

ABSTRACT PROCEEDING

The
7th
Rencontres de
Quy Nhon

INTERNATIONAL BIOLOGY CONFERENCE 2024

October, 02-04, 2024
ICISE, Quy Nhon, Vietnam

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Nº	Full name	Academic Title	Institution/Address	Position of Program Chairmanship
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7	Trịnh Duy Chi	Ph.D.	University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam	Member

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5	Phạm Hoàng Nam	Ph.D.	University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam	Member
6	Nguyễn Thị Kiều Oanh	Assoc. Prof. Ph.D.	University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam	Member
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Program Chairmanship: Human Biology

Nº	Full name	Academic Title	Institution/Address	Position of Program Chairmanship
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2	Ngô Thị Hoa	Assoc. Prof. Ph.D	Oxford University Clinical Unit in Ho Chi Minh City, Vietnam	Co-Chair
3	Nguyễn Thị Thu Hoài	Assoc. Prof. Ph.D	International University, Vietnam National University, Ho Chi Minh City, Vietnam	Co-Chair
4	Akira Kurisaki	Prof. Ph.D	Nara Institute of Science and Technology (NAIST), Japan	Co-Chair
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Program Chairmanship: Animal Biology

Nº	Full name	Academic Title	Institution/Address	Position of Program Chairmanship
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4	Jalanie S. Marohomsalic	Ph.D.	Department of Biological Sciences, College of Science and Mathematics, Mindanao State University–Iligan Institute of Technology, Iligan City, Philippines	Member
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6	Thạch Út Đồng	Ph.D.	Ton Duc Thang University, HCMC, Vietnam	Member
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15	Nguyễn Hồng Phương	MA.	Marketing, USTH
16	Nguyễn Thị Phương	M.Sc	Chief Accountant, USTH

Organizers



Organizing Team



Sponsors



EXHIBITORS



Preface

Active scientific exchange is one of the critical factors for the success of scientists from their early education to throughout their careers. Within Vietnam, there are limited opportunities for research funding and qualified scientific conferences for young researchers to update with state-of-the-art technologies and advanced discoveries. With the aim to promote active and professional scientific exchanges among biological researchers, we have formed a network of young Vietnamese biologists via a series of meetings at the International Center for Interdisciplinary Science and Education (ICISE), Quy Nhon, Binh Dinh since 2017. Since then, Four Biology Conferences-LifeScienceLinks 1-4 have been successfully organized during the second week of December with the enthusiastic participation of young and iconic scientists from all over Vietnam.

Continuing this success, to celebrate the 5th year milestone and according to the international year of Basic Science for Sustainable Development 2022, the **Rencontres de Quy Nhon V: International Biology Conference 2022** (RdQIBC2022) was taken place from August 17-19, 2022. Respecting to the growth of the conference, it was scaled up to the international level. Therefore, the young Vietnamese biologists have more chance to connect with other scientists over the world. The 5th edition attracted more than 400 scientists from 18 countries worldwide.

The Rencontres de Quy Nhon VI: International Biology Conference 2023 (BIO2023) has been organized from September 20-22, 2023 with the identified format focusing on focus on the aspects related to the life sciences including humans, animals, plants, and microbiology. The BIO2023 attracted 14 Keynote lectures, 44 Oral presentations, and 101 Posters.

During the past six years, International Biology Conference brought together scientists from more than 30 countries to report research progress and exchange ideas in the life science. As a result, several national and international research teams have been established with great promise. **The Rencontres de Quy Nhon VII: International Biology Conference 2024 (BIO2024)** will cover recent, exciting breakthroughs in multidisciplinary research – pushing current scientific knowledge to address the need of sustainable development in different aspects of life science, environment, and food security.

For the successful organizing, we would like to express our gratitude to all supporters. Without them, this conference could not take place. We thank **Prof. Jean Tran Thanh Van** – President of RDV, Director of ICISE Quy Nhon, **Prof. Le Kim Ngoc** (RDV), and the **Rector Board of USTH** for their bighearted financial support. We are truly grateful to the scientific companies for their partnership and generous support. The special thanks are especially dedicated to ICISE, USTH, RDV, Department of Life Sciences, USTH, National University of Singapore, Nong Lam University – HCMC, Hanoi University of Science – VNU, International University – VNU HCM, Ton Duc Thang University, Tra Vinh University, Tien Giang University, and VNU HCM for their great supports with human resource.

Welcome all of you to the “**Rencontres de Quy Nhon VII: International Biology Conference 2024**” (BIO2024) from October 02 – 04, 2024 at ICISE.

Please join us for a 3-day exciting meeting to discuss cutting-edge science with many of the world’s top scientists. Meet old friends, make new ones, and forge novel collaborations in the beautiful setting and hospitality of Quy Nhon – Happy City.

We thank you for your presence and we wish you all the best at the conference!

Quy Nhon, October 2024

Organizing Committee

Life Science Links

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THE RENCONTRES de QUY NHON VII: INTERNATIONAL BIOLOGY CONFERENCE 2023
FROM CONNECTIONS TO COLLABORATIONS

October 02 – 04, 2024, ICISE, Quy Nhon, Vietnam

Program Overview

Time	Pre-conference day (Tuesday, October 01, 2024)			
10:00 – 16:00	Welcome Invited guests and delegates to Quy Nhon City			
16:00 – 18:00	Registration at Seagull Hotel Welcome sponsors to ICISE and set up exhibition places			
Day 1 (Wednesday, October 02, 2024)				
07:30 – 08:00	Picking up delegates from allocated points to ICISE by buses			
08:00 – 09:00	Registration and Poster hanging (lobby)			
09:00 – 09:40	Opening – Conference Hall 1			
09:40 – 10:30	Group photos & Coffee break			
10:30 – 12:30	Plenary session 1 – Conference Hall 1			
10:30 – 11:10	Plenary Keynote talk 1			
11:10 – 11:50	Plenary Keynote talk 2			
11:50 – 12:30	Plenary Keynote talk 3			
12:30 – 14:00	Lunch @ Dining room, ICISE			
14:00 – 16:05	Concurrent sessions 1			
14:00 – 16:05	Plant Biology Conference Hall 2	Microbiology Conference Hall 1	Human Biology Seminar room 2	Animal Biology Seminar room 1
14:00 – 14:25	Delegate talk 1	Delegate talk 1	Delegate talk 1	Delegate talk 1
14:25 – 14:50	Delegate talk 2	Delegate talk 2	Delegate talk 2	Delegate talk 2
14:50 – 15:15	Delegate talk 3	Delegate talk 3	Delegate talk 3	Delegate talk 3
15:15 – 15:40	Delegate talk 4	Delegate talk 4	Delegate talk 4	Delegate talk 4
15:40 – 16:05	Delegate talk 5	Delegate talk 5	Delegate talk 5	Delegate talk 5
16:05 – 16:30	Coffee break @ Dining room, ICISE			
16:30 – 18:00	Poster parallel sessions 1			
16:30 – 18:00	Plant Biology Eastern Corridor	Microbiology Eastern Corridor	Human Biology Eastern Corridor	Animal Biology Eastern Corridor
16:30 – 18:00	PB_P01 : PB_P08	MB_P01 : MB_P11	HB_P01 : HB_P04	AB_P01 : AB_P04
18:00 – 19:30	Dinner @ Dining room, ICISE & Back to hotel by buses			
End of day 1				

Day 2 (Thursday, October 03, 2024)				
07:30 – 08:30	Picking up delegates from allocated points to ICISE by buses			
08:30 – 11:50	Plenary session 2 – Conference Hall 1			
08:30 – 09:10	Plenary keynote talk 4			
09:10 – 09:50	Plenary keynote talk 5			
09:50 – 10:30	Coffee break @ Dining room, ICISE			
10:30 – 11:10	Plenary keynote talk 6			
11:10 – 12:00	General discussion			
12:00 – 13:30	Lunch @ Dining room, ICISE			
13:30 – 15:35	Concurrent sessions 2			
13:30 – 15:35	Plant Biology Conference Hall 2	Microbiology Conference Hall 1	Human Biology Seminar room 2	Animal Biology Seminar room 1
13:30 – 13:55	Delegate talk 6	Delegate talk 6	Delegate talk 6	Delegate talk 6
13:55 – 14:20	Delegate talk 7	Delegate talk 7	Delegate talk 7	RIVN Talk
14:20 – 14:45	Delegate talk 8	Delegate talk 8	Delegate talk 8	Delegate talk 7
14:45 – 15:10	Delegate talk 9	Delegate talk 9	Delegate talk 9	Delegate talk 8
15:10 – 15:35	Delegate talk 10	General discussion within session		
15:35 – 16:00	Coffee break @ Dining room, ICISE			
16:00 – 17:30	Poster session 2			
16:00 – 17:30	Plant Biology Eastern Corridor	Microbiology Eastern Corridor	Human Biology Eastern Corridor	Animal Biology Eastern Corridor
16:00 – 17:30	PB-P09 : PB-P14	MB-P12 : MB-P23	HB-P05 : HB-P08	AB_P05 : AB_P09
17:30 – 18:00	Free discussion and discover ICISE			
18:00 – 21:00	Gala dinner @ ICISE, & back to the hotel by bus			
End of day 2				

	Day 3 (Friday, October 04, 2024)
07:30 – 08:30	Picking up delegates from allocated points to ICISE by buses
08:30 – 10:30	Plenary session 3 – Conference Hall 1
08:30 – 09:10	Plenary keynote talk 7
09:10 – 09:50	Plenary keynote talk 8
09:50 – 10:30	Plenary keynote talk 9
10:30 – 11:00	Coffee break @ Dining room, ICISE
11:00 – 11:30	General discussion– Conference hall 1
11:30 – 12:30	Conclusion remarks - Awards for the best oral/poster presentation, most active attendee, excellent woman scientist, and active researcher who are Vietnamese minor ethnic people. Certificate awards to the Sponsors and Partners Closing
12:30 – 14:00	Lunch @ Dining room, ICISE
14:00 – 19:00	Excursion & Connection
19:00 –	Freely discover Quy Nhon City and Farwell
End of Program	
<i>This schedule can be adjusted to be fitted to the real situations</i>	

Detailed Program

Day 1 (Wednesday, October 02, 2023)				
06:30 – 07:30	Breakfast at hotels			
07:30 – 08:00	Picking up delegates from hotels to ICISE by buses			
08:00 – 09:00	Welcoming & Registration			
09:00 – 09:40	Opening session – Conference Hall 1			
09:00 – 09:10	Opening speech from Organizing Team <i>Ph.D. NGUYEN Van Phuong – USTH, VAST</i>			
09:10 – 09:40	Opening speech from organizers			
09:10 – 09:40	Prof. Ph.D. Jean TRAN Thanh Van <i>President of The Scientific Association Rencontres du Vietnam (RDV)</i> <i>Director of ICISE</i> Ph.D. NGUYEN Hai Dang <i>Vice Rector of University of Science and Technology of Hanoi (USTH), VAST</i>			
09:40 – 10:30	Group photos & Mini Coffee @ Dining room, ICISE			
10:30 – 12:30	Plenary session 1- Conference hall 1			
<i>Chair: Prof. Ph.D. DUONG Tan Nhut ; Co-Chair: Assoc. Prof. Ph.D. NGUYEN Thien Tao</i>				
10:30 – 11:10	[PS-01] IUCN’s, “One Plan Approach”, “Reverse the Red” and topical conservation zoo campaigns highlighting Vietnam’s unique biodiversity <i>Prof. Ph.D. Thomas ZIEGLER – Zoological Institute of Cologne University, Germany</i>			
11:10 – 11:50	[PS-02] Exploring metabolic polymorphism of antioxidant phytochemicals in plants <i>Prof. Ph.D. Takayuki TOHGE – Nara Institute of Science and Technology (NAIST), Division of Biological Science, Ikoma, Nara, Japan</i>			
11:50 – 12:30	[PS-03] Effect of astaxanthin on gastrointestinal microbiota of the human digestive system <i>Prof. Ph.D. Hui-Min David WANG – Graduate Institute of Biomedical Engineering, National Chung Hsing University, Taiwan</i>			
12:30 – 14:00	Lunch @ Dining room, ICISE			
14:00 – 16:05	Concurrent sessions 1			
14:00 – 16:05	Plant Biology Conference Hall 2	Microbiology Conference Hall 1	Human Biology Seminar room 2	Animal Biology Seminar room 1
16:05 – 16:30	Coffee break @ Dining room, ICISE, & Networking			
16:30 – 18:00	Poster parallel sessions 1			
16:30 – 18:00	Plant Biology Eastern Corridor	Microbiology Eastern Corridor	Human Biology Eastern Corridor	Animal Biology Eastern Corridor
16:30 – 18:00	PB_P01 : PB_P08	MB_P01 : MB_P11	HB_P01 : HB_P04	AB_P01 : AB_P04
18:00 – 19:00	Dinner @ Dining room, ICISE & Back to hotel by bus			
End of day 1				

Day 2 (Thursday, October 03, 2024)				
06:30 – 07:30	Breakfast at hotels			
07:30 – 08:30	Picking up delegates from hotels to ICISE by buses			
08:30 – 11:50	Plenary session 2 – Conference Hall 1			
<i>Chair: Prof. Ph.D. NGUYEN Huy Hoang; Co-Chair: Assoc. Prof. Ph.D. NGUYEN Hai Dang</i>				
08:30 – 09:10	[PS-04] Cancer Research and Nanotechnology <i>Prof. Ph.D. Hui-Min David WANG – Graduate Institute of Biomedical Engineering, National Chung Hsing University, Taiwan</i>			
09:10 – 09:50	[PS-05] Explore antibiotic resistance in environment microbiomes with AI <i>Ph.D. Phuc Loi LUU – Head of Data Science Division, Tam Anh Research Institute</i>			
09:50 – 10:30	Coffee break @ Dining room, ICISE			
10:30 – 11:10	[PS-06] Nanoengineering Technology in Precision Medicine <i>Mr. Chien Ju Louis LEE – General Manager, WIDE Technology Corp. Ltd., Taiwan</i>			
11:10 – 12:00	General discussion			
12:00 – 13:30	Lunch @ Dining room, ICISE			
13:30 – 15:35	Concurrent sessions 2			
13:30 – 15:35	Plant Biology Conference Hall 2	Microbiology Conference Hall 1	Human Biology Seminar room 2	Animal Biology Seminar room 1
15:35 – 16:00	Coffee break @ Dining room, ICISE			
16:00 – 17:30	Poster session 2			
16:00 – 17:30	Plant Biology Eastern Corridor	Microbiology Eastern Corridor	Human Biology Eastern Corridor	Animal Biology Eastern Corridor
16:00 – 17:30	PB-P09 : PB-P14	MB-P11 : MB-P22	HB-P05 : HB-P08	AB_P05 : AB_P09
17:30 – 18:00	Free discussion & discover ICISE			
18:00 – 21:00	Gala dinner @ ICISE & back to hotel by buses			
End of day 2				

Day 3 (Friday, October 04, 2024)	
06:30 – 07:30	Breakfast at hotels
07:30 – 08:30	Picking up delegates from allocated points to ICISE by buses
08:30 – 10:30	Plenary session 3 – Conference Hall 1
<i>Chair: Prof. Ph.D. TRUONG Xuan Lam; Co-Chair: Prof. Ph.D. Hui-Min David WANG</i>	
08:30 – 09:10	[PS-07] Antimicrobial resistance of <i>Streptococcus pneumoniae</i> in Vietnam 2011-2023 – from molecular findings to solutions <i>Ph.D. Thomas KESTEMAN – Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK</i>
09:10 – 09:50	[PS-08] Differentiation of stomach tissue cells from stem cells and their mechanisms <i>Prof. Ph.D. Akira KURISAKI – Laboratory of Stem Cell Technologies, Division of Biological Science, Graduate School of Science and Technology, NAIST, Japan</i>
09:50 – 10:30	[PS-09] Unraveling the role of Ethylene in Petunia flower senescence, seed germination, and abiotic stress tolerance <i>Prof. Ph.D. Aung Htay NAING – Department of Horticulture, College of Agriculture and Life Science, Kyungpook National University, South Korea</i>
10:30 – 11:00	Coffee break @ Dining room, ICISE, Poster session 2 of Microbiology
11:00 – 11:30	General discussion – Conference Hall 1
11:30 – 12:30	Conclusion remarks - Awards for the best oral/poster presentation, most active attendee, excellent woman scientist, and active researcher who are Vietnamese minor ethnic people. Certificate awards to the Sponsors and Partners Closing
12:30 – 14:00	Lunch @ Dining room, ICISE
14:00 – 19:00	Excursion & Connection
19:00 –	Freely discover Quy Nhon City and Farwell
<i>End of Program</i>	

Day 1 (Wednesday, October 02, 2024)	
14:00 – 16:05	Plant Biology: Concurrent session 1 – Conference Hall 2
<u>Chairmanship:</u> Prof. Ph.D. DUONG Tan Nhut – Chair Assoc. Prof. Ph.D. NGUYEN Van Tang – Member Ph.D. MAI Thi Phuong Nga – Secretary	
14:00 – 14:25	[PB-O01] Arabidopsis floral buds are locked through differential growth-induced sepal tip curving Ph.D. TRINH Duy Chi – Department of Life Sciences, University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam
14:25 – 14:50	[PB-O02] Exploring the interactions between food ligands with soybean and zein film proteins: a molecular dynamics study Assoc. Prof. Ph.D. PHAM The Hai – Department of Life Sciences, University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam
14:50 – 15:15	[PB-O03] Optimization of microwave-assisted extraction parameters for total saponin content and antioxidant activity from leaves of <i>Launaea sarmentosa</i> M.Sc. candidate TRAN The Tai – Department of Chemistry, Vinh University, Vinh City, Nghe An province, Vietnam.
15:15 – 15:40	[PB-O04] Characterization of Seed Germination-Promoting Fungi in Cymbidium Orchids Student PHAN Thi Kim Ngan – Faculty of Agronomy, Nong Lam University Ho Chi Minh City, HCMC, Vietnam
15:40 – 16:05	[PB-O05] Innovations and Challenges in Developing a Biodegradable Antimicrobial Film from Agricultural By-Products for Fruit Preservation Student NGUYEN Thi Hong Ngoc – Department of Life Sciences, University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam
16:05 – 16:30	Coffee break @ Dining room, ICISE
16:30 – 18:00	Plant Biology: Poster session 1 (PB-P01 : PB-P08) – Eastern Corridor
<u>Chairmanship:</u> Ph.D. TRINH Ngoc Ai – Chair Ph.D. TRINH Duy Chi – Member Ph.D. LE Quynh Mai – Secretary	
18:00 – 19:00	Dinner @ Dining room, ICISE & Back to hotel by buses
<i>End of day 1</i>	

Day 2 (Thursday, October 03, 2024)	
13:30 – 15:35	Plant Biology: Concurrent session 2 – Conference Hall 1
<u>Chairmanship:</u> <i>Prof. Ph.D. Aung Htay NAING – Chair</i> <i>Ph.D. TRINH Ngoc Ai – Member</i> <i>Ph.D. LE Quynh Mai – Secretary</i>	
13:30 – 13:55	[PB-O06] Creating Emulgel from Medicinal Herbs to Support Treatment of Dermatitis <i>M.Sc. candidate LAM Quang Duc – Division of Medical Biotechnology - Biotechnology Center of Ho Chi Minh city, HCMC, Vietnam</i>
13:55 – 14:20	[PB-O07] GWAS Exploration of Proanthocyanidin and Bran Color Diversity in Vietnamese Landrace Rice <i>B.Sc. LE Hoang Nhat Minh – Department of Life Sciences, University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam</i>
14:20 – 14:45	[PB-O08] Developing tea bag products named “Lục trà sam” from medicinal herbs specifically for diabetic patients <i>M.Sc. candidate NGUYEN Thi Van Anh – Faculty of Biological Sciences - Nong Lam University, Ho Chi Minh City, Vietnam</i>
14:45 – 15:10	[PB-O09] Evaluation of Agarwood Formation Induced by Bacteria Isolated from <i>Aquilaria cumingiana</i> Trees in Albay, Bicol Region of the Philippines <i>M.Sc. candidate Ralph Kenneth ARBES – The Graduate School, University of Santo Tomas, Manila 1015, Philippines</i>
15:10 – 15:35	[PB-O10] Plant Secondary Metabolites on Efflux-Mediated Antibiotic Resistant <i>Stenotrophomonas Maltophilia</i>: Potential of Herbal-Derived Efflux Pump Inhibitors <i>Ph.D. PHAM Hoang Nam – Department of Life Sciences, University of Science and Technology of Hanoi (USTH), VAST, Hanoi, Vietnam</i>
15:35 – 16:00	Coffee break @ Dining room, ICISE
16:00 – 17:30	Plant Biology: Poster session 2 (PB-P09 : PB-P14) – Eastern corridor
<u>Chairmanship:</u> <i>Ph.D. TRINH Ngoc Ai – Chair</i> <i>Ph.D. TRINH Duy Chi – Member</i> <i>Ph.D. MAI Thi Phuong Nga – Secretary</i>	

17:30 – 18:00	Free discussion & Connection
18:00 – 21:00	Gala dinner @ ICISE, & back to hotel by buses
<i>End of day 2</i>	

Day 3 (Friday, October 04, 2024)	
06:30 – 07:30	Breakfast at hotels
07:30 – 08:30	Picking up delegates from allocated points to ICISE by buses
08:30 – 10:30	Plenary session 3 – Conference Hall 1
10:30 – 11:00	Coffee break @ Dining room, ICISE
11:00 – 11:30	General discussion– Conference Hall 1
11:30 – 12:30	Conclusion remarks - Awards for the best oral/poster presentation, most active attendee, excellent woman scientist, and active researcher who are Vietnamese minor ethnic people. Certificate awards to the Sponsors and Partners Closing
12:30 – 14:00	Lunch @ Dining room, ICISE
14:00 – 19:00	Excursion & Connection
19:00 –	Freely discover Quy Nhon City and Farwell
<i>End of Program</i>	

Day 1 (Wednesday, October 02, 2024)	
14:00 – 16:05	Microbiology: Concurrent session 1 – Conference Hall 1
Chairmanship: Ph.D. Thomas KESTEMAN – Chair Ph.D. PHAM Hoang Nam – Member Ph.D. NGUYEN Quang Huy – Secretary	
14:00 – 14:25	[MB-O01] Exploring Antibiotic Resistance Genes from the Microbiome of Barbour's Seahorses and its Habitat Ph.D. candidate Rose Chinly Mae H. ORTEGA-KINDICA Department of Biology and Environmental Science, College of Science, University of the Philippines Cebu, Gorordo Avenue, Lahug, Cebu City, Philippines
14:25 – 14:50	[MB-O02] Evaluating the Effect of Hyperaccumulator Plant and Biochar Intervention in Hg-Contaminated Soil Using Microbial Community Composition as Bioindicator for Soil Health M.Sc. Kryzzyl M. MAULAS Department of Biological Sciences, Mindanao State University- Iligan Institute of Technology, Iligan City, Philippines
14:50 – 15:15	[MB-O03] Scrutinization of plant-based multivalent antigens for subunit vaccine against African Swine Fever Virus M.Sc. NGUYEN Thu Giang Institute of Biotechnology, Vietnam Academy of Science and Technology, Hanoi, Vietnam
15:15 – 15:40	[MB-O04] Administration of Viable <i>Lactocaseibacillus rhamnosus</i> CLR1505 as a Potential Adjuvant for Oral Yeast COVID-19 Vaccine M.Sc. candidate Bainadzma AKMAD The Graduate School, University of Santo Tomas, Manila 1015, Philippines; UST Laboratories for Vaccine Science, Molecular Biology and Biotechnology, Research Center for the Natural and Applied Sciences, University of Santo Tomas, Manila 1015, Philippines
15:40 – 16:05	[MB-O05] Plant secondary metabolites reducing antibacterial resistance: Virtual screening efficiency Ph.D. NGUYEN Phuong Nhung Department of Life Sciences, University of Science and Technology of Hanoi, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet, Cau Giay, Hanoi, Vietnam
16:05 – 16:30	Coffee break @ Dining room, ICISE
16:30 – 18:00	Microbiology: Poster session 1 (MB-P01 : MB-P11) – Eastern Corridor
Chairmanship: Assoc. Prof. Ph.D. NGUYEN Thi Thu Hoai– Chair Ph.D. PHAM Hoang Nam – Member Ph.D. NGUYEN Quang Huy – Secretary	
18:00 – 19:00	Dinner @ Dining room, ICISE & Back to hotel by buses
<i>End of day 1</i>	

Day 2 (Thursday, October 03, 2024)	
13:30 – 15:10	Microbiology: Concurrent session 2 – Conference Hall 1
<u>Chairmanship:</u> Prof. Ph.D. Hui-Min David Wang – Chair Ph.D. PHAM Hoang Nam – Member Ph.D. NGUYEN Quang Huy – Secretary	
13:30 – 13:55	[MB-O06] Agarwood Formation Induced by Fungi Isolated from <i>Aquilaria cumingiana</i> Trees in Albay, Philippines M.Sc. candidate Angeli AGUSTIN The Graduate School, University of Santo Tomas [UST], Manila 1015, Philippines; UST Laboratories for Vaccine Science, Molecular Biology, and Biotechnology, Research Center for the Natural and Applied Sciences, University of Santo Tomas, Manila 1015, Philippines
13:55 – 14:20	[MB-O07] A member of myosin V plays a role in the hyphal growth and virulence of the human pathogenic fungus <i>Mucor lusitanicus</i> Ph.D. TRIEU Anh Trung Hanoi National University of Education, 136 Xuan Thuy, Cau Giay, Hanoi, Vietnam
14:20 – 14:45	[MB-O08] Prevalence of <i>Pseudomonas aeruginosa</i> in the environment and its detection using Loop Mediated Isothermal Amplification Assay B.Sc. LIM Đình Kỳ School of Biotechnology, International University, Vietnam National University HCMC, Vietnam; Vietnam National University, Ho Chi Minh City, Vietnam
14:45 – 15:10	[MB-O09] Antifungal activity of endophytic <i>Burkholderia</i> spp., and curcumin silver nanoparticles against <i>Aspergillus</i> spp. and <i>Fusarium</i> sp. M.Sc. PHAM Thi Thu Trang University of Science and Technology of Hanoi, Vietnam Academy of Science and Technology (VAST); 18 Hoang Quoc Viet Street, Nghia Do Ward, Cau Giay District, Hanoi, Vietnam
15:10 – 15:35	General discussion & connection within session
<u>Chairmanship:</u> Prof. Ph.D. Hui-Min David Wang – Chair Ph.D. PHAM Hoang Nam – Member Ph.D. NGUYEN Quang Huy – Member Assoc. Prof. Ph.D. NGUYEN Thi Thu Hoai – Member	
15:35 – 16:00	Coffee break @ Dining room, ICISE
16:00 – 18:00	Microbiology: Poster session 2 (MB-P12 : MB-P23) – Eastern Corridor

Chairmanship:

Assoc. Prof. Ph.D. NGUYEN Thi Thu Hoai – Chair

Ph.D. PHAM Hoang Nam – Member

Ph.D. NGUYEN Quang Huy – Secretary

18:00 – 21:00**Gala dinner @ ICISE, & back to hotel by buses***End of day 2***Day 3 (Friday, October 04, 2024)**

06:30 – 07:30

Breakfast at hotels

07:30 – 08:30

Picking up delegates from allocated points to ICISE by buses

08:30 – 10:30**Plenary session 3 – Conference Hall 1****10:30 – 11:00****Coffee break @ Dining room, ICISE****11:00 – 11:30****General discussion– Conference Hall 1**

11:30 – 12:30

Conclusion remarks - Awards for the best oral/poster presentation, most active attendee, excellent woman scientist, and active researcher who are Vietnamese minor ethnic people.

Certificate awards to the Sponsors and Partners

Closing

12:30 – 14:00**Lunch @ Dining room, ICISE**

14:00 – 19:00

Excursion & Connection

19:00 –

Freely discover Quy Nhon City and Farwell

End of Program

Day 1 (Wednesday, October 02, 2024)	
14:00 – 16:05	Human Biology: Concurrent session 1 – Seminar room 2
<u>Chairmanship:</u> Assoc. Prof. Ph.D. NGUYEN Hai Dang – Chair Assoc. Prof. Ph.D. NGUYEN Thi Kieu Oanh – Member Ph.D. PHAN Quang Tien – Secretary	
14:00 – 14:25	[HB-O01] The effect of human serum albumin concentration in biphasic in-vitro maturation (CAPA-IVM) B.Sc. NGUYEN Huynh Hue Tuyet IVFMD Phu Nhuan, My Duc Phu Nhuan Hospital, Ho Chi Minh City, Vietnam
14:25 – 14:50	[HB-O02] Waste-derived TiO₂ nanoparticles synthesized from <i>Hordeum vulgare</i> L.: A Bridge for Sustainable Ovarian Cancer Therapy Joining Agriculture to Oncology Ph.D. candidate Shreya CHAKRABORTY Research Scholar, Department of Bio-Medical Sciences, School of Biosciences and Technology, Vellore Institute of Technology, Vellore, Tamil Nadu, India
14:50 – 15:15	[HB-O03] Plant exosomes extracted from <i>Elettaria Cardamomum</i> inhibit Triple-Negative Breast cancer Ph.D. candidate Manosi BANERJEE Research Scholar, Department of Bio-Medical Sciences, School of Biosciences and Technology, Vellore Institute of Technology, Vellore, Tamil Nadu, India
15:15 – 15:40	[HB-O04] Green synthesis of Magnesium Oxide nanoparticles from <i>Musa acuminata</i> and its anti-diabetic effect on <i>Danio rerio</i> model Assoc. Prpf. Ph.D. Devi RAJESWARI V Department of Biomedical Science, School of Bioscience and Technology, Vellore Institute of Technology, Vellore, Tamil Nadu, India
15:40 – 16:05	[HB-O05] Effect of post-warming culture time of vitrified-warmed oocyte on embryological outcomes M.Sc. Nhung Thi Cam NGUYEN IVFMD, My Duc Hospital, Ho Chi Minh City, Vietnam HOPE Research Center, My Duc Hospital, Ho Chi Minh City, Vietnam
16:05 – 16:30	Coffee break @ Dining room, ICISE
16:30 – 18:00	Human Biology: Poster session 1 (HB-P01 : HB-P04) – Eastern Corridor
<u>Chairmanship:</u> Assoc. Prof. Ph.D. NGUYEN Hai Dang – Chair Ph.D. PHAN Quang Tien – Member Assoc. Prof. Ph.D. NGUYEN Thi Kieu Oanh – Secretary	
18:00 – 19:00	Dinner @ Dining room, ICISE & Back to hotel by buses
<i>End of day 1</i>	

Day 2 (Thursday, October 03, 2024)	
13:30 – 15:10	Human Biology: Concurrent session 2 – Seminar room 2
<u>Chairmanship:</u> Prof. Ph.D. Akira KURISAKI – Chair Assoc. Prof. Ph.D. NGUYEN Hai Dang – Member Assoc. Prof. Ph.D. NGUYEN Thi Kieu Oanh – Secretary	
13:30 – 13:55	[HB-O06] Association of <i>Fusobacterium nucleatum</i> with Breast Cancer Progression and Virulence Factor Profiling in South Indian Patients Ph.D. candidate Kiruthika VIJAYAKUMAR Department of Biotechnology, Faculty of Biomedical Sciences and Technology, Sri Ramachandra Institute of Higher Education and Research, (Deemed to be University), Porur, Chennai - 600116, Tamil Nadu State, India
13:55 – 14:20	[HB-O07] A gender-specific role for the chemokine receptor Cxcr3.2 in medaka bone homeostasis Ph.D. PHAN Quang Tien Department of Biological Sciences and Centre for Bioimaging Sciences, National University of Singapore; 14 Science Dr 4, Singapore 117543, S1A-06-05
14:20 – 14:45	[HB-O08] Decoding Vietnam's Measles Epidemic: A Comprehensive Look Since 2010 B.Sc. Kim Ngan NGUYEN School of Biotechnology, International University, Vietnam National University HCMC, Vietnam
14:45 – 15:10	[HP-O09] Lipid nanoparticles for enhancing the therapeutic effectiveness of berberine Ph.D. Van Hong NGUYEN Department of Life Sciences, University of Science and Technology of Hanoi, Vietnam Academy of Science and Technology, 18- Hoang Quoc Viet, Cau Giay, Hanoi, Vietnam
15:10 – 15:35	General discussion & connection
<u>Chairmanship:</u> Prof. Ph.D. Akira KURISAKI – Chair Assoc. Prof. Ph.D. NGUYEN Hai Dang – Member Assoc. Prof. Ph.D. NGUYEN Thi Kieu Oanh – Member	
15:35 – 16:00	Coffee break @ Dining room, ICISE

16:00 – 17:00	Human Biology: Poster session 1 (HB-P05 : HB-P08) – Eastern Corridor
<i>Chairmanship:</i> <i>Assoc. Prof. Ph.D. NGUYEN Hai Dang – Chair</i> <i>Ph.D. PHAN Quang Tien – Member</i> <i>Assoc. Prof. Ph.D. NGUYEN Thi Kieu Oanh – Secretary</i>	
17:00 – 18:00	Free discussion & discover ICISE
18:00 – 21:00	Gala dinner @ ICISE, & back to hotel by buses
<i>End of day 2</i>	

Day 3 (Friday, October 04, 2024)	
06:30 – 07:30	Breakfast at hotels
07:30 – 08:30	Picking up delegates from allocated points to ICISE by buses
08:30 – 10:30	Plenary session 3 – Conference Hall 1
10:30 – 11:00	Coffee break @ Dining room, ICISE
11:00 – 11:30	General discussion– Conference Hall 1
11:30 – 12:30	Conclusion remarks - Awards for the best oral/poster presentation, most active attendee, excellent woman scientist, and active researcher who are Vietnamese minor ethnic people. Certificate awards to the Sponsors and Partners Closing
12:30 – 14:00	Lunch @ Dining room, ICISE
14:00 – 19:00	Excursion & Connection
19:00 –	Freely discover Quy Nhon City and Farwell
<i>End of Program</i>	

Day 1 (Wednesday, October 02, 2024)	
14:00 – 16:05	Animal Biology: Concurrent session 1 – Seminar room 1
<u>Chairmanship:</u> <i>Prof. Ph.D. Thomas ZIEGLER – Chair</i> <i>Assoc. Ph.D. NGUYEN Thien Tao – Member</i> <i>Ph.D. DOAN Thi Ngoc Thanh – Secretary</i>	
14:00 – 14:25	[AB-O01] Effect of Heavy Metals on the Life History Trait of <i>Heterocephalobellus</i> sp. and <i>Cephalobus</i> sp. (Nematode: Cephalobidae) Collected from a Small-Scale Mining Site, Davao de Oro, Philippines <i>M.Sc. Alissa Jane S. MONDEJAR</i> <i>Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Tibanga, Iligan City, 9200 Philippines</i> <i>Center for Natural Products and Drug Discovery, PRISM, Mindanao State University-Iligan Institute of Technology, Tibanga, Iligan City, 9200 Philippines</i>
14:25 – 14:50	[AB-O02] ASGM-impacted Soil Assessment and its Heavy Metal Contamination Influence on the Life History Traits of Free-living Nematodes in a Small-scale Mining Area in Nabunturan Davao de Oro, Philippines <i>M.Sc. Florifern C. PAGLINAWAN</i> <i>Molecular and Developmental Biology Laboratory, PRISM, MSU - Iligan Institute of Technology, Iligan City, Philippines</i>
14:50 – 15:15	[AB-O03] Knowledge, Perception, and Management of Fall Armyworm (FAW) <i>Spodoptera frugiperda</i> Among Farmers in Iligan City, Northern Mindanao, the Philippines <i>Ph.D. Mark Anthony TORRES</i> <i>Center of Integrative Health and Climate Change Laboratory, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Tibanga, Iligan City, 9200 Philippines</i>
15:15 – 15:40	[AB-O04] Displaying Immunostimulants on Gram-Positive Enhancer Matrix (GEM) Particles as Mucosal Adjuvants <i>Ph.D. Thu-Dung DOAN</i> <i>International Degree Program in Animal Vaccine Technology, International College, National Pingtung University of Science and Technology, 1, Shuefu Road, Neipu, Pingtung, 91201 Taiwan</i> <i>Graduate Institute of Animal Vaccine Technology, College of Veterinary Medicine, National Pingtung University of Science and Technology, 1, Shuefu Road, Neipu, Pingtung, 91201 Taiwan</i>
15:40 – 16:05	[AB-O05] Insect Fauna of the Bangsamoro Region and Where to Find Them: Integrative Taxonomy and Strategies for Environmental Tactics <i>Ph.D. Jalandie S. MAROHOMSALIC</i> <i>Biology Department, College of Arts and Sciences, Iligan Medical Center College, San Miguel Village, Palao, 9200 Iligan City, Lanao del Norte, Philippines</i>
16:05 – 16:30	Coffee break @ Dining room, ICISE

16:30 – 18:00	Animal Biology: Poster session 1 (AB-P01 : AB-P04) – Eastern Corridor 1
<u>Chairmanship:</u> <i>Ph.D. DOAN Thi Ngoc Thanh – Chair</i> <i>Ph.D. DOAN Thu Dung – Member</i> <i>Ph.D. THACH Ut Dong – Secretary</i>	
18:00 – 19:00	Dinner @ Dining room, ICISE & Back to hotel by buses
<i>End of day 1</i>	

Day 2 (Thursday, October 03, 2024)	
13:30 – 15:10	Animal Biology: Concurrent session 2 – Seminar room 1
<u>Chairmanship:</u> <i>Assoc. Ph.D. NGUYEN Thien Tao – Chair</i> <i>Ph.D. Jalandie S. MAROHOMSALIC – Member</i> <i>Ph.D. THACH Ut Dong – Secretary</i>	
13:30 – 13:55	[AB-O06] Assessing Interspecific Shape Variability in Two Congeneric Species of Epigeic Tiger Beetles (Coleoptera: Cicindelidae) Using Landmark-Based Geometric Morphometric Analysis. <i>Ph.D. candidate Jamalia M. MACATANONG</i> <i>Biology Department, College of Arts and Sciences, Iligan Medical Center College, San Miguel Village, Palao, 9200 Iligan City, Lanao del Norte, Philippines</i> <i>Department of Biological Sciences, Mindanao State University – Iligan Institute of Technology, A. Bonifacio Avenue, Tibanga, 9200 Iligan City, Lanao del Norte, Philippines</i>
13:55 – 14:20	[RIVN] The Ultra-Sensitive Simoa™ Technology Introduction <i>M.Sc. Ngau NGUYEN</i> <i>Quanterix Company; Everlife - Research Instruments Vietnam</i>
14:20 – 14:45	[AB-O07] Species Diversity, Distribution, and Microhabitat Preferences of Anurans in Forested Areas of Brgy. Napangan, Don Victoriano Chiongbian, Philippines <i>Mr. Junville RULE</i> <i>Northwestern Mindanao State College of Science and Technology, Philippines</i>
14:45 – 15:10	[AB-O08] Snakebite in Northern Vietnam: Statistics from a major hospital with notes on challenges and opportunities <i>M.Sc. Linh Tu Hoang LE</i> <i>Institute of Genome Research, Vietnam Academy of Science and Technology, Hanoi, Vietnam</i>

15:10 – 15:35	General discussion and connection within session
<u>Chairmanship:</u> <i>Prof. Ph.D. Thomas ZIEGLER – Chair</i> <i>Assoc. Ph.D. NGUYEN Thien Tao – Member</i> <i>Ph.D. Jalandie S. MAROHOMSALIC – Member</i> <i>Ph.D. DOAN Thu Dung – Member</i> <i>Ph.D. DOAN Thi Ngoc Thanh – Member</i>	
15:35 – 16:00	Coffee break @ Dining room, ICISE
16:00 – 17:00	Animal Biology: Poster session 3 (AB-P05 : AB-P09) – Eastern Corridor 1
<u>Chairmanship:</u> <i>Ph.D. DOAN Thi Ngoc Thanh – Chair</i> <i>Ph.D. DOAN Thu Dung – Member</i> <i>Ph.D. THACH Ut Dong – Secretary</i>	
17:00 – 18:00	Free discussion & discover ICISE
18:00 – 21:00	Gala dinner @ ICISE, & back to hotel by buses
<i>End of day 2</i>	

Day 3 (Friday, October 04, 2024)	
06:30 – 07:30	Breakfast at hotels
07:30 – 08:30	Picking up delegates from allocated points to ICISE by buses
08:30 – 10:30	Plenary session 3 – Conference Hall 1
10:30 – 11:00	Coffee break @ Dining room, ICISE
11:00 – 11:30	General discussion– Conference Hall 1
11:30 – 12:30	Conclusion remarks - Awards for the best oral/poster presentation, most active attendee, excellent woman scientist, and active researcher who are Vietnamese minor ethnic people. Certificate awards to the Sponsors and Partners Closing
12:30 – 14:00	Lunch @ Dining room, ICISE
14:00 – 19:00	Excursion & Connection
19:00 –	Freely discover Quy Nhon City and Farwell
<i>End of Program</i>	

PLENARY SESSIONS



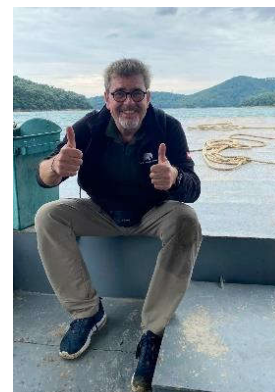
[PS-01] IUCN's, "One Plan Approach", "Reverse the Red" and topical conservation zoo campaigns highlighting Vietnam's unique biodiversity

Thomas ZIEGLER, Ph.D.

Zoological Institute of Cologne University, Germany

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Instagram: [thomas_ziegler_work_group](#)



Abstract: The central theme of Cologne Zoo's Aquarium house, which recently has developed into a species conservation center, is the "*One Plan Approach to Conservation*" by the IUCN/SSC Conservation Planning Specialist Group, which refers to the interaction of different measures involving various expertise and all responsible parties, thus enabling optimized, contemporary species conservation, whether inside or outside the natural range. This includes the discovery of new amphibian and reptile species in the Southeast Asian tropics – you can only protect what is known – to administrative assistance for the conservation authorities in confiscation cases of threatened animals and to the development of conservation breeding programs for invertebrates, fish, amphibians and reptiles classified as threatened with extinction by IUCN Red List. More than 100 of the species kept in Cologne Zoo's Aquarium are threatened according to the IUCN Red List. Concerning the amphibian and reptile species kept, about half of them are listed in the appendices of CITES, 25 of which derive from confiscations. Molecular analyses of rescued animals from official confiscations also provide proper identification and allocation to geographical lineages so that they or their offspring are suitable for repatriation. More than half of the amphibians and reptile species kept (54), with a designated focus on species from Vietnam, are successfully reproduced. Students in the working group carry out analyses in order to be able to promote improved species conservation in an even more targeted manner. This is done, for example, by evaluating zoo databases as a means for improved ex situ measures. Furthermore, endemism analyses are carried out and protected area coverage is examined as a basis for further conservation measures, i.e., inclusion of species in the IUCN Red List, suggestion of the designation of new protected areas, or the establishment of conservation breeding programs. For many species, the keeping and breeding in Cologne Zoo's Aquarium house is linked to projects in the tropics, mainly in Southeast Asia, particularly in Vietnam, but also in the Philippines. Field work for species conservation is performed by means of population and threat analyzes. This is carried out by students and cooperation partners on-site, which allows species to first be assigned an international protection status. There are also cooperation programs with local partners in reserve establishment, building up stations and in-country breeding programs, as well as in terms of release / repatriations of threatened amphibians and reptiles.

[PS-02] Exploring metabolic polymorphism of antioxidant phytochemicals in plants

Takayuki TOHGE, Ph.D.

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Abstract: To acclimate to environmental changes in environmental stress factors, plants produce such antioxidant compounds and pigments. Plant polyphenolic antioxidant compounds are widely diversified in their chemical structures, since during the long evolutionary period wherein plants have adapted to the environmental niches, several strategies such as gene duplication and convergent evolution of some key genes have contributed to the evolution of the plant metabolism. On the other hand, plant polyphenolics are also known as important major components within numerous many herbal plants and health-beneficial vegetables. Utilizing mass spectrometry (MS)-based global metabolomics integrated with genomics and transcriptomics, comprehensively elucidation of target metabolism across closely related species, aiding in productivity of target metabolites and the discovery of novel functional compounds, can be performed. Through MS-based metabolomics-assisted phytochemical surveys of wild plants and their relatives, we identified several metabolic polymorphisms within a class of polyphenolic antioxidants which have can confer greater antioxidant activity and UV absorption. We established a metabolomics-assisted functional genomics approach using model plant species, leading to the discovery of key genes involved in the diversification of metabolic polymorphisms in polyphenolics, and extend our approach to vegetable species as well as herbal plant species. Our findings present the importance of understanding plant polyphenolic metabolism for harnessing the full potential of these compounds in enhancing human health and addressing environmental challenges.

[PS-03] Effect of astaxanthin on gastrointestinal microbiota of the human digestive system

Hui-Min David WANG, Ph.D.

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Abstract: Astaxanthin (polyphenol) was selected as an anticancer drug due to our previous research finding that astaxanthin has extremely high antioxidant, anti-ultraviolet damage, and anti-tumor properties. In recent years, astaxanthin has been confirmed by various medical and biotechnology researchers to have excellent anti-oxidation, vision improvement, immunity enhancement, and even excellent anti-tumor abilities, a large number of related healthcare and nutrition products have gradually come into the market. Polyphenols have beneficial properties for human health, while their biological activities are significantly related to intestinal transformations, particularly the action of microbiota metabolism. On the other hand, studies have highlighted the role of gut microbiota in developing obesity. We found that about 90–95% of the total polyphenols from dietary intake might accumulate in the large intestinal lumen, where the gut microbiota enzymatically digests them. Notably, the composition of microbiota could also be affected by polyphenols. Hence, dietary polyphenols influence the host's health by interacting with the intestinal microbiota. Meanwhile, following the research that a transferrable microbiota could increase body mass in lean mice, numerous studies have shown differences in the microbiota between obese and lean individuals.

References

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[PS-04] Cancer Research and Nanobiotechnology

Hui-Min David WANG, Ph.D.

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Abstract: Cancer is a major global health challenge, and nanomedicine therapies are viewed as potential therapeutic breakthroughs. Nanomedicines are currently a hot research topic in biotech medicine, combined with precision medicine to use environmentally sensitive and multifunctional biomolecules as a precise treatment and tracking platform for cancer-related diseases. They can even customize novel administration dosage forms and drug designs for new development routes on clinically available preparations. Over the past few decades, considerable research interest has been in drug delivery systems using nano-scale vehicles as small biomolecular carriers. Systems like nanoparticles have been used as physical methods to develop various drug-lead compound molecule pharmacokinetic and pharmacodynamic properties. They have been applied *in vivo* to protect the drug in the systemic circulation, increase its reach to specific site locations, and exert its effect at a sustained and stable concentration while minimizing side effects. Studying the molecular mechanism and target pathway of nanocarriers will help clinicians and researchers to understand the role of clinical nanomedicines, improve efficacy, be an essential innovation for developing pioneering targets to overcome drug resistance, and provide information for treating other diseases.

Based on these critical problems and new strategies, our team has successfully searched for tumor protein-protein interaction inhibitors and developed novel nanocarriers to fight cancer over the years.

David Wang's Lab

Tissue Biomedical Engineering & Cancer Translational Medicine Laboratory

Prof. Hui-Min David Wang

Research Interests

Precision medicine; Tissue engineering; Regenerative medicine; Oncology; Drug design; Food chemistry; Skin physiology; Chemical engineering; Biochemistry; proteomics; Molecular biology

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<https://www.scopus.com/authid/detail.uri?authorId=58493103100>

https://scholar.google.com.tw/citations?hl=zh-TW&user=sFFCI7kAAAJ&view_op=list_works

(WANG HUI MIN DAVID)

Website: <https://sites.google.com/site/davidbiocosme/home>

[PS-05] Explore antibiotic resistance in environmental microbiomes with AI

Phuc Loi LUU, Ph.D.

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**Bio**

Dr. Loi currently serves as the head of the Data Science Division at the Tam Anh Research Institute in Vietnam. Prior to relocating to Vietnam in 2023, he worked as a medical researcher at the Garvan Institute of Medical Research in Sydney, Australia, from 2015 to 2023. His interest in clinical epigenetics and genomics using next-generation sequencing (NGS) technologies dates back to his Bioinformatics Master's training at the Max Planck Institute for Informatics in 2011 and his doctoral studies at the Max Planck Institute for Molecular Biomedicine in Germany in 2014. During his post-doc, Dr. Loi developed multiple bioinformatics tools and experimental protocols for diverse studies, ranging from mechanistic investigations to translational research.

At the Garvan Institute of Medical Research, Dr. Loi established his own research program focusing on both fundamental and translational studies. His work explores the interplay of genomics and epigenomics, including DNA methylation, histone modification, and non-coding RNA, in regulating cancer gene expression. He has also contributed to pharmacogenomics and pharmaco-epigenetics, developing epigenetic biomarkers for cancer prognosis, diagnosis, treatment guidance, and disease progression monitoring in cancer and genetic disorders.

Currently, Dr. Loi's research is centered on investigating microbial antibiotic and drug resistance using metagenomics and metabolomics approaches.

Abstract:

Introduction: Antimicrobial resistance (AMR) is a pressing global health threat exacerbated by the overuse of antibiotics in agriculture and healthcare. Vietnam, a major agricultural producer, has been identified as a hotspot for AMR. This study aims to characterize the soil microbiome, identify potential pathogens, and assess AMR profiles in Vietnamese agricultural soils to inform sustainable agricultural practices.

Methods: Shotgun metagenomic sequencing was performed on soil samples collected from Lam Dong province, Vietnam, across three cultivation phases: control, fertilization, and pesticide application. A total of 64 Vietnamese soil samples and 9 international soil samples were analyzed to investigate microbial community composition, potential pathogens, AMR profiles, and the presence of mobile genetic elements. A support vector machine (SVM) model was developed to classify soil microbiomes based on their origin (forest, cropland, or water).

Results: Our analysis revealed distinct microbial communities in Vietnamese soils compared to international samples, highlighting the importance of region-specific AMR assessments. Potential pathogens, including *Mycobacterium mantanii*, were identified, and AMR genes were detected on plasmids. Pesticide application was found to reduce microbial diversity and the prevalence of AMR genes, suggesting its potential impact on AMR dissemination. The SVM model accurately classified soil microbiomes based on their origin.

Conclusion: This study provides valuable insights into the factors driving AMR in Vietnamese agricultural soils. The findings highlight the need for sustainable agricultural practices that minimize antibiotic use and the importance of region-specific AMR monitoring and control strategies.

[PS-06] Nanoengineering Technology in Precision Medicine

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Abstract: The mission of my group is to develop advanced healthcare units with a multidiscipline that spans the fields of nanotechnology, molecular/cellular physiology, and engineering. The research directions can be divided into the following categories: (1) Tissue Engineering. (2) Biomedical Instrumentation. (3) Biosensor. (4) Biomedical Imaging. We also collaborate with business companies, and now we set two. (1) **DuoGenic StemCells Corporation**: Founded in 2018, DuoGenic StemCells Corp. was formed by a team of passionate researchers focused on stem cell cultivation. The company aims to push its products as the future standard for stem cell culture by providing high-quality and certified stem cell culture media that can be used for both 2D and 3D cultures. The products are intended for research use and can be upgraded for clinical applications. We are constantly looking for prospective distributors to increase the outreach of our products. (2) **"TWBIO" (Trade Wind Biotech Co. Ltd)**: Taiwan's first synthetic biology (synthetic biology) concept biotechnology company. Its core value comes from the team's efforts to cope with global ecological resource consumption, use synthetic technology biology to edit cells, use safe probiotics to produce natural products, use patented technology to explore "rare natural product cell factories", replace traditional natural product agriculture or chemical cumbersome and highly polluting production processes, and produce safe and sustainable natural products rare raw materials.

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[PS-07] Antimicrobial resistance of *Streptococcus pneumoniae* in Vietnam 2011-2023 – from molecular findings to solutions

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Abstract: In Vietnam, no formal surveillance of serotypes of *Streptococcus pneumoniae* exist and data was missing since 2009. Although pneumococcal conjugate vaccine (PCV) is registered and recommended in Vietnam, it is not yet part of routine immunization. We aimed to update the serotype distribution of *S. pneumoniae* isolated from invasive pneumococcal disease (IPD) in Vietnam during last 13 years and to evaluate their genetic and resistance profiles.

We conducted a retrospective, multicenter, hospital-based study. We included IPD patients of all age from ten hospitals across Vietnam between 2011 and 2023. Isolates were cultured, susceptibility was tested using etests, DNA extracted, and whole-genome sequenced using Illumina MiSeq. Reads were analyzed using PathogenWatch. Unculturable isolates have been serotyped using a multiplex Real-Time PCR assay.

Among the 288 pneumococci successfully analyzed, almost all isolates originated from blood (51%) and cerebrospinal fluid (45%), and the majority were from adult patients (65%). Almost one third (30%) belonged to non-PCV serotypes. Resistance to beta-lactams increased dramatically between 2011-2012 and 2022-2023: median MIC penicillin increased 6-fold (from 0.25 to 1.5 µg/mL) and ceftriaxone increased 4-fold (from 0.125 to 0.5 µg/mL). This phenomenon was not associated with clonal diffusion of resistant serotypes, MLST or cluster types.

Conclusion

Antimicrobial resistance is widespread in Vietnam, increasing, and concerning. Results suggest population-wide emergence of resistance rather than clonal dispersion. Besides, the addition of serotypes 15A and 11A would likely improve the expected impact of PCV in a future large-scale implementation. These results highlight the importance of surveillance and research for control of antimicrobial resistance.

Keywords: Public health & surveillance, antimicrobial resistance, *Streptococcus pneumoniae*, serotyping, whole-genome sequencing, Vietnam.

[PS-08] Differentiation of stomach tissue cells from stem cells and their mechanisms

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Research Interest: Differentiation of stem cells and the regulatory mechanisms

Educational Experience

1997	Ph.D. Tohoku University, Sendai, Japan
1989-1991	M.S. Tohoku University, Sendai, Japan
1985-1989	B.S. Tohoku University, Sendai, Japan

Professional Experience

2017-	Professor, Nara Institute of Science and Technology (NAIST)
2007-2017	Senior Researcher, National Institute of Advanced Science and Technology (AIST), Japan
2006-2007	Researcher, ICORP Organ Regeneration Project, JST, Japan
2002-2006	Assistant Professor, Tokushima University, Japan
1999-2002	Post-doc fellow, Ludwig Institute for Cancer Research, Sweden
1997-1999	lecturer, Tokushima University, Japan

Abstract: The stomach is a unique organ that secrete various enzymes, gastric acid, and hormones. In the adult stomach tissues, defects in gastric tissue stem cell differentiation are associated with various gastric disorders, including atrophic gastritis, intestinal metaplasia, and gastric cancer. However, the mechanisms underlying the multilineage differentiation of gastric stem cells during healthy homeostasis remain poorly understood. Using a single-cell RNA sequencing method, we analyzed the gene expression dynamics of progenitor cell differentiation toward pit cell, neck cell, and parietal cell lineages in healthy adult mouse corpus tissues. Enrichment analysis of pseudotime-dependent genes and a gastric organoid assay revealed that EGFR-ERK signaling promotes pit cell differentiation, whereas NF- κ B signaling maintains gastric progenitor cells in an undifferentiated state. In addition, pharmacological inhibition of EGFR in vivo resulted in fewer pit cells. Although activation of EGFR signaling in gastric progenitor cells has been suggested as one of the major inducers of gastric cancers, our findings unexpectedly identified that EGFR signaling exerts a differentiation-promoting function, not a mitogenic function, in normal gastric homeostasis.

[PS-09] Unraveling the Role of Ethylene in Petunia Flower Senescence, Seed Germination, and Abiotic Stress Tolerance

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Abstract: Ethylene is a pivotal plant hormone known for its involvement in various physiological processes, including flower senescence, seed germination, and abiotic stress responses. The intricate relationship between ethylene production and the genetic regulation of key ethylene biosynthesis genes (PhACO1, PhACO3, and PhACO4) in *Petunia hybrida* cv. 'Mirage Rose' was explored. Following this, these genes were edited utilizing the CRISPR/Cas9 genome editing system to elucidate their roles in flower longevity, seed germination, and abiotic stress tolerance. CRISPR/Cas9-mediated editing of these genes resulted in significantly reduced ethylene production and extended flower longevity. However, seeds of the *phaco1*, *phaco3*, and *phaco4* mutants exhibited reduced germination rates. Exogenous ACC and gibberellic acid supplementation restored germination activity, underscoring ethylene's pivotal role in seed germination mechanisms in *petunia*. Expanding our investigation into the role of ethylene in abiotic stress tolerance, it was observed that *phaco1* and *phaco3* mutants were more sensitive to salt and drought stress than wild type (WT), while *phaco4* mutants exhibited greater tolerance to abiotic stress than WT, indicating the contrasting roles of the ethylene biosynthesis genes in abiotic stress tolerance.

In summary, these findings uncover the multifaceted roles of ethylene in *petunia* flower senescence, seed germination, and abiotic stress tolerance. Furthermore, they underscore the importance of considering the potential positive or negative effects of ethylene reduction on seed germination and abiotic stress tolerance when selecting ethylene biosynthesis genes for editing to improve flower longevity.

ORAL PRESENTATIONS

Concurrent session 1 – Conference Hall

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Plant Biology



[PB-O01] Arabidopsis floral buds are locked through differential growth-induced sepal tip curving

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Abstract: Plant reproduction is critical not only for plants themselves but also for humans because it provides us with flowers, fruits and seeds. The reproductive organs (carpels and stamens) are fragile and often requires a good protection. In most plant species, this protective function is provided by the outer floral organs such as sepals or petals. There are probably several different mechanisms to close the flower bud, but none has been described in detail. This research aims to explain mechanistically how floral bud is closed, using the sepals of the plant *Arabidopsis thaliana* as the model. In *Arabidopsis*, we identified a small region at the sepal tip that is markedly curved inward early on and remains curved even after flowering. Through modelling and quantitative growth analysis, we find that this hook emerges from a sharp difference in growth rates between the sepal tip and the sepal body. Prolonging the growth at the tip hindered hook formation and resulted in open floral buds, leading to reduced fertilization. In addition, sepals of the mutant with defective growth pattern at the tip failed to curve inwards. We propose that floral buds are locked due to a sharp differential growth between sepal regions, which curves the sepal tip and forms a rigid hook early on during flower development.

Keywords: floral closure, differential growth, biomechanics, microtubules, curvature.

[PB-O02] Exploring the interactions between food ligands with soybean and zein film proteins: a molecular dynamics study

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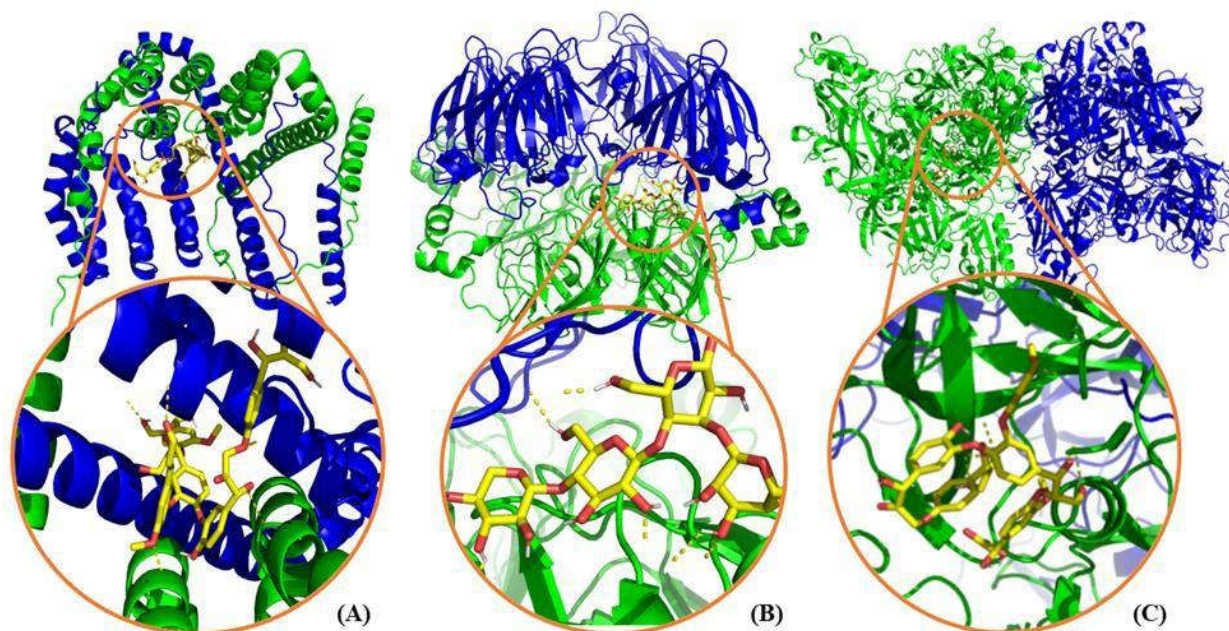


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Abstract: Food packaging is critical in preserving the quality and extending the shelf life of food. As the global concern for environmental sustainability continues to grow, there is a pressing need for sustainable alternatives to replace the traditional petroleum-based plastics in the food packaging industry. Plant-based protein biomaterials have emerged as promising candidates for sustainable food packaging. Soybean and Zein proteins have garnered significant attention from this group due to their abundance, renewability, biodegradability, and excellent film-forming properties. Zein-based films (Z-films) are known for their strength and water resistance but may lack flexibility. On the other hand, Soy-based films (S-films) offer good flexibility but may exhibit lower strength and water resistance. However, combining these films through layering and altering their properties by incorporating additives could lead to aggregative benefits, thereby improving their mechanical and physiochemical properties. This study combines molecular docking (MD) and molecular dynamics (MDS) to investigate the influence of incorporating Microfibrillated cellulose (MFC) and Olive stone ligands (OSP), like cellulose, hemicellulose, and lignin, in Proteoposites. Proteoposites are bio-based composite films composed of plant-based proteins like Z-films and S-films. The MDS analysis revealed stable systems for most protein-ligand incorporations. It confirmed the influence of LCL on residue fluctuations, their cascade effects on protein structure upon incorporation, and the exposure or screening of residues that influence film characteristics. Observations based on MDS analysis indicate that lignin shows strong and stable interactions when incorporated into the Zein protein. It shows cellulose exhibits strong and stable interactions when incorporated in 3AUP and 1OD5 Soy proteins. An alternate occurrence would be the lignin-bound 3AUP complex. However, cellulose-bound 3AUP shows a familiar hydrophobic resultant effect. Incorporating hemicellulose appears puzzling to all complexes. However, MDS analysis indicates hemicellulose behaves as a plasticizer, displaying stronger and better interactions with Zein-Zein and 1OD5-1OD5 complexes. An alternative would be lignin-bound Zein-Zein, but hemicellulose-bound shows better H-Bond interactions. Lignin and cellulose may perform better as potential plasticizers for zein and soy than hemicellulose. The tensile strength properties of proteoposite could be attributed to the strength of binding, reflected in the Free energy of binding (FEB). Observations show Zein-Zein complexes have exceptionally high FEB. Their individual spring-like and complex hinge-like conformation and energetics play a role in improving the tensile strength of Proteoposite films. These insights enable the

identification of ligand selectivity, ligand modification, and synthesis routes for Proteoposite, which will contribute significantly to future efforts.

Keywords: *Molecular dynamics (MDS), Molecular docking (MD), Soy film (S-film), Zein film (Z-film), Olive Stone ligands (OSP), microfibrillated cellulose (MFC), Proteoposites.*



[PB-O03] Optimization of microwave-assisted extraction parameters for total saponin content and antioxidant activity from leaves of *Launaea sarmentosa*

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Abstract: This research aimed to enhance the efficiency of extracting the total saponin content (TSC) and increase the radical scavenging activities (DPPH) of extract from the leaves of *Launaea sarmentosa*. Response Surface Methodology (RSM) along with the Box-Behnken design (BBD) were employed, incorporating three distinct factors (microwave power, extraction time, and ethanol concentration) to optimize the extraction procedure. The highest values of the responses (TSC and DPPH) were determined at conditions of microwave power 330 W, extraction time 22 min, and ethanol concentration 64 %. The results showed that the TSC and DPPH radical scavenging activity were 9.56 ± 0.24 (mg DE/g dw) and $87.62 \pm 0.46\%$, respectively.

Keywords: antioxidant activities, *launaea sarmentosa*, microwave-assisted extraction, response surface methodology, saponin.

[PB-O04] Characterization of Seed Germination-Promoting Fungi in Cymbidium Orchids

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Abstract: The Orchidaceae family is among the most diverse plant families globally. In natural environments, orchid seeds rely on a symbiotic relationship with specific mycorrhizal fungi, known as orchid mycorrhizal fungi (OMFs), to germinate. This study aimed to identify and characterize OMFs present in the roots of Cymbidium and evaluate their influence on seed germination. Roots from thirty Cymbidium accessions, collected in Southern Vietnam, were stained with Trypan Blue and examined under a light microscope. The OMFs isolated on potato dextrose agar (PDA) medium were tested for their ability to promote seed germination on sterilized black sphagnum. The fungal isolates that exhibited high germination rates were identified through morphological analysis and sequencing of the internal transcribed spacer (ITS) region using ITS1/ITS4 primers, followed by BLAST analysis against NCBI database sequences. Five distinct fungal morphotypes were observed in the Cymbidium roots, with two types, designated as S1 and S3, significantly enhancing seed germination rates up to 15.3% and 13.7%, respectively. Morphological and molecular analyses suggested that S1 belongs to the genus *Fusarium*, while S3 belongs to the genus *Trichoderma*. These findings highlight the potential application of specific OMF strains in Cymbidium breeding, sexual propagation, and conservation efforts.

Keywords: *Cymbidium*, seed germination, Orchid Mycorrhizal Fungi (OMF), internal transcribed spacer (ITS).

[PB-O05] Innovations and Challenges in Developing a Biodegradable Antimicrobial Film from Agricultural By-Products for Fruit Preservation

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Abstract: Among commonly used foods, fruits stand out for their high nutritional and economic value, but they are also highly susceptible to spoilage due to oxidation and pathogen attack. Traditional preservation methods raise concerns regarding environmental impact, health risks, and associated costs while failing to fully address the underlying causes of post-harvest fruit spoilage. In addition to the issue of waste during storage and transportation, the large-scale agricultural production results in significant amounts of agricultural by-products being discarded, without fully utilizing their potential. This study aims to integrate bioactive agricultural by-products into biodegradable films, leveraging their antimicrobial and antioxidant properties, and then applying these films to protect fresh fruits. Initially, agricultural by-products are processed to obtain extracts using organic solvents, then applied for antimicrobial and antioxidant activity evaluation. Among the 18 Vietnamese agricultural by-products, for example: orange peels, kumquat peels, mushroom substrate, and peanut shells, antioxidant assays demonstrated robust efficacy in most samples ($IC_{50} < 300 \mu\text{g/mL}$). Besides, antimicrobial activity against common ATTC strains and bacteria isolated from spoiled fruit revealed strong effectiveness across some extracts. During antimicrobial testing using a 96-well microplate, several challenges were encountered: While using a single solvent for extraction often led to suboptimal activity, the varied solubility of extracts in activity assessment required concentration adjustments to accurately measure bioactivity. Limitations of the microplate reader, such as non-uniform light scattering, overlapping extract colors, and microbial metabolic activity, caused measurement fluctuations, complicating the assessment of extract activity. Despite these challenges, bioactive extracts were successfully incorporated into food wrap films, with some exhibiting expected bioactivity, pending further evaluation on fresh fruit.

Keywords: fruit preservation, agricultural byproducts, biodegradable food wraps, antioxidant, antimicrobial testing challenges

[PB-O06] Creating Emulgel from Medicinal Herbs to Support Treatment of Dermatitis

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Abstract: The development of herbal-based products is an increasingly prominent trend within the cosmetic and pharmaceutical industries, driven by the growing demand for sustainable and green alternatives. Emulgel dosage forms offer an efficient method for delivering high concentrations of active ingredients to the skin surface, presenting several notable advantages. Accordingly, recent research efforts have focused on formulating herbal emulsions for treating dermatitis. Herbal extracts with proven anti-inflammatory and antibacterial properties were selected as the foundational components for the formulation of an emulsion aimed at dermatitis treatment. The composition of the emulsion formulation was determined by identifying the emulsification zone within a ternary phase diagram, consisting of an oil phase, an aqueous phase, and a surfactant-co-surfactant mixture, such as Tween 20, Tween 80, and Span 80. Preliminary evaluations of the emulsion formulations were conducted to assess parameters including appearance, droplet size, pH, and stability. These emulsions were subsequently integrated with various gel-forming excipients, such as Sodium Carbomer, NaCMC, HPMC, and Carbopol 934, to develop a gel matrix suitable for topical application. The resulting formulation exhibited nanoscale particle size, a pH of approximately 5.0, and maintained stability after exposure to six heat shock cycles. The herbal emulgel demonstrated a transparent and soft gel consistency, was easy to apply and remove from the skin, maintained a pH of around 6.5, and showed no signs of phase separation or morphological changes following six heat shock cycles.

Keywords: emulgel, gel emulsion, dermatitis, herbs, topical delivery.

[PB-O07] GWAS Exploration of Proanthocyanidin and Bran Color Diversity in Vietnamese Landrace Rice

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Abstract: Rice (*Oryza sativa*) domestication has led to diverse phenotypes, with pericarp color and proanthocyanidin content being key traits influenced by human selection. This study investigated these traits in 165 Vietnamese landrace rice accessions to elucidate domestication and evolutionary processes. Pericarp color was quantified using standardized ImageJ analysis, while total proanthocyanidin content was determined through spectrophotometric assays. Proanthocyanidin content ranged from around 1.57 to nearly 4000 mg catechin-equivalent/100g rice sample, with darker-pericarp varieties showing significantly higher levels ($p < 0.001$). Genome-wide association studies identified the Rc gene as a primary regulator of both traits. Analysis of SNP data from the 3K rice genome project and TASUKE+ genome browser revealed distinct haplotypes in the Rc gene, including functional, nonsense, and loss-of-function deletion mutations, correlating with variations in pericarp color and proanthocyanidin content. The Vietnamese collection predominantly exhibited white pericarp, associated with the loss-of-function deletion in Rc, consistent with global domestication patterns. Notably, a nonsense mutation previously reported only in Indian rice was detected in some Vietnamese accessions, suggesting potential gene flow. These findings provide insights into rice domestication, highlighting the role of human selection in favoring white pericarp. The unexpected genetic similarity between some Vietnamese and Indian rice accessions warrants further investigation into historical dispersal patterns. This study underscores the value of integrating phenotypic, biochemical, and genomic approaches in understanding crop evolution and sets the stage for more comprehensive analyses of rice diversity and domestication history, with implications for future breeding programs and germplasm conservation efforts.

Keywords: Crop evolution, Gene flow, Genome-wide association study, Haplotype, Pericarp color, Proanthocyanidin content, Rc gene, Rice domestication, SNP analysis, Vietnamese rice landraces

[PB-O08] Developing tea bag products named “Lục trà sam” from medicinal herbs specifically for diabetic patients

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Abstract: Purslane (*Portulaca oleracea* L.) is a nutrient-dense plant commonly used in traditional medicine and various culinary preparations. Building on positive findings from LC-QTOF-MS analysis and various bioactivities, including antioxidant activity, α -amylase enzyme inhibition, and toxicity testing on animal models, the authors developed a purslane tea bag product named “Lục trà sam,” which primarily featured purslane (50%), complemented by ingredients such as lingzhi mushroom (16%), sweet grass (16%), ming aralia (2%), peppermint (1%), and honey (15%), targeting diabetic patients. The product was further evaluated for sensory qualities and key quality indicators such as heavy metals, total yeast, mold, coliform, *Salmonella* sp., and *Staphylococcus aureus*. The findings revealed that purslane contained nearly 100 beneficial secondary active compounds across various subgroups, including fatty acids, flavonols, flavones, flavan-3-ols, flavanones, isoflavonoids, anthocyanins, phenolic acids, stilbenes, lignans, and tannins. This product also met Vietnamese standards, with an ash content of 7.6%, moisture content of 5.75%, no detectable levels of toxic metals like lead and cadmium or harmful microorganisms, and showed no acute toxicity in animal models. “Lục trà sam” demonstrated 50% inhibition of the α -glucosidase enzyme, with effectiveness equivalent to 381.90 μ g/mL and antioxidant activity with IC_{50} values of 5.77 mg/mL and 7.19 mg/L, as measured by 2,2-azinobis (3-ethylbenzothiazoline-6-sulfonic acid) and 2,2-diphenyl-1-picrylhydrazyl free radical scavenging assays, respectively. The results of the study are expected to provide scientific evidence and prospects for developing functional foods from Vietnamese medicinal herbs aimed at stabilizing blood sugar and minimizing the impact of complications on patients.

Keywords: Diabetic mellitus, “Lục trà sam” tea bags, *Portulaca oleracea* L..

[PB-09] Evaluation of Agarwood Formation Induced by Bacteria Isolated from *Aquilaria cumingiana* Trees in Albay, Bicol Region of the Philippines

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Abstract: Agarwood, a highly valuable aromatic resinous heartwood produced by *Aquilaria* species, holds significant economic importance due to its use in incense, perfumes, and traditional medicines. The resin forms in response to natural or artificial wounding of the trees. However, the rising global demand for agarwood has led to the overexploitation of natural *Aquilaria* populations, resulting in several species being listed as vulnerable by Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and the International Union for Conservation of Nature (IUCN). In this study, the role of bacteria as bioinoculants to stimulate artificial agarwood formation was explored. Bacterial endophytes were collected from plantation (n=4) and forest (n=4) *A. cumingiana* trees in Albay, Philippines, yielding a total of 48 samples. Dominance analysis revealed that *Bacillus* is the dominant bacterial genus among the endophytes, with *B. cereus*, *B. pumilus*, and *B. velezensis* as the top three species. A mixed culture method using these three bacteria was utilized for artificial inoculation in *A. cumingiana* trees, which were incubated for 3 months. Preliminary results showed the presence of dark to dark-brownish wood along the inoculation area, indicative of artificial agarwood formation. Further experiments, including measuring the resulting infection length in the trees and performing Gas Chromatography - Mass Spectroscopy for agarwood biomarker compound analysis, are ongoing. Notably, this represents the first attempt in the Philippines to explore artificial agarwood induction through bacterial inoculation. Furthermore, this study presents significant opportunities for scientific collaboration, particularly in the areas of sustainable agarwood production, microbial biotechnology, and conservation. Collaborative efforts could further explore the role of bacterial endophytes in agarwood formation, potentially leading to innovative approaches for artificial induction and preservation of *Aquilaria* species.

Keywords: agarwood, *Aquilaria cumingiana*, artificial induction, bacterial endophytes, bioinoculant, GC - MS

[PB-O10] Plant Secondary Metabolites on Efflux-Mediated Antibiotic Resistant *Stenotrophomonas Maltophilia*: Potential of Herbal-Derived Efflux Pump Inhibitors

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Abstract: During the process of adapting to metal contamination, plants produce secondary metabolites that have the potential to modulate multidrug-resistant (MDR) phenotypes; this is achieved by inhibiting the activity of efflux pumps to reduce the minimum inhibitory concentrations (MICs) of antimicrobial substrates. Our study evaluated the effect of secondary metabolites of belowground parts of *Pteris vittata* L. and *Fallopia japonica*, two metal-tolerant plants from northern Vietnam, on six antibiotic-resistant *Stenotrophomonas maltophilia* strains possessing efflux pump resistance mechanisms that were isolated from soil and clinical samples. The chemical composition of aqueous and dichloromethane (DCM) fractions extracted from *P. vittata* and *F. japonica* was determined using UHPLC-DAD-ESI/QTOF analysis. The antibacterial and efflux pump inhibitory activities of the four fractions were evaluated for the six strains (K279a, 0366, BurA1, BurE1, PierC1, and 502) using a microdilution assay at fraction concentrations of 62.5, 125, and 250 µg/mL. The DCM fraction of *F. japonica* exhibited remarkable antibacterial activity against strain 0366, with a MIC of 31.25 µg/mL. Furthermore, this fraction also significantly decreased gentamicin MIC: four-fold and eight-fold reductions for BurA1 and BurE1 strains, respectively (when tested at 250 µg/mL), and two-fold and eight-fold reductions for K279a and BurE1 strains, respectively (when tested at 125 µg/mL). Pure emodin, the main component identified in the DCM fraction of *F. japonica*, and sennidine A&B only reduced by half the MIC of gentamicin (when tested at 30 µg/mL). Our results suggest that the DCM fraction components of *F. japonica* underground parts may be potential candidates for new bacterial efflux pump inhibitors (EPIs)

Keywords: Efflux pump inhibitor; plant metabolites; antimicrobial activity; bacterial multidrug resistance; metal contamination.

ORAL PRESENTATIONS

Concurrent session 2 – Conference Hall

1

Microbiology



[MB-O01] Exploring Antibiotic Resistance Genes from the Microbiome of Barbour's Seahorses and its Habitat

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Abstract: This study aimed to determine the antibiotic resistance genes (ARGs) and mobile genetic elements (MGEs) associated with the cutaneous and intestinal mucus of *Hippocampus barbouri* collected from Cantiasay Island. Three liters of water and 300 grams of sediments were also collected and analyzed for comparative purposes. Using shotgun metagenomics, this study revealed that genes conferring resistance to aminoglycosides (*acrD* and *kdpE*), aminocoumarin (*mdtA*, *mdtB*, and *mdtC*), beta-lactams (CMY-83, HERA-1, OmpK35, *pbp2*, *penA*, and porin), fluoroquinolones (*mfd*, *emrA*, *emrB*, *hmrM*, *mdtH*, *patA*, and *pmrA*), macrolides (*efmA*, *smpC*, *macA*, and *macB*), sulfonamides (*leuO*) and tetracyclines (*tet39*, *tetC*, and *tetM*) are present in all samples. For MGEs, genes that showed high prevalence were associated with the Tn3-family transposase (Tn21, Tn3, Tn4401, and Tn501), IS5-family transposases (IS5), IS6-family transposases (IS26, IS1216, and IS1216E), ISCR elements (ISCR1 and ISCR2), IS4-family transposase (ISSba6), MOB relaxases (MOBF, MOVP, MOVQ, MOBT, and MOBV). The relative abundance of MGEs in this study establishes their influence on the mobilization of ARGs in this set of samples associated with *H. barbouri*. These findings could potentially lay the groundwork for future research into the mechanisms that promote the emergence, evolution, and spread of antibiotic resistance in bacteria associated with wild and farmed seahorses.

Keywords: *Hippocampus barbouri*, antibiotic resistance, mobile genetic elements, seahorses

[MB-O02] Evaluating the Effect of Hyperaccumulator Plant and Biochar Intervention in Hg-Contaminated Soil Using Microbial Community Composition as Bioindicator for Soil Health

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Abstract: Artisanal small-scale gold mining (ASGM) is a method of mineral extraction that relies on minimal mechanical assistance, but it has significant drawbacks such as mercury pollution and health risks. This study aimed to assess the effectiveness of using hyperaccumulator plants and biochar as soil amendments for the bioremediation of mercury-contaminated ASGM site, using a mesocosm setup. Our findings indicated that *Christella dentata*, the selected plant species, exhibited potential for phytoremediation based on the root-to-shoot translocation of Hg. The addition of biochar and plants appeared to stabilize the Hg-contaminated soil, as evidenced by changes in physicochemical properties and a decrease in mercury levels in the treated samples. Our microbial analysis revealed the presence of 30 phyla and 21 families in the samples. Notably, three phyla (Proteobacteria, Myxococcota, and Bacteroidota) exhibited consistent abundance across all time intervals and treatments, indicating their resilience. However, there were significant variations in the relative abundance of different families. While the abundant families remained somewhat consistent during the first three-time intervals (0, 30, and 60 days), an increase in nitrogen-fixing bacteria and nitrogen levels was observed on day 160, suggesting a potential shift in nutrient dynamics in the soil. Principal Coordinate Analysis (PCoA) confirmed differences in the microbial community composition between day 0, day 35, and day 60, compared to day 160. It also revealed that the composition variation was lower during the initial four time intervals, implying that time might have played a role in driving changes in microbial community composition.

Keywords: Heavy metal Hyperaccumulation, Mercury, Microbial Community Structure, Bioindicator, Soil Health, ASGM, Phytoremediation

[MB-O03] Scrutinization of plant-based multivalent antigens for subunit vaccine against African Swine Fever Virus

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Abstract: African swine fever (ASF), caused by the African swine fever virus (ASFV), is a deadly, highly contagious disease in both domestic pigs and wild boar. With mortality up to 100%, the disease has been making a serious impact on the swine industry worldwide. Because no effective antiviral treatment has been observed, proactive prevention such as vaccination remains the key to controlling the outbreak. In the pursuit of expediting vaccine development, our current work has focused on heterologous production of the viral antigens in the “green” synthetic host *Nicotiana benthamiana*. Protein oligomerization strategies via the C-terminal fusion of target genes with GCN4pII trimerization motif and GCN4pII_TP oligomerization motif were implemented to increase their immunogenicity. Herein, CD2vpII, p72pII, p30pIItp, p54pIItp, and p17pIItp were expressed in oligomeric forms in tobacco, which were indicated in western blot assays. The results of purification and size determination by size exclusion chromatography (SEC) illustrated that these antigens were successfully produced in stable oligomeric forms throughout the extraction, purification, and analysis process. Further, the immunogenicity of antigens were assessed via the vaccination in mice with three dose of 10 µg of recombinant protein. Indirect ELISA results demonstrated highly humoral immunity responses induced by antigens, suggesting them as the potential subunit vaccine candidates for preventing ASFV.

Keywords: African swine fever virus, oligomer antigen, GCN4pII-isoleucine zipper, transient expression, tp motif

[MB-O04] Administration of Viable *Lactocaseibacillus rhamnosus* CLR1505 as a Potential Adjuvant for Oral Yeast COVID-19 Vaccine

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Abstract: *Lactocaseibacillus rhamnosus* CRL1505 (LR1505) is a probiotic and immunobiotic strain known for its remarkable efficiency in regulating and enhancing hosts' immune responses against pathogens through oral delivery. It is considered one of the immune-boosting probiotics that could be explored for COVID-19 vaccine optimization. The present study was done to investigate whether oral administration of LR1505 as an adjuvant for the oral yeast COVID-19 vaccine, a vaccine delivery system made of recombinant yeast *Saccharomyces boulardii* expressing the RBD-spike protein of SARS-CoV-2 virus, will produce significant humoral and cell-mediated immune response in BALB/c mice models. Mice blood serum, fecal, and spleen samples were used to evaluate the levels of varying COVID-19 cytokine profiles, and SARS-CoV-2 RBD-specific IgG and IgA antibodies titers using enzyme-linked immunosorbent assay (ELISA) and flow cytometry analysis. Furthermore, since both organisms to be administered are viable, the biological activity of LR1505 with *S. boulardii* was also evaluated in vitro. LR1505 has a great survival rate in simulated gastrointestinal conditions and exhibited a synergistic relationship with *S. boulardii* in vitro. In addition, preliminary findings in orally vaccinated small cohort of mice using the yeast COVID-19 vaccine and LR1505, trigger robust humoral immune responses. Experiments are ongoing which explore the levels of different COVID-19 cytokine profiles, and antibodies titers in a bigger cohort of mice for further evaluation of LR1505's efficacy as an adjuvant, and its impact on mice gut microbiome composition after oral administration. With that, we are open to insights and collaborations that can contribute to the advancement and refinement of these probiotic-adjuvant strategies for enhanced vaccine efficacy.

Keywords: *Lactocaseibacillus rhamnosus* CRL1505, *Saccharomyces boulardii*, Oral Yeast COVID-19 Vaccine, Adjuvants, Immune Response.

[MP-O05] Plant secondary metabolites reducing antibacterial resistance: Virtual screening efficiency

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Abstract: Recently, plants growing in polluted areas including heavy metal contamination have been explored as a pool of molecules with multidrug-resistant (MDR) bacteria inhibition as the consequences of their metabolic modification under the effect of stress conditions. In this study, we examined the chemical and biological profile of *Pteris vittata* L., which is a heavy metal hyperaccumulator plant abundant in these high metal exposure environments. Metabolomic profiling was characterized by ultra-performance liquid chromatography–triple quadrupole tandem mass spectrometry system (UPLC-QqQ-MS/MS) with targeted mass spectra analysis versus in-house spectral library. For antibacterial activity, the representative model was a resistant bacteria *Stenotrophomonas maltophilia* strain K279a which is an opportunistic nosocomial pathogen and can cause severe respiratory tract infection and focused on the resistance-nodulation-division (RND)-type efflux pump specially SmeDEF as protein target in virtual screening. The structure of the protein was constructed by homology modeling. Through binding affinity prediction in molecular docking and then *in vitro* confirmation, two flavonoid derivatives (Procyanidin C1 and neohesperidin) showed a remarkably synergistic effect with levofloxacin through reduction of minimum inhibitory concentration (MIC) by 32 and 21.33 folds respectively despite their own neglectable bacterial inhibitory effects. These results bring out not only new pharmacological effects of two compounds but also novel directions to develop antibacterial lead compounds for treating clinical infection of *Stenotrophomonas maltophilia* K279a and other MDR bacteria.

Keywords: *Pteris vittata*, *S. maltophilia*, antibiotic resistance, *in-silico*, efflux pump

[MB-O06] Agarwood Formation Induced by Fungi Isolated from *Aquilaria cumingiana* Trees in Albay, Philippines

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Abstract: Agarwood is a highly-prized commodity formed in the agarwood-producing genus *Aquilaria*. *Aquilaria cumingiana*, a tree species native to the Philippines with no recorded studies on its agarwood-producing capability, was investigated for its potential to form agarwood. An artificial induction method using endophytic fungi isolated from the host trees was utilized to stimulate agarwood formation. A total of 47 fungi were isolated from the stem samples of domesticated and wild trees. Fungal endophytes were identified using both traditional and molecular methods. The three predominant fungal isolates were *Lasiodiplodia theobromae*, *Phomopsis* sp., and *Penicillium oxalicum*. The three predominant fungal species were used to develop a mixed culture, formulated in mature coconut juice, and served as the experimental treatment, while a chemical stick inducer and sterile distilled water were used as the positive and negative control, respectively. Artificial infection was induced using the syringe method, and agarwood formation will be evaluated three months after the artificial infection. This approach seeks to produce agarwood in a shorter time than the natural process, which takes years. Currently, the trees are in the second month of the incubation period, and preliminary signs of agarwood formation have already been observed. The agarwood resin will be collected in the third month and will be subjected to gas chromatography-mass spectrometry (GC-MS) analysis to determine its chemical composition and evaluate the presence and concentration of key aromatic compounds. This study could provide valuable insights into the fungal diversity linked to agarwood formation in *A. cumingiana*, and could potentially contribute to the development of sustainable agarwood production methods, conservation strategies, and economic development to support farmers reliant on agarwood trade.

Keywords: agarwood, *Aquilaria cumingiana*, artificial infection, endophytic fungi, GC-MS.

[MB-O07] A member of myosin V plays a role in the hyphal growth and virulence of the human pathogenic fungus *Mucor lusitanicus*

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Abstract: Mucormycosis, commonly known as 'black fungus,' is a rare but deadly invasive fungal infection caused by fungi from the order Mucorales. It primarily affects immunocompromised individuals and is associated with high mortality rates. The incidence of mucormycosis has been rising rapidly due to increasing risk factors and has recently emerged as a prevalent fungal infection among severe COVID-19 patients. One of the challenges in managing this infection is the limited understanding of its pathogenesis, especially at the molecular level. Our previous research has highlighted the role of various myosin V family members in pathogenic fungi. However, the functions of the protein members in this family are different. In this study, we focused on the myosin superfamily, which includes diverse actin-based motor proteins involved in various cellular functions. Specifically, we explored the role of the Myo5C (ID 154518) protein from the myosin class V family in *Mucor lusitanicus* by generating silencing phenotypes and null mutants of the *myo5C* gene. Fungal transformants with silenced *myo5C* exhibited a significantly reduced growth rate and almost complete loss of sporulation compared to the wild-type strain. The *myo5CΔ* null mutant strain displayed unusual characteristics, such as abnormally short septa and swollen hyphae. Notably, the mutant produced predominantly small yeast-like cells instead of filamentous hyphae, and these yeast-like cells failed to germinate normally, resulting in a loss of polarity. *In vivo* virulence assays using the *Galleria mellonella* invertebrate model demonstrated that the *myo5CΔ* mutant strain was avirulent. These findings underscore the essential role of the Myo5C protein in the dimorphism and pathogenicity of *M. lusitanicus*. Overall, the myosin V family presents a promising target for future therapeutic strategies against mucormycosis.

Keywords: dimorphism, fungal infection, *Mucor lusitanicus*, mucormycosis, *myo5C*, myosin V

[HB-O08] Prevalence of *Pseudomonas aeruginosa* in the environment and its detection using Loop Mediated Isothermal Amplification Assay

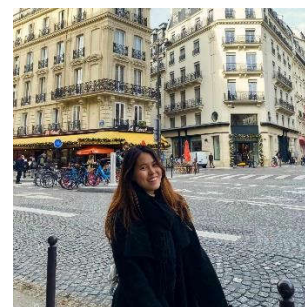
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Abstract: *Pseudomonas aeruginosa* (*P. aeruginosa*) is an opportunistic pathogen commonly found in clinical and environmental samples. Rapid detection of this bacterium is crucial for the effective diagnosis and treatment of *P. aeruginosa* infections. This study aimed to develop a high-efficiency loop-mediated isothermal amplification (LAMP) assay targeting a *P. aeruginosa*-specific gene encoding a hypothetical protein (GenBank ID: 882161). The study involved two main parts: 1) Isolation and identification of *P. aeruginosa* from environmental samples, and 2) Evaluation of the established LAMP assay on these environmental *P. aeruginosa* isolates. A total of 52 samples were collected from various geographical regions in Ho Chi Minh City, with 50 samples (96%) containing *Pseudomonas* species, characterized as rod-shaped, Gram-negative bacteria growing on selective media. Following duplex PCR screening, 14 *P. aeruginosa*-like environmental strains were isolated, and 5 randomly selected isolates were confirmed as *P. aeruginosa* through 16S rRNA sequencing. The LAMP assay was optimized at 60°C, 63°C, and 65°C for 30 and 45 minutes, using specific primers, and tested on all five confirmed *P. aeruginosa* isolates. The results demonstrated that the LAMP assay was highly specific (100%) for detecting environmental *P. aeruginosa*, with a detection limit of 1 pg/μL. In conclusion, *P. aeruginosa* is prevalent in the environment, and the developed LAMP assay shows strong potential for identifying environmental *P. aeruginosa* isolates.

Keywords: Duplex-PCR, environmental isolates, LAMP, *P. aeruginosa*

[MB-O09] Antifungal activity of endophytic *Burkholderia* spp., and curcumin silver nanoparticles against *Aspergillus* spp. and *Fusarium* sp.

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Abstract: Numerous members of *Aspergillus* spp. and *Fusarium* spp. are pathogens possessing a broad spectrum of their host including plants, animals, and humans. In this study, five endophytic *Burkholderia* spp., five plant extracts, and curcumin silver nanoparticles (C-AgNPs) were used to screen their antifungal activities against *Aspergillus fumigatus*, *Aspergillus flavus*, *Aspergillus terreus*, and *Fusarium* sp. ATCC 60289 (*F. sp.*). The results of dual assays showed that all five *Burkholderia* spp. strains NC119, NC148, NC160, NC166, and NC206 exhibited the antifungal activities with the percentage of inhibition (PI) ranging from 34.34 % to 76.01 %, in which the strain NC166 showed the strongest antifungal activity against all four studied fungi. Notably, *Burkholderia* spp. appeared to be effective against *F. sp.*, with the PI greater than 50% in four out of five bacterial strains. In addition, the C-AgNPs performed considerable effectiveness in inhibiting the growth of all four fungi, with the highest PI of 71.17 ± 1.44 % against *Aspergillus terreus*. These outcomes emphasize the potential of *Burkholderia* spp. and C-AgNPs as antimicrobial agents for the management of *Aspergillus* spp. and *Fusarium* spp.

Keywords: Antifungal activity, *Aspergillus* spp., *Burkholderia* spp., curcumin silver nanoparticles, endophytic bacteria, *Fusarium* sp.

ORAL PRESENTATIONS

Concurrent session 3 – Seminar Room 1

Human Biology



[HB-O01] The effect of human serum albumin concentration in biphasic *in vitro* maturation (CAPA-IVM)

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Abstract:

Objective: The supplementation of human serum albumin (HSA) in CAPA-IVM medium is crucial for the maturation of human oocytes, but the optimal concentration of HSA remains controversial. This study aimed to investigate the effectiveness of the CAPA-IVM when adding HSA at two different concentrations (5 mg/ml versus 10 mg/ml).

Methods: This multicenter, retrospective cohort study included 298 polycystic ovary syndrome (PCOS) patients who underwent CAPA-IVM treatment between January 2018 and September 2023 at IVFMD, My Duc Hospital, and IVFMD Phu Nhuan, My Duc Phu Nhuan Hospital. The patients were categorized into two groups based on the concentration of HSA in oocyte maturation medium: 10mg/mL HSA group (HSA10, 183 patients), and 5 mg/mL HSA group (HSA5, 115 patients). The primary outcome was the maturation rate.

Results: The maturation rate was decreased significantly in the HSA5 group when compared to the HSA10 group (60.00% vs 65.00%, $p < 0.005$). However, the rate of good-quality day 3 embryo was significantly higher in the HSA5 group compared to the HSA10 group (83.33% vs 68.97%, $p < 0.005$). There were six cases (7.14%) in the HSA10 group that could not reach the blastocyst stage compared to no case in the HSA5 group. Moreover, the proportion of good-quality blastocysts and the total number of frozen embryos among the two groups were similar ($p > 0.005$). There was no significant difference in the rates of ongoing pregnancy, implantation and miscarriage after the first frozen embryo transfer between two groups ($p > 0.005$).

Conclusion: In the CAPA-IVM cycles, the HSA concentration of 5 mg/mL in the oocyte maturation medium decreased by 5% maturation rate when compared to that of 10 mg/mL. However, there was no significant difference in laboratory outcomes and clinical outcomes between the two groups. The study demonstrates that the HSA concentration of 5 mg/mL can be alternative to the HSA concentration of 10mg/mL in CAPA-IVM.

Keywords: *in-vitro* maturation of oocytes, human serum albumin (HSA), CAPA-IVM.

[HB-O02] Waste-derived TiO₂ nanoparticles synthesized from *Hordeum vulgare* L.: A Bridge for Sustainable Ovarian Cancer Therapy Joining Agriculture to Oncology

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Abstract: Eco-friendly and sustainable methods for synthesizing nanomaterials have attracted significant interest, particularly in biomedical applications. Among these, TiO₂NPs have been extensively studied for their use in medical implants, photodynamic therapy, drug delivery systems, and many more. Due to their robust photocatalytic properties, TiO₂ nanoparticles offer a promising approach for treating ovarian cancer, especially targeting the PA1 cell line with novel applications emerging in photodynamic therapy, drug delivery, and apoptosis induction. With ongoing advancements in nanoparticle design and application strategies, TiO₂ has significant potential for improving therapeutic outcomes in ovarian cancer and beyond. This study explores the use of TiO₂ nanoparticles synthesized using waste from *Hordeum vulgare* L. as a novel therapeutic against the PA1 ovarian cancer cell line. The green synthesis route leverages the bioactive compounds in *Hordeum vulgare* L., which serve as natural reducing agents, to produce TiO₂ nanoparticles with enhanced biocompatibility and a reduced environmental impact. In vitro studies demonstrated that these waste-derived TiO₂ nanoparticles exhibit notable cytotoxic effects on the PA1 cell line, primarily by inducing oxidative stress and apoptosis. The increase in ROS production and subsequent apoptotic events were confirmed through flow cytometry and fluorescence microscopy. Moreover, these nanoparticles displayed selective toxicity towards cancerous cells, highlighting their potential for targeted cancer therapy. This study also focuses on making the best use of the waste from *Hordeum vulgare* L. to synthesize biogenic TiO₂ nanoparticles as a sustainable and effective treatment strategy for ovarian cancer, paving the way for future research. Notably, to our knowledge, this is the first time we are reporting the cytotoxic properties of TiO₂ nanoparticles synthesized from *Hordeum vulgare* L. waste making it an efficient approach connecting agriculture to oncology.

Keywords: Cytotoxic effects, Green synthesis approach, *Hordeum vulgare* L, PA1 Ovarian cancer cell lines, TiO₂ nanoparticles

[HB-O03] Plant exosomes extracted from *Elettaria Cardamomum* inhibit Triple-Negative Breast cancer

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Abstract: Triple-negative breast cancer (TNBC) does not express HER2, the progesterone receptor (PR), or the estrogen receptor (ER); traditional endocrine and HER2-targeted therapies are not successful in treating TNBC. Chemotherapy is still the major therapeutic choice as a result, even though it frequently fails and has negative effects. Exosomes, in particular, are important for cell-to-cell communication and can affect both normal and abnormal processes. Plant micro-vesicles (MVs), which include bioactive substances such as proteins, nucleic acids, metabolites, and lipids with anti-tumorigenic, anti-oxidative, and anti-inflammatory qualities, have been shown to have therapeutic promise in recent research. In this study, we used a variety of techniques, such as SEM, TEM, DLS, AFM, NTA, and zeta potential analysis, to characterize micro-vesicles that were isolated from *Elettaria cardamomum* seeds (ECS MVs). The exosomes from 1 mg of *E. cardamomum* seed extract yielded approximately 3.0×10^7 particles/mL vesicles. We quantified the protein and then used SDS-PAGE to determine the molecular weight. Using a variety of in vitro tests, the anti-cancer properties of ECS MVs were examined on two TNBC cell lines, MDA-MB-231 and 4T1. Assays for colony formation evaluated inhibition, while MTT assays evaluated cell survival and provided IC₅₀ values for the exosomes. Cell migration was analyzed using a scratch assay. Live and dead cells were distinguished using ethidium bromide and acridine orange staining. Furthermore, fluorescence-activated cell sorting (FACS) was used to identify the cell cycle arrest stage by exosomes, and fluorometry and a fluorescence microscope were used to detect the amounts of reactive oxygen species (ROS). Trypan blue staining further quantified cell viability by identifying nonviable cells. PI staining was done, and the cell death was quantified through a fluorescence spectrophotometer. As per our knowledge, this is the first time we are reporting the anti-cancer properties of plant-derived exosomes from *Elettaria cardamomum*'s seed on TNBC.

Keywords: Exosomes, Triple-negative breast cancer, Plant-exosomes, *Elettaria Cardamomum*

[HB-O04] Green synthesis of Magnesium Oxide nanoparticles from *Musa acuminata* and its anti-diabetic effect on *Danio rerio* model

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Abstract: Diabetes mellitus is a significant global health issue, prompting research into innovative treatment methods. In this study, magnesium nanoparticles were synthesized using banana peel extract from *Musa acuminata*. The synthesized nanoparticles were characterized through various techniques, including dynamic light scattering (DLS), zeta potential analysis, UV-visible spectroscopy, Fourier-transform infrared spectroscopy (FTIR), scanning electron microscopy (SEM), and X-ray diffraction (XRD). The DLS results indicated that the magnesium oxide nanoparticles had an average size of 6 nm. We evaluated their antioxidant, anti-inflammatory, and anti-diabetic properties using multiple assays: DPPH and FRAP for antioxidant activity, BSA and albumin denaturation assays for anti-inflammatory effects, and α -amylase inhibition and glucose uptake by yeast for anti-diabetic evaluation. Notably, the magnesium oxide nanoparticles demonstrated significant antioxidant activity with IC₅₀ values of 102.5 μ g for DPPH and 100 μ g for FRAP. Additionally, we assessed their anti-diabetic effects and toxicity using an adult *Danio rerio* (zebra fish) model. The study employed a full factorial method to examine dye degradation by the magnesium oxide nanoparticles. This research marks the first report on the anti-diabetic properties of magnesium oxide nanoparticles, highlighting their potential therapeutic benefits.

Keywords: MgO, Anti-diabetic, Anti-oxidant, Anti-inflammatory, toxicity effect, *Musa acuminata*, *Danio rerio*

[HB-O05] Effect of post-warming culture time of vitrified-warmed oocyte on embryological outcomes

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Abstract:

Background and Aims

Vitrification-warming oocytes have become increasingly popular due to technological advancements resulting in a high post-warming survival rate. However, the vitrification-warming process has been found to influence tubulin depolymerization, causing structural disruptions and errors in embryo division, especially in women of advanced age. Therefore, it was suggested to extend the post-thaw culture time of oocytes to compromised spindle stabilization regulators before ICSI. This study aims to evaluate the effect of post-warming oocyte culture time on embryological outcomes.

Methods:

This multicenter, retrospective cohort study conducted at IVFMD, My Duc Hospital, and IVFMD Phu Nhuan, My Duc Phu Nhuan Hospital, Vietnam, included patients who underwent in vitro fertilization with warming oocytes from January 2020 to December 2023.

The primary outcome was the effect of post-warming culture time on embryo development to cleavage state, which was evaluated using the logistic regression in the Generalized Estimating Equations (GEE) model adjusted with the maternal age. The other effect on the degeneration of oocytes after ICSI, fertilization, and blastocyst development also performed as a secondary outcome.

Results:

The study analyzed 1570 warmed oocytes from 322 women, with a mean maternal age of 37.3 (5.36) years. The median duration of post-warming culture was 2.83 [2.26;3.29] hours. After adjusting for female age, the duration of post-warming culture had a significant impact on the development of embryos at the cleavage stage (OR=0.78; 95% CI:0.67-0.91; p=0.002). A post-warming duration of 3 hours or higher increased oocyte degeneration and decreased the cleavage embryo rate. The optimal duration time was found to be 2.3 hours. However, there were no significant effects observed on fertilization or blastocyst development.

Conclusions:

In this study, Post-warming oocyte culture time 2- 3 hour is better than >3h for embryo development during the cleavage stage.

[HB-O06] Association of *Fusobacterium nucleatum* with Breast Cancer Progression and Virulence Factor Profiling in South Indian Patients

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Abstract: Background: Breast cancer is a multifaceted disease with various factors influencing its progression, metastasis, and treatment response. Recent studies suggest a significant association between *Fusobacterium nucleatum*, a common oral bacterium, and the development, progression, and chemotherapeutic resistance of various cancers, including breast cancer. *F. nucleatum* can colonize tumors, protecting them against the host's anti-tumor immunity. Its ability to coaggregate with other oral bacteria and form multi-species biofilm communities can significantly alter the tumor microenvironment by facilitating the recruitment of other pathogenic bacteria, enhancing inflammatory responses, and creating a protective niche that shields tumor cells from immune detection, thereby promoting cancer progression and metastasis. Additionally, its translocation via hematogenous routes suggests a systemic link between oral health and distant tumor sites. The virulence factors associated with *F. nucleatum* *fadA* and *fipA* are particularly notable; *fadA* binds to endothelial cells, activating β -catenin and promoting cancer-related gene expression, while *fipA* inhibits immune responses by arresting T cells in the G1 phase. Understanding *F. nucleatum*'s influence on tumor progression, metastasis, and treatment resistance is crucial for improving breast cancer management. **Methods:** This study investigated the incidence of *F. nucleatum* and its virulence factors, *fadA* and *fipA*, in oral samples from South Indian breast cancer patients (n=30) at Sri Ramachandra Medical Center. Ethical clearance was obtained, and patients with all breast cancer stages were included. Oral wash samples were collected and subjected to PCR amplification using 16S rRNA primers to identify *F. nucleatum* positive samples. The presence of *fadA* and *fipA* was determined using sequence-specific oligonucleotide primers. **Results:** Among the samples, 73.3% (n=22) were positive for *F. nucleatum*; 45.45% (n=10) were positive for *fadA*, and 54.54% (n=12) were positive for *fipA*. Data analysis, conducted using R programming, revealed a higher frequency of *F. nucleatum* in later stages of breast cancer. However, *fadA* and *fipA* did not significantly influence disease progression. Notably, *F. nucleatum* incidence was higher in hormone-sensitive breast cancer, with no significant presence in triple-negative cases. **Conclusion:** This study provides preliminary evidence linking *F. nucleatum* to breast cancer progression. While a larger sample size is needed, the data suggest other virulence factors may be involved in disease progression. Comprehensive profiling of virulence factors could enhance our understanding of pathogenic mechanisms and improve therapeutic strategies.

Keywords: *Fusobacterium nucleatum*, Breast Cancer, Virulence Factors, Tumor Microenvironment, Chemotherapeutic Resistance.

[HB-O07] A gender-specific role for the chemokine receptor Cxcr3.2 in medaka bone homeostasis

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Abstract: During remodeling of ossified bone matrix, osteoclasts continuously resorb old and brittle bone that is replaced by deposition of new bone produced by osteoblasts. Therefore, to maintain healthy bone, a balanced activity of osteoblasts and osteoclasts is needed. In a previous study using a transgenic medaka fish osteoporosis model where ectopic osteoclast formation and osteoporotic lesions are induced by transgenic Rankl expression, we showed that bone-forming osteoblast progenitors strongly express the chemokine Cxcl9 upon Rankl induction. This in turn triggers the recruitment of Cxcr3.2-expressing macrophages toward the bone surface. There, the macrophages dynamically interact with osteoblast progenitors and differentiate into cathepsin K-positive osteoclasts. These osteoclasts then excessively resorb bone matrix and cause severe bone lesions. Blocking Cxcl9-Cxcr3.2 signaling in medaka by CRISPR-induced mutations or treatment with chemical CXCR3 antagonists prevented macrophage recruitment and osteoclast formation, and protected ossified tissues from Rankl-induced bone loss. Together, this showed that in early larval stages, Cxcl9l and Cxcr3.2 are required for osteoclast formation under osteoporotic conditions. In the present study, we furthermore showed that under non-osteoporotic conditions, adult male *cxcr3.2* mutant medaka have a higher bone density when compared to female mutants or wildtype fish. This is particularly obvious in teeth, jaws, and the vertebral columns. This osteoporotic phenotype suggests a possible osteoclast deficiency, and opens the possibility that Cxcr3.2 and its ligand Cxcl9l are also required for endogenous osteoclast formation specifically in males. These observations are consistent with our earlier findings that men with increased CXCL9 serum levels are more susceptible to hip fractures (Phan et al., *J Bone Min Res* 2022). Our results therefore suggest that Cxcl9-Cxcr3.2 signaling is important for osteoclast formation and bone homeostasis of males, while alternative mechanisms should exist in females.

Keywords: CXCL9-CXCR3 signaling, Osteogenic progenitor, Macrophage, Osteoporosis.

Acknowledgements: This study was supported by funding from the Singapore Ministry of Education (MOE2016-T2-2-086 and MOE-T2EP30221-0008).

[HB-O08] Decoding Vietnam's Measles Epidemic: A Comprehensive Look Since 2010

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Abstract: Vietnam, as a tropical Southeast Asia country, has been dealing with diverse pathogens and their potential to develop into epidemics anytime. The rapid fluctuations in climate contribute to the increased spread of viruses, with measles being particularly prone to outbreaks. This work reviews the epidemiology of measles in Vietnam since 2010, tracking its transmission patterns and impact through different period of time, including pre-COVID-19, during COVID-19, and post-COVID-19. The analysis delves into the virology and pathogenesis of measles, highlighting its highly contagious nature and severe health consequences. Besides, diagnostic methods, treatment options, and preventive measures, notably immunization strategies, are discussed in detail. Interestingly, it seems that in Vietnam, boys who are in populated and remarkably humid rural areas are more susceptible to contracting the virus over the first few months of a year. Despite the positive increase in vaccine coverage, challenges such as anti-vaccination attitudes and wellness access disparities persist and push the measles outbreaks into managing struggle. Overall, the review underscores the ongoing battle against measles and the importance of comprehensive public health interventions to protect populations at substantial risk and prevent upcoming threats.

Keywords: measles, Measles morbillivirus, epidemiology, vaccine coverage

[HP-O09] Lipid nanoparticles for enhancing the therapeutic effectiveness of berberine

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Abstract: Berberine (BBR) is a Vietnamese traditional herbal drug, that has been used for the local treatment of gastrointestinal tract diseases. Recently, novel biological activities of BBR have been reported, especially for chronic diseases like diabetes, hyperlipemia, hypertension, Alzheimer's disease. However, low solubility and permeability of BBR limited applications on these treatments. Hence, solid lipid nanoparticles (SLNs) and nano lipid carriers (NLCs) were investigated for therapeutic improvement of berberine via various administration routes. Lipid screening, formulation ingredients and processing parameters were carried out. Berberine nanoparticles (NPs) were successfully prepared by ultrasonication method. The characterization of berberine NPs were carefully evaluated, including particle size, zeta potential, drug loading, and *in-vitro* release profile. Optimum berberine NPs had a reasonable size below 200 nm with PDI value < 0.3; the absolute value of the zeta potential above of 50 mV and high entrapment efficiency, more than 95%. Both SLNs and NLCs expressed sustained release of berberine, especially in initial period, in *in-vitro* oral release model and *in-vitro* dermal release model, respectively. Moreover, blank lipid carriers increased the cell viability and reduced the cytotoxicity of berberine on the specific cell lines. The resulted BBR-NPs could be considered as potential drug delivery systems to enhance berberine absorption into our human body.

Keywords: berberine, solid lipid nanoparticles, nano lipid carriers

ORAL PRESENTATIONS

Concurrent session 4 – Seminar Room 1

Animal Biology



[AB-O01] Effect of Heavy Metals on the Life History Trait of *Heterocephalobellus* sp. and *Cephalobus* sp. (Nematode: Cephalobidae) Collected from a Small-Scale Mining Site, Davao de Oro, Philippines

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Abstract: Mining is notorious for causing heavy metal contamination of the environment, disrupting the activities of soil fauna, such as nematodes, and causing changes in the functions of organisms in the soil ecosystem. This study investigated the survival, reproduction, and the typical life history traits (LHTs) of free-living nematodes collected from an artisanal and small-scale gold mine (ASGM) site, including how heavy metals influenced these parameters. Morphological and molecular analyses identified *Heterocephalobellus* sp. and *Cephalobus* sp. (Rhabditida: Cephalobidae) from the soil, which were cultured in a bacteriological agar to assess their LHT using the hanging drop technique. These cultured nematodes were then exposed to different temperatures (20, 25 and 30°C) to determine the optimum condition for their survival and reproduction. Cultured nematodes were also exposed to copper (Cu), lead (Pb) and zinc (Zn) to elucidate their effects on the nematode's survival, reproduction, and LHT. Our results suggest that the ideal temperature for survival with high reproduction rate for both species was at 25°C. Exposure to heavy metals led to decreased survival and reproduction at 25°C and 30°C in both nematodes. In contrast, these nematodes survived longer at 20°C with delayed reproductive maturity. At 25°C, the LHT of *Heterocephalobellus* sp. showed shorter population generation time with decreased number of offsprings. Although shorter population generation time was also observed in *Cephalobus* sp., more offsprings were produced when exposed to heavy metal contaminants. Altogether, these results suggest that when exposed to heavy metal contaminants, *Heterocephalobellus* sp. and *Cephalobus* sp. led to changes in their survival and reproduction. To the best of our knowledge, this is the first report evaluating the survival, reproduction and LHTs of *Heterocephalobellus* sp. and *Cephalobus* sp. in the Philippines and how these parameters are affected by heavy metals ubiquitous in mine sites.

Keywords: Artisanal and small-scale gold mining (ASGM), hanging drop method, heavy metals, life history trait

[AB-O02] ASGM-impacted Soil Assessment and its Heavy Metal Contamination Influence on the Life History Traits of Free-living Nematodes in a Small-scale Mining Area in Nabunturan Davao de Oro, Philippines

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Abstract: The poor proper methods and techniques in recovering gold conducted by artisanal and small-scale gold mining (ASGM) including the improper release of mine wastes, has greatly contributed to the contamination of the soil. In effect, organisms in the soil are directly affected by it, such as the free-living nematodes. Nematodes are responsible for many soil processes and are important bio-indicators of the soil environment. In this study, soil contamination due to ASGM activities and the Life History Traits (LHT) of soil nematodes in Nabunturan Davao de Oro, Philippines were investigated. Results showed that ASGM-impacted soils had Cu, Pb, Zn and As up to 3.6, 83, 73 and 68 times higher than background levels respectively and were classified as 'extremely' polluted (CD = 30-228; PLI = 5.5-34.8). Minerals typically found in samples were copper-gold ores like pyrite, chalcopyrite, malachite, galena, sphalerite and goethite were identified by XRD and SEM-EDS analyses. Cu and As released from the historic ASGM site samples exceeded the environmental limits for Class A and Class C effluents, which is likely attributed to the removal of calcite and dolomite by weathering. As for the soil nematodes, the isolated *Acrobeloides thornei*'s basic morphology showed that species from impacted soils are bigger than from non-impacted sites by 62µm in body length and 2.62µm in body width, suggesting that despite the intense heavy metal contamination, these nematodes were able to thrive. LHT of these species were observed with 1×10^9 cells ml⁻¹ and 5×10^9 cells ml⁻¹ bacterial densities and under 20°C, 25°C and 30°C. Results showed no difference in their survivability, fecundity and life cycle parameters under two bacterial densities but has significant differences under varying temperatures under specific ages.

Keywords: ASGM, heavy metal, *Acrobeloides thornei*

[AB-O03] Knowledge, Perception, and Management of Fall Armyworm (FAW) *Spodoptera frugiperda* Among Farmers in Iligan City, Northern Mindanao, the Philippines

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Abstract: The fall armyworm (FAW) *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae) is a major corn pest in the Philippines. This study was conducted from November 2023 to February 2024 through local assessment of affected corn farms in Iligan City, Northern Mindanao through field evaluations and surveys of farmers' knowledge, perception, and management strategies. FAW larvae were collected from all the farms. A potential biotype of *S. frugiperda* that consumes Bt maize and displays pesticide tolerance was observed. A high yield loss (48.76%, $p < 0.0001$) and substantial income reduction (50.93%, $p < 0.0001$) caused by FAW damage were recorded. The majority of farmers (75%) experienced moderate-to-severe FAW infestation in 2023 and a resurgence in 2024. Farmers have limited knowledge and a low perception of fall armyworm, which has led to ineffective management strategies allowing the pest to persist in corn fields. Community-based programs and agricultural services integrating local knowledge could contribute to the sustainable management of FAW.

Keywords: Corn, farmers' knowledge, FAW, pest management

[AB-O04] Displaying Immunostimulants on Gram-Positive Enhancer Matrix (GEM) Particles as Mucosal Adjuvants

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Abstract: The recent COVID-19 pandemic has highlighted the crucial role of vaccines, especially in preparing for future potential pandemics. The efficacy of vaccines depends on the essential properties of antigens and the contributions of adjuvants. In recent years, developing successful mucosal vaccines remains challenging, as they often fail to induce a sufficient specific secretory immunoglobulin A (sIgA) response. Therefore, our objective is to establish a platform that uses Gram-positive bacteria carrying immunostimulants as mucosal adjuvants. In our previous study, we demonstrated that the full-length suilysin protein from *Streptococcus suis* serves as a potent biological adjuvant. In this study, we identified the immunostimulant domain of suilysin using in silico analysis. We successfully expressed the truncated suilysin (tSly), achieving the expected size of 43 kDa. The recombinant protein was then displayed on treated *Lactococcus lactis* bacteria, referred to as GEM-tSly. The GEM-tSly platform was characterized via SDS-PAGE, Western blotting and Transmission Electron Microscopy (TEM). The immunoenhancing potential of the GEM-tSly will be further evaluated by combining it with an antigen for vaccination and challenge test. Our adjuvant platform holds promise as a potential mucosal adjuvant for vaccine development.

Keywords: *Streptococcus suis*, Suilysin, Recombinant protein, Immunostimulant, Adjuvant.

[AB-O05] Insect Fauna of the Bangsamoro Region and Where to Find Them: Integrative Taxonomy and Strategies for Environmental Tactics

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Abstract: Insects are essential group of invertebrates in the functioning of ecosystem and are useful bioindicator species for environmental change and pollution. Despite their importance, they are remain poorly understood and understudied. The present study aimed to assess the diversity of insect fauna in the Bangsamoro region, classify them according to morphological and molecular data, and document their current geographical distribution. Eleven (11) sites were surveyed from 25 February to 26 March 2024 in Lanao del Sur province. Specimens were collected through opportunistic sampling using entomological hand nets such as sweep net, beating sheet, and tree bark net. A total of 228 individual species belonging to Orders Coleoptera, Dermaptera, Hemeptera, Mantodea, Orthoptera, Siphonaptera, and Odonata were documented, all of which are new distribution record in the Bangsamoro region. The Curculionidae under order Coleoptera are the most encountered, widely distributed family with higher species abundance. Among the studied sites, S4 (agroforest) had higher species richness with six (6) Orders. Most of the studied species are associated to plants (e.g. ferns and flowering plants). However, further investigations are necessary to determine such relationship. Other than perching behavior, it is interestingly to note that some genera were observed copulating while some are hiding in abaxial part of leaves. Some are active during the night whereas others are perching on the leaves and active during day time. Despite the importance of insects in the ecosystem, they are vulnerable to human activities such as agricultural activities, illegal logging, and conversion of forest ecosystem to highways and villages. Therefore, this study highly recommends to protect the natural environment of insect fauna in the Bangsamoro region.

Keywords: *Coleoptera, Dermaptera, Hemeptera, Mantodea, Odonata.*

[AB-O06] Assessing Interspecific Shape Variability in Two Congeneric Species of Epigeic Tiger Beetles (Coleoptera: Cicindelidae) Using Landmark-Based Geometric Morphometric Analysis

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Abstract: Tiger beetles are among the insects with a broad geographic distribution worldwide and are regarded as flagship bioindicator species. Ninety-percent (90%) of the more than 170 taxa that make up the Philippine tiger beetle fauna are indigenous. According to studies, tiger beetles exhibit morphological polymorphism that is impacted by various circumstances. In two species of *Cylindera*, the head, pronotum, and abdomen can vary in shape. This study looked at this shape variability from the riparian habitat along the Tubod River in Brgy. Merila, Iligan City, samples of *Cylindera (Eugrapha) minuta* (Olivier, 1790) and *Cylindera (Ifasina) discreta elaphroides* (Dokhtouroff, 1882) were sporadically obtained. The study employed a total of 25 samples. The shape of the head, pronotum, and ventral abdomen was captured with two-dimensional Cartesian coordinates of 16, 10, and 16 markers. The samples were digitally captured three times to lower structure measurement errors. The findings reveal significant form variation between the two species in the investigated body units. In terms of total diversity in the forms of the head (68.59%), pronotum (80.26%), and abdomen (65.59%), the first three primary components account for and make up the most significant percentage. For all three morphological features, Procrustes ANOVA indicated significant differences in the forms with a determined p-value of 0.0001. The observed variability was verified using discriminant function analysis, showing that the collected data were utterly distinct. The observed form diversity is thought to be the outcome of the species' environmental adaptation and evolution, which has allowed them to coexist and prosper in the same habitat.

Keywords: *Cicindelids, Variability, Morphology, Tropical Beetles, Riparian*

[AB-O07] Species Diversity, Distribution, and Microhabitat Preferences of Anurans in Forested Areas of Brgy. Napangan, Don Victoriano Chiongbian, Philippines

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Abstract: Anurans are a group of amphibians that are severely threatened by anthropogenic disturbances. Therefore, this study sought to determine the diversity, distribution and microhabitat preferences of anuran fauna in Don Victoriano Chiongbian, Misamis Occidental, contributing to the overall understanding of anuran populations and their habitats in the region. A total of 8 days of fieldwork were conducted using opportunistic methods and active transect line walks from January 12-17, 2024, and April 4-7, 2024. Environmental factors were also measured in attempt to determine its possible influence on their distribution. A total of 97 individuals, representing 7 species belonging to 5 families were recorded. Site 3 (1050 masl) has the highest species richness followed closely by site 2 (850 masl) and site 1 (750 masl). All of the sites have relatively moderate diversity. Around 57.14% of the species recorded are Philippine endemic. Most of the species are categorized as least concern, however, the vulnerable *Pelobatrachus stejnegeri* and *Ansonia muelleri* were also recorded. Most species were found in aquatic (Type I) and ground (Type III) microhabitats, with multiple microhabitats while some are microhabitat specific. In terms of Canonical correspondence analysis, it revealed that few species in site 1 such as the *Leymnonectes leytensis* has strong correlation with stream width, leaf litter, water pH, and stream velocity. This area in Brgy. Napangan appears to support a relatively rich anuran species. Thus, it is essential to protect it in order to conserve these species, especially the vulnerable and the other threatened anuran population.

Keywords: *Anurans, distribution, microhabitat preferences, species diversity*

[AB-O08] Snakebite in Northern Vietnam: Statistics from a major hospital with notes on challenges and opportunities

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Abstract: Vietnam hosts a rich diversity of snakes, with approximately 246 species, including over 60 venomous species. This diversity, though ecologically significant, may contribute to the increasing incidence of snakebites. However, there is a notable lack of research on venomous snakes and snakebite epidemiology in the country, particularly in Northern Vietnam. This retrospective study recorded snakebite data from 2008 to 2020 at the Poison Control Center (PCC) of Bach Mai Hospital, one of the largest treatment center in Northern Vietnam, aimed to characterize snakebite incidents and identify risk factors. The study documented and analyzed around 5,805 snakebite cases at PCC over 12 years with Cobra species (*Naja* spp.) accounting for majority of cases (39%). Snakebite cases showed an annual increase throughout the study period. Key risk factors for snakebite incidents included male gender, rainy season occurrence, rural residency, and snake farming activities. Our findings underscore that snakebite envenoming is a complex issue involving various technical, environmental and social factors. Thus, a comprehensive One Health approach is crucial to address this multifaceted problem and can present an opportunity for collaborations from a variety of expertise.

Keywords: *venomous snake, snakebite, taxonomy, database, One Health, call for collaboration*

POSTER PRESENTATIONS

Plant Biology



[PB-P01] Synthesis of cabraleahydroxylactone and its activity toward α -glucosidase

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Abstract: Cabraleahydroxylactone (1a) is a naturally existed compound in *Aglaia abbreviata* plant that exhibits potential biological activities. While the natural resources yielded negligible quantities which are insufficient for further investigation, it is crucial to develop synthetic methods to overcome the limitation. This project was able to utilize cabralealactone (2) as a starting material for obtaining 1a. By employing aluminum trichloride hexahydrate and sodium cyanoborohydride, a reduction of cabralealactone (2) successfully produced both diastereomers 1a and 1b (3-epi-cabraleahydroxylactone). The yield of 1a surprisingly increased in a mixture with 1b, which was the only diastereomer observed in previous reports. Interestingly, the inhibitory activity against α -glucosidase illustrated an improvement with the diastereomers compared to cabralealactone and its precursor dipterocarpol (3). Compound 1a displayed the strongest inhibition with IC₅₀ at $43.79 \pm 1.81 \mu\text{g/mL}$, followed by 1b ($66.82 \pm 0.758 \mu\text{g/mL}$) and 2 ($63.55 \pm 0.96 \mu\text{g/mL}$), while 3 exhibited the weakest inhibition ($105.85 \pm 2.75 \mu\text{g/mL}$). Enzymatic kinetic study revealed that 1a and 1b functioned as partially non-competitive and partially competitive inhibitors, respectively. Notably, a synergistic effect of 1a and 1b was observed, suggesting a potential advantage of using the diastereomeric mixture over the separated forms. Furthermore, the mixture of these diastereomers from a practical reduction reaction also illustrated a combined effect on α -glucosidase inhibition. The observed synergistic effect between the diastereomers suggests that a combinatorial approach may be beneficial for optimizing the inhibitory activity against α -glucosidase, providing insights for future drug design strategies.

Keywords: α -glucosidase inhibition, Cabreahydroxylactone, 3-epi-cabraleahydroxylactone, cabralealactone, dipterocarpol, diastereomers, synergistic effect.

[PB-P13] The deep-dive analysis of the crown root formation in Vietnamese rice collection

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Abstract: Crown roots play a pivotal role in water absorption, nutrient uptake, and the adaptation of *Oryza sativa* (rice) to stressful conditions. In this study, we focus on investigating the crown root emergence process at the histological level within a Vietnamese rice collection by assessing the number of crown roots, number of primordia, and their respective ratios across different rice varieties in the two-weeks stage. The results revealed variations in the number of roots within two-weeks old rice accessions, ranging from 2 to 14. Out of them, 34 varieties were analyzed for primordia evaluation, demonstrating a fluctuation from 2 to 11, with the number of primordia versus number of crown roots ratio varying between 0.3 to 1.7. This indicates that root formation relies not only on initiation but also on emergence. Haplotype analysis delivered no genetic polymorphism in gene sequence of *CRL1* – a key gene in initiation and *CAND1* – a crucial gene in emergence. However, there are two single nucleotide polymorphisms (SNPs), Chr7_1300807 and Chr7_1300911, located on intron 7 of chromosome 7 of *CRL5* sequence, which is also a gene related to initiation. Through qPCR analysis targeting *CRL5* and *CAND1* on two groups of different haplotypes, varieties with CC genotype, whose ratio greater than 1, emerged with higher *CRL5* expression than varieties with TT genotype, whose ratio smaller than 1. This outcome indicated that mutants at this position make a notable contribution to expression level of *CRL5*, thus proposing a novel pathway in crown root formation. This study represents the first histological investigation into crown root formation within a collection of rice plants. These findings contribute to a deeper understanding of the mechanisms underlying crown root formation and development, offering initial data for the exploration of genes associated with rice root emergence.

Keywords: *CAND1*, *CRL1*, *CRL5*, Crown root emergence, Crown root initiation, *Oryza sativa*, Rice root anatomy.

[PB-P03] Phytochemical screening, antioxidant, and cytotoxicity activity of the ethanolic leaf extract of *Ficus fiskei* Elm.

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Abstract: *Ficus fiskei* Elmer is one of the 150 endemic *Ficus* species in the Philippines that remains understudied and underutilized. The objective of the present study is to determine the bioactive compounds present in the ethanolic leaf extract of *Ficus fiskei* through phytochemical screening. Assess its antioxidative capacity through DPPH. And evaluate its cytotoxicity through MTT assay on the A549 lung cancer cell line. Phytochemical screening revealed the presence of bioactive compounds such as alkaloids, flavonoids, and steroids. Data indicated that the ethanolic leaf extract exhibited weak antioxidant activity, with an EC₅₀ of 1092 µg/mL. Furthermore, the results indicate that plant sample extract has a mild cytotoxicity value to A549 cancer cells only at 62.5 µg/mL concentration. Future studies will identify the level of chemical components of *F. fiskei* major extracts responsible for anticancer activity and elucidate more detailed molecular mechanisms of cell death.

Keywords: A549 lung cancer cell line, DPPH scavenging activity, *Ficus fiskei* Elm., MTT assay, phytochemical screening,

[PB-P04] Investigation of antimicrobial and antibiofilm effects of some ethnopharmacological based Vietnamese medicinal plants

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Abstract: Multidrug-resistant bacteria are posing a threat to our global health, therefore finding out new potential medication is a priority. In our search for antimicrobial and antibiofilm properties of *Opuntia ficus-indica* L., as well as the metabolite profile of the plant in numerous extracts and fractions. The herbal aqueous fraction of *Opuntia ficus-indica* L., shows promising antifungal ability on *S. aureus*, *P. aeruginosa*, *S. maltophilia* while the extracts in 80% methanol solution and aqueous fraction can be applied for biofilm-formation resistance on *S. aureus*. During the metabolite profiling, various compounds were annotated, with terpenes and terpenoids accounting for the majority. In the future, our contribution might be continued research to precisely identify the composition in the plant, or to screen for potential drug-like compounds. Although further studies are required, the chance for *O. ficus-indica* L., in modern medication is clearly wide open.

Keywords: *Opuntia ficus-indica* L., metabolomics approach, antimicrobial, antibiofilm, metabolite profiling, UPLC-QToF-MS.

[PB-P05] Evaluation of salinity tolerance of mutant rice variety (*Oryza sativa* L.) using irradiation method

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Abstract: Rice (*Oryza sativa* L.) is a vital staple crop globally, but its susceptibility to salt stress poses significant challenges to productivity, particularly in regions like the Mekong Delta. Saline intrusion in this area induces osmotic stress, hampers germination, and alters root morphology. Our study explores the potential of low-dose gamma radiation, especially at 100 Gray, to mitigate these effects. We found that exposure to this radiation level enhances germination rates and seedling height, activating endogenous antioxidant enzymes to boost growth under salt stress. Additionally, gamma radiation increases chlorophyll and relative water content, while effectively counteracting the accumulation of Na⁺ and K⁺ ions induced by salt stress. However, higher doses, such as 300 Gray, exhibit adverse effects, including DNA damage, metabolic disruptions, altered root morphology, and inhibition of seedling growth and development. These findings underscore the nuanced effects of gamma radiation on rice resilience to salt stress and highlight the importance of dosage optimization for agricultural applications.

Keywords: *Gamma Ray, Irradiation, Oryza sativa, Salinity stress, antioxidant enzymes*

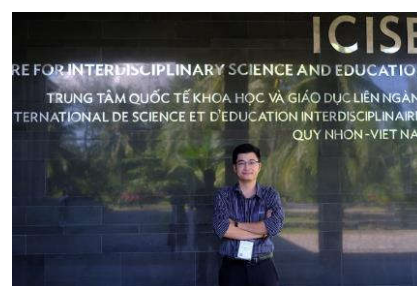
[PB-P06] Biomass and bioactive compound production in *Anoectochilus* sp. rhizome culture

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Abstract: *Anoectochilus* sp. is a valuable medicinal plant with a long history of use in traditional medicine. This study aims to optimize the culture conditions for rhizome biomass cultivation in *Anoectochilus lylei*, offering a sustainable alternative for biomass and bioactive compounds production. The highest rhizome induction rate of 98.9%, with a fresh weight (FW) of 12.64 g and a dry weight (DW) of 1.14 g, was achieved using MS medium supplemented with 2 g/L Hyponex I, 2 g/L Hyponex II, 2 g/L peptone, and 1.0 g/L activated charcoal. Rhizome proliferation peaked in 3/4 MS medium supplemented with 2 mg/L BA, 0.2 mg/L Kin, and 35 g/L sucrose. Among the various salt strengths tested (MS, SH, B5) in liquid cultures, 3/4 MS medium resulted in the highest rhizome proliferation, with 127.33 g/L FW and 20.40 g/L DW. The highest total phenolic content (4.9 mg/g DW) was observed in 1/2 MS medium, while the highest total flavonoid content (1.05 mg/g DW) and the highest polysaccharide content (150.66 mg/g DW) were recorded in control. However, 3/4 MS medium yielded the highest productivity for total phenolics, flavonoids, and polysaccharides. Additionally, the best results for rapid rhizome multiplication were obtained with 35 g/L sucrose (157.17 g/L FW; 20.67 g/L DW), followed by 20 g/L sucrose (109.42 g/L FW; 11.88 g/L DW) when tested in difference sucrose concentration. The highest total phenolic content (4.44 mg/g DW) and total flavonoid content (1.15 mg/g DW) were achieved with 10 g/L sucrose, while the highest polysaccharide content (115.87 mg/g DW) was found in the medium supplemented with 35 g/L sucrose. The optimal bioactive compound productivity was recorded at 35 g/L sucrose concentration. These findings can be applied to large-scale bioreactor cultures for biomass and bioactive compound production of *Anoectochilus lylei* rhizomes.

Keywords: *Anoectochilus lylei*, bioactive compounds, medium salt-strength, rhizome culture, sucrose concentration.

Acknowledgements: Dr. Ho Thanh Tam was funded by the Postdoctoral Scholarship Programme of Vingroup Innovation Foundation (VINIF), code VINIF.2023.STS.82.

[PB-P07] Identification of Alpha-Galactosidase gene in tomato plant

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Abstract: In recent years, Alpha-Galactosidase enzyme has been a growing interest in applying renewable resources for biorefineries, helping in xenotransplantation, transforming blood group from B to O, removing flatulence-causing factors in soy milk, and managing of Fabray's illness. Tomatoes are widely consumed around the world and are the second most economically valuable vegetable. It is the best fruit or vegetable in terms of vitamin and mineral content. This project intends to isolate the α -Galactosidase gene from tomato leaves and seeds. The selected samples were prepared, and their RNA was extracted using Total RNA Extraction Kit-Mini-Plant. The total RNA elution was checked for its concentration by the UV-Vis spectrophotometer. For complementary DNA synthesis, the isolated RNA was converted into cDNA by reverse transcription using TOYOBO Company reagents, then the PCR was used with the forward primer (ATGTCATCAACTTCACCACCCTCGTTGT) and reverse primer (TTTTTTTGGAGTAAGAACATACATGCTGCA) to detect α -Galactosidase gene. As the results, the targeted DNA band size (1.3 Kbp) of α -Galactosidase gene was detected in germinating of tomato seeds, where it involves in the mobilization of carbohydrate reserves during and following tomato's seed germination; while there was no evidence that illustrates the appearance of α -Galactosidase in tomato leaves. This result is significant for further research on α -Galactosidase gene overexpression to increase the enzyme α -Galactosidase amount for medical application.

Keywords: *Alpha-Galactosidase, cDNA, Oligosaccharides, PCR, Tomato plants*

[PB-P08] Preliminary morphological and molecular biological data of yellowcress plants (*Rorippa* sp.) in Vietnam

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Abstract: The wild crucifer plants, particularly *Rorippa* species, represent an important yet understudied component of Vietnam's biodiversity. Among them, yellowcress (cải đất), an annual herb in the Brassicaceae family, is commonly found across Asia. It grows year-round but is most prevalent from March to May and is widely used as a vegetable in several Asian countries. The natural aphid tolerance observed in yellowcress offers significant potential for agricultural applications, particularly in mustard oil production, where aphid infestations by *Lipaphis erysimi* pose significant threats. Plant samples were collected from gardens in Hanoi, Hung Yen, and Quang Ninh provinces. These samples have herbaceous stems that are either erect or branching, reaching heights of 10-50 cm. The leaves vary in shape, initially measuring 4-10 cm long and 1.5-2 cm wide during the early growth stage, with a green or green-purple hue. The leaf blades are lanceolate or elongate, with entire or serrated edges and lobes at the base. The flowers are small, predominantly yellow, and arranged in racemes. They generally lack petals, have four sepals, and typically six stamens. The siliques are linear and cylindrical, about 2-3 cm long, with seeds arranged in two rows. PCR was performed to amplify four key genes: *HSPRO* (1303 bp), *rbcL* (1198 bp), *matK* (2244 bp), and *18S* rRNA (996 bp). The amplified fragments were sent to 1stBase (Axil Scientific Pte Ltd, Singapore) for sequencing. Phylogenetic analyses of yellowcress plants revealed a close genetic relationship between *Rorippa indica* and *Rorippa dubia*. In conclusion, the preliminary morphological and molecular data on *Rorippa* species in Vietnam, particularly the identification of the *HSPRO* gene associated with aphid resistance in yellowcress, suggest that this wild crucifer species could serve as a valuable genetic resource in breeding aphid-resistant mustard varieties. The combination of aphid resistance and adaptability to environmental stress makes this wild crucifer plant a promising candidate for sustainable agriculture, warranting further research and exploration.

Keywords: *Lipaphis erysimi* resistance gene, *Rorippa dubia*, *Rorippa indica*, wild crucifer, yellowcress

[PB-P09] A Comparison of Orchid Mycorrhizal Fungi Communities in the Rhizosphere of *Dendrobium* and *Cymbidium* Orchids

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Abstract: *Cymbidium* and *Dendrobium* are two prominent genera within the Orchidaceae family, representing distinct growth forms: terrestrial and epiphytic, respectively. However, the growth and development of these orchids must be closely linked to their symbiotic relationships with appropriate Orchid Mycorrhizal Fungi (OMFs). This study aimed to identify and compare the OMF communities in the rhizosphere of *Cymbidium* sp. and *Dendrobium* sp. A total of 60 root samples (30 from each species) were collected, stained with Trypan Blue, and examined under a light microscope. The OMF spores were then isolated, cultured on potato dextrose agar (PDA) medium, and assessed for their ability to promote *Cymbidium* seed germination on sterilized black sphagnum. The fungal strains with high germination-promoting potential were then, selected and identified through morphological characteristics and sequencing of the Internal Transcribed Spacer (ITS) region using ITS1/ITS4 primers. The results revealed five filamentous OMF forms in the roots of *Cymbidium* sp. and six OMF forms in *Dendrobium* sp. Morphological and molecular analyses indicated that the S3 strain, presented in both genera belonging to the genus *Trichoderma* and promoted seed germination at rates ranging from 13.5% to 18.0%. These findings suggested a complex role of OMFs in orchid root symbiosis, with implications for their potential application in orchid breeding and sexual propagation without the need for in vitro culture techniques.

Keywords: *Cymbidium*, *Dendrobium*, Internal Transcribed Spacer (ITS), Orchid Mycorrhizal Fungi (OMFs), propagation.

[PB-P10] Influence of the elicitors on the accumulation of secondary metabolites and antioxidant activity in the *Polyscias fruticosa* (L.) Harms *in vitro* roots

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Abstract: *Polyscias fruticosa* (L.) Harms, belonging to the Ginseng family (*Araliaceae*), is a valuable medicinal plant in Vietnam. Recognized in the Vietnamese Pharmacopoeia, it is esteemed for its antioxidant, anti-inflammatory, and antipyretic properties, making it a significant contributor to traditional medicine. This research contributes to the understanding of elicitor-induced changes in antioxidant activity, and secondary metabolite content of *in vitro* root extracts of *P. fruticosa*. The results showed that the antioxidant activity of the root extract tested by DPPH radical scavenging assay with an IC₅₀ value of 1.28 mg/mL in the baseline and the lowest IC₅₀ value of 0.89 mg/mL in the medium treated with yeast extract (YE). The highest total phenolic and flavonoid content were displayed in jasmonic acid-treated samples at 24.31 ± 2.86 mg galic acid/g extract and 29.25 ± 0.26 mg quercetin/g extract, respectively. The highest saponin was also produced in roots elicited by jasmonic acid, where it reached about 167.19 ± 3.29 mg aescin/g extract. Furthermore, investigation with antioxidant enzyme activities showed another superiority when using elicitors YE (64.4 ± 3.14 U/mg protein) and mannitol (Man) (65.39 ± 3.85 U/mg protein) in peroxidase (POD) activity and using jasmonic acid (8.87 ± 0.74 U/mg) in catalase (CAT) activity. Lastly, TPC and TFC exhibited a positive correlation of $r = 0.53$, while the TPC and DPPH scavenging activity and TFC and POD showed a remarkably negative correlation of r around -0.8. In conclusion, this study highlights the advancements in eliciting root cultures to enhance specific phytochemicals and antioxidant activity. The information provided holds significant value and will be of interest to scientists engaged in plant biotechnology, particularly in the elicitation of medicinal plant roots.

Keywords: Antioxidant, elicitors, *in vitro* tissue culture, *Polyscias fruticosa* (L.) Harms, secondary metabolites.

[PB-P11] Endogenous auxin from bacteria stimulated IR64 rice plant growth (*Oryza sativa* L.)

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Abstract: *Oryza sativa* L. is a member of the Poaceae family, renowned for its exceptional plant productivity, capacity to thrive in many environmental circumstances, and resilience to some pests and diseases. This study focused on the positive effects of a phytohormone from bacterial suspension, a bacteria known for promoting plant growth by producing essential phytohormones such as auxins, cytokinins, and gibberellins. The bacterial suspension was pre-treated using two methods: autoclaving and filtration with a syringe filter. The phenotypic parameters were measured after 14 days of culturing IR64 rice seedlings on MS medium supplemented with bacterial phytohormones. It was observed that when applying autoclaved bacteria suspension, it produced superior results in number of roots (16 ± 1), shoot length (22.27 ± 1.33 cm), root length (9.03 ± 0.68 cm), shoot weight (112.7 ± 2.97 mg), and root weight (99.55 ± 15.48 mg) of rice plants compared to control. Besides, the content of hormone IAA and antioxidant enzyme activities in the IR64 plants grown on the medium containing autoclaved bacterial suspension was higher than the filter bacterial suspension and control. In addition, the study emphasized the notable difference in gene expression. The roots of plants treated with autoclaved bacteria suspension showed much-increased expression of genes encoding catalase and peroxidase antioxidant enzymes, with fold changes that were 3.7 and 1.5 times greater than the control. Notably, the plantlets derived from the medium containing autoclaved bacterial suspension had better acclimatization and growth under *in vitro* conditions than the ones in the medium with the filter bacterial suspension and control. The study emphasizes the potential of bacterial phytohormones in enhancing rice growth and suggests future exploration of their synergistic effects with other growth-promoting mechanisms. Overall, these findings highlight promising agricultural applications for bacterial phytohormones.

Keywords: antioxidant, auxin, bacterial suspension, phytohormone, plant-microbial interaction.

[PB-P12] Characteristics of the proteins in vacuolar iron transporter (VIT) family and expression level of some OsVIT genes in rice (*Oryza sativa* L.)

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Abstract: Vacuolar Iron Transporters (VITs) are the transport proteins by which iron in plant cells can be transported into the vacuole for storage, helping to reduce the adverse effects of excess iron. Vacuolar Iron Transporter-like (VTLs) also participate in the process of transporting iron into the vacuole. In this study, using bioinformatics tools, based on comparison with EgVIT1, 9 VITs in rice were identified along with the same family proteins in *Arabidopsis thaliana* (6 proteins) and in maize (8 proteins). The data show that VIT family proteins in rice range from 69 to 252 a.a. in length, molecular mass from 7.263 to 26.551 kDa, isoelectric point from 4.69 to 8.57. Most of the VIT family proteins in rice have five transmembrane domains and were identified to be expressed in the vacuolar membrane. The protein sequences were compared, homology motifs were identified, and a phylogenetic tree was constructed, showing a close relationship between VIT proteins in monocots and dicots. Expression data of four of the VIT family genes in rice showed that *OsVIT2*, *OsVTL1*, and *OsVTL2* genes were highly expressed in early-seeded seeds and then decreased as the seeds developed. In particular, *OsVIT1* was highly expressed in roots and leaves but not at any other stage of the seeds. *OsVIT1* has the potential to be a target gene for studies on improving iron content in seeds.

Keywords: bioinformatics, gene expression level, iron transport, *OsVIT* gene family, vacuolar iron transporter (VIT), .

[PB-P13] Investigating the phytochemical production and antioxidant activity in four plant species belonging to the *Asteraceae* family

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Abstract: Vietnam has a rich and profound traditional medicine system that is widely used today. Medicinal plants are used to treat colds, coughs, bone and joint diseases, digestion, respiratory diseases, etc. In this study, leaves of *Artemisia vulgaris*, *Taraxacum*, *Blumea balsamifera* and flowers of *Xerochrysum bracteatum* from the *Asteraceae* family were selected to determine the antioxidant capacity and relationship with the active ingredients in the plants. The methanolic extracts were screened for antioxidative activity and chemical compositions via the total phenolic content (TPC) assay, the total flavonoid content (TFC) assay, and DPPH radical scavenging activity. The highest radical scavenging activity was observed in the flowers of *X. bracteatum* ($IC_{50} = 0.0608$ mg/mL), followed by the leaves of *Taraxacum* ($IC_{50} = 0.3132$ mg/mL), *A. vulgaris* ($IC_{50} = 1.367$ mg/mL), and *B. balsamifera* ($IC_{50} = 1.4502$ mg/mL). The TPC of the studied plants ranged from 19.98 ± 1.355 to 195.78 ± 42.518 mgGAE/g extract, while the TFC ranged from 60.31 ± 1.725 to 339.14 ± 26.299 mgQE/g extract. The highest TPC and TFC were recorded in the methanol extract of *X. bracteatum*. The strongly negative correlation between the TPC and TFC and the IC_{50} values ($R^2 = -0.78$, $R^2 = -0.76$) suggests that TFC and TPC could strongly contribute to the antioxidant activity of these plants. *X. bracteatum* was observed to have the highest antioxidant activity, followed by *Taraxacum*, *A. vulgaris*, and *B. balsamifera*. These results not only highlight the relevance of these plants in traditional medicine but also scientifically validate their use, particularly in the context of their antioxidant properties. The study underscores the close relationship between the traditional use of these plants and their scientifically observed effects, reinforcing the value of folk remedies.

Keywords: Antioxidant, *Asteraceae*, flavonoid, free radical scavenging activity, phenolic, secondary metabolites.

POSTER PRESENTATIONS

Microbiology



[MB-P01] Enhancing bioactive content and selective antibacterial activity of *Hylocereus undatus* peel extract via *Aspergillus niger* solid-state fermentation

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Abstract: Improper management of agro-industrial waste not only poses environmental and public health risks, but also squanders valuable resources. This study explores the potential of *Aspergillus niger* solid-state fermentation (SSF) as a sustainable approach to valorize *Hylocereus undatus* peel extract (DFPE) by enriching its bioactive content. Response surface methodology (RSM) was employed to optimize post-SSF extraction conditions specifically for maximizing total phenolic content (TPC). The optimal parameters identified for extraction were 41.9% ethanol concentration, 51.8 mL/g solvent-to-solid ratio, 21.4 minutes sonication time, and 28.7°C temperature. Fermented DFPE exhibited significantly higher TPC and TFC levels (5 times) compared to the unfermented extract. This enhancement was directly correlated with a twofold improvement in antioxidant and antibacterial selectivity. The fermented DFPE exhibited strong antibacterial activity against both *Escherichia coli* and *Staphylococcus aureus* with larger inhibition zone and lower inhibitory concentration. Notably, the fermented extract displayed higher selectivity, with lower inhibitory effects on the probiotic bacteria *Lactobacillus delbrueckii subsp. bulgaricus* and *Streptococcus thermophilus* at higher concentration of fermented extract, compared to the unfermented extract. Overall, this study establishes optimal conditions and demonstrