human gut[1]. As its important role in maintaining human health, many studies have been conducted to investigate the association of gut microbiota with human disease[2,3]. This study aimed to investigate gut microbiota composition and diversity in colorectal cancer patients (CRCs) compared to healthy controls by 16s rRNA sequencing in feacal samples. Clinical information and feacal samples from 10 newly diagnosed CRCs and 05 healthy control were collected at 108 Central Military Hospital. Total genomic DNA were extracted from feacal samples and subjected to 16S rRNA V3-V4 region sequencing. Bioinformatics and statistical analysis allowed to compare the microbiota composition and diversity between CRC patients and healthy controls. Our study presented CRC patients matched well with healthy controls with respect to age, BMI, gender and hypertension but other clinical characteristics need further investigate a larger sample size. There was no significant difference in alpha and beta diversity between the two groups. The composition of bacterial species belonging to 25 genera, 16 families, and 5 phyla accounted for a high proportion in CRC and healthy samples. The relative abundance of bacterial taxa varied between the two studied groups and also between participants within the same group. In short, initially using 16s rRNA gene sequencing technique, we have successfully determined the composition of gut bacteria to genus. This pilot study works as a good foundation for further analysis in a larger sample size to increase statistical power and to allow for differences between CRC patients and healthy controls to be detected.

References

1) Ahn, J., Sinha, R., Pei, Z., Dominianni, C., Wu, J., Shi, J., et al. (2013). Human gut microbiome and risk for colorectal cancer. J Natl Cancer Inst 105(24), 1907-1911. doi: 10.1093/jnci/djt300.
2) Ley, R.E., Turnbaugh, P.J., Klein, S., and Gordon, J.I. (2006). Microbial ecology: human gut microbes associated with obesity. Nature 444(7122), 1022-1023. doi: 10.1038/4441022a.
3) Qin, J., Li, R., Raes, J., Arumugam, M., Burgdorf, K.S., Manichanh, C., et al. (2010). A human gut microbial gene catalogue established by metagenomic sequencing. Nature 464(7285), 59-65. doi: 10.1038/nature08821.

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[IO-10] Investigating the circulation of AMR between animals, humans and their environment using (meta)genomics approaches

Antimicrobial resistance (AMR) is an increasing public health concern and threatens decades of infectious disease control efforts. The emergence and spread of AMR are mainly attributed to the overuse of antibiotics, whether in humans, animals, or the environment. We observe the emergence of bacteria resistant to multiple antibiotics, which directly impact human health. Today, we still do not know why and where AMR emerges and how it circulates between humans, animals, and the environment. This information is nevertheless essential for the establishment of effective control strategies. In the framework of the various AMR projects, we aimed at understanding the circulation of AMR at the interface between humans, animals and the environment, with a "One Health" approach. These studies were conducted utilizing genomic and metagenomic sequencing and through the extensive use of bioinformatics workflows.

Enterobacteriaceae strains isolated from patients, animal, and environmental samples, have been submitted to Whole Genome Sequencing (WGS) on the Illumina NovaSeq platform. For analyzing the WGS datasets, we have implemented a bioinformatics workflow: Bacterial Assembly and Antimicrobial Resistance Genes detection In Nextflow (*baargin*). It allows to assemble the genomes, check for contamination, detect the sequences of plasmid origin, identify the Antimicrobial Resistance Genes, annotate the genomes, and perform a pangenome analysis of all the datasets provided to the workflow. I will present some results that we obtained from the genomics and metagenomics approaches, in the context of various projects, notably in South-East Asia.

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- 2017-2021 Researcher, Swedish University of Agricultural Sciences, coordinator of the SLU Bioinformatics Infrastructure (SLUBI)
- 2021-present Researcher, French Research Institute for Sustainable Development (IRD) – MIVEGEC Unit – Montpellier, France

[IO-11] Optimizing Electrode Surfaces in Electrowetting-on-Dielectric-Based Digital Microfluidic Platforms for Automated Molecular Biology Assays

Electrowetting-on-dielectric based digital microfluidics (DMF) has emerged as a promising technology for precise liquid manipulation in miniaturized systems, finding applications in various fields such as healthcare, diagnostics, and chemical analysis. The choice of substrate surface significantly influences the performance and reliability of DMF devices especially when it comes to application on biological samples. This study presents a comprehensive investigation into three surface types to assess their impact on DMF functionality. The study employs a systematic approach, involving surface characterization techniques, wetting behavior analysis, and experimental validation through digital microfluidic operations. Additionally, the study evaluates the long-term stability and durability of DMF devices on each surface type, addressing concerns related to surface degradation and performance degradation over time. Our results reveal distinct advantages and challenges associated with each surface type. Cost effective surface that adheres to standard manufacturing practices as well as environmentally friendly alternative protocols may present challenges in terms of surface uniformity and therefore, may pose issues in achieving optimal electrowetting behavior. In opposite, surfaces exhibit improved smoothness, stability and enhanced electrowetting characteristics come at a higher manufacturing cost. Our study underscores the importance of surface selection in optimizing digital microfluidic systems for diverse applications, paving the way for advancements in this rapidly evolving field.

References

1) Thien Hoang, Bao-Han Ly, Thanh-Xuan Le, Thanh-Thao Huynh, Hoang-Tuan Nguyen, Toi Van Vo, Thi Thu Hien Pham, Khon Huynh. Minimal microfabrication required digital microfluidic system toward point-of-care nucleic acid amplification test application for developing countries. Microsystem Technology 26, 1863–1873 (2020)

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- Field of research: Lab-on-a-chip, microfluidics, Vascular biology

[IO-12] Genomic sequencing and a novel mouse-adapted *Helicobacter pylori* model for hpEastAsia genotype

Different strains of *H. pylori* have a high genetic diversity due to a substantial incidence of intraspecies genetic recombination and mutation. Vietnam has a notable prevalence of *H. pylori* infection and its associated stomach cancer. However, the existing body of knowledge about genomic information of *H. pylori* isolates in Vietnam still needs to be expanded. To investigate the correlation between pathogenicity and the geographic distribution of *H. pylori*, it is essential to acquire a comprehensive genome of the bacterial isolates.

We employed Illumina and Oxford Nanopore sequencing to assemble the complete genome sequence of an *H. pylori* clinical isolate from Vietnam. Combining long-read and short-read sequences results in a single contig of the circular genome of the HP34 isolate with a length of 1,600,602bp. The genome analysis of the HP34 isolate unveiled genetic alterations that conferred resistance to Quinolone, Metronidazole, and Amoxilicin. Also, it revealed that the HP34 was closely related to previously reported *H. pylori* isolates from Vietnam. We then used the isolate to develop a novel mouse-adapted H. pylori model for the hpEastAsia genotype in Vietnam and Southeast Asia. In brief, the high quality of the *H. pylori* genome can be utilized as a novel isolate reference, while the mouse model has significant promise for advancing our understanding and developing region-specific interventions for *H. pylori*-associated diseases.

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organoEZ Media Growth Medium Established for Organoid Culture

Product	Cat No.	Volume	Price(-VAT)
CM-Wnt3a	oscm-001	30 mL	$164
		100 mL	$455
CM-WRN	oscm-002	30 mL	$182
		100 mL	$500
CM-RSPO1	oscm-003	30 mL	$164
		100 mL	$455

organoEZ Protein Growth Factors And Proteins for Organoid Culture

Product	Cat No.	Volume	Price(-VAT)
hRSPO1 human RSPO1 (R-Spondin1)	ospr-001	100 µg	$650
		200 µg	$1,100
		500 µg	$2,300
		1 mg	$4,100
hRSPO3 human RSPO3 (R-Spondin3)	ospr-002	50 µg	$450
		100 µg	$850
		200 µg	$1,300
		500 µg	$2,800
hNOG human NOG (noggin)	ospr-003	100 µg	$600
		200 µg	$850
		500 µg	$1,800
		1 mg	$3,150
hEGF human EGF (epidermal growth factor)	ospr-004	100 µg	$81
		200 µg	$125
		500 µg	$240
		1 mg	$440
hIGF1 human IGF1 (insulin-like growh factor 1)	ospr-005	100 µg	$100
		200 µg	$160
		500 µg	$240
		1 mg	$440
hFGF2 human FGF2 (fibroblast growth factor 2)	ospr-006	100 µg	$240
		200 µg	$450
		500 µg	$860
		1 mg	$1,300

Product	Cat No.	Volume	Price(-VAT)
hFGF4 human FGF4 (fibroblast growth factor 4)	ospr-007	100 µg	$800
		200 µg	$1,100
		500 µg	$2,300
		1 mg	$4,100
hFGF7 human FGF7 (fibroblast growth factor 7)	ospr-008	100 µg	$1,200
		200 µg	$2,000
		500 µg	$3,300
		1 mg	$5,500
hFGF10 human FGF10 (fibroblast growth factor 10)	ospr-009	100 µg	$450
		200 µg	$650
		500 µg	$1,500
		1 mg	$2,700
hHGF human HGF (hepatocyte growth factor)	ospr-010	100 µg	$450
		200 µg	$750
		500 µg	$1,800
		1 mg	$3,200
hNRG1 human NRG1 (neuregulin1)	ospr-011	100 µg	$360
		200 µg	$510
		500 µg	$1,300
		1 mg	$2,300
mEGF mouse EGF (epidermal growth factor)	ospr-012	100 µg	$125
		200 µg	$200
		500 µg	$350
		1 mg	$650

organoEZ ECM Extracellular Matrix Which Maintains A Three-dimensional Structure for Organoid Growth

Product	Cat No.	Volume	Price(-VAT)
GelMatrix	osem-001	100 µg	Coming soon
		500 µg	Coming soon
		1000 µg	Coming soon

Tel. 070-8802-2889
E-mail. organoez@organoidrx.com
kakao. ORGANOIDSCIENCES

SCAN HERE FOR INQUIRY



Vazyme

A Global Supplier Specializing in

Design, Manufacture and Application of

Bioactive Compounds

Innovation in Enzyme Technology

Our mission is to create value for our customers by pursuing the highest standards in quality of products and services.

2012 – 2023

Vazyme (688105.SH) is a global supplier that has been digging deep into the field of bioactive compounds since 2012.

A publicly listed company on the **Shanghai Stock Exchange** in 2021.

Who We Are

Vazyme

Our Vision

For Science For Health

Our Culture

- We care for our customers
- We strive for excellence
- We live by our principles
- We thrive on innovation
- We own our company
- We achieve as a team



CÔNG TY TNHH THIẾT BỊ KHOA HỌC VÀ CÔNG NGHỆ QMEDIC được biết đến là đơn vị phân phối thiết bị, vật tư, hóa chất sinh học phân tử dùng trong xét nghiệm y tế, nghiên cứu khoa học cơ bản và pháp y. QMEDIC tự hào là đối tác của các hãng lớn trên thế giới như QIAGEN GmbH (Đức), VeroGen (Mỹ) ...

QMEDIC đem đến giải pháp toàn diện về sinh học phân tử cho các phòng lab với đa dạng quy mô

- Thiết bị & hóa chất tách chiết, tinh sạch DNA/RNA
- Thiết bị & hóa chất phân tích nồng độ DNA/RNA tự động
- Thiết bị & hóa chất chuẩn bị phản ứng tự động, dùng cho PCR, Realtime PCR, chuẩn bị thư viện NGS...
- Thiết bị & hóa chất phát hiện các tác nhân gây bệnh truyền nhiễm, các đột biến gây bệnh ở người dùng trong chẩn đoán in vitro và các giải pháp pháp y, định danh người...
- Phần mềm phân tích kết quả NGS...

Các giải pháp tiên tiến dùng trong phát hiện các bệnh truyền nhiễm



Hệ thống tách chiết nucleic axit và chuẩn bị mẫu tự động QIAsymphony SP/AS



Hệ thống real time PCR Rotor Gene Q MDx



Hệ thống xét nghiệm real time pcr tự động hoàn toàn



Hệ thống Xét nghiệm Hội chứng lên đến 48 tác nhân

CÔNG TY TNHH THIẾT BỊ KHOA HỌC VÀ CÔNG NGHỆ QMEDIC
Địa chỉ: Tầng 4, Toà nhà D1, ô đất CT2, KĐT Kim Văn - Kim Lũ, P. Đại Kim, Q. Hoàng Mai, Hà Nội
Điện thoại: +84 963520800
Website: www.tbytphuongdong.com.vn

Phương Đông

CÔNG TY TNHH THIẾT BỊ Y TẾ PHƯƠNG ĐÔNG là đơn vị tiên phong và luôn dẫn đầu tại Việt Nam trong lĩnh vực cung cấp thiết bị Y tế bệnh viện. Phương Đông tự hào là nhà phân phối các thiết bị, hóa chất vật tư xét nghiệm đa tác nhân gây bệnh bằng phương pháp sinh học phân tử của hãng Seegene Inc. – Hàn Quốc tại Việt Nam.

- Đậu mùa khỉ
- Nhiễm SARS-CoV-2
- Nhiễm trùng hô hấp
- Nhiễm trùng HPV
- Nhiễm trùng lây qua đường tình dục
- Nhiễm trùng tiêu hóa
- Lao
- Nhiễm trùng tại bệnh viện
- Viêm màng não

Seegene

HỆ THỐNG XÉT NGHIỆM REAL-TIME PCR ĐA TÁC NHÂN CỦA SEEGENE HOÀN TOÀN TỰ ĐỘNG

- Cho kết quả xét nghiệm toàn diện
- Danh mục xét nghiệm đa dạng
- Xét nghiệm định lượng
- Hệ thống tự động hoàn toàn xét nghiệm dựa trên hội chứng
- Quy trình xét nghiệm đơn giản và tối ưu hóa



Hệ thống tự động hoàn toàn
Seegene STARlet-AIOS

CÔNG TY TNHH THIẾT BỊ Y TẾ PHƯƠNG ĐÔNG
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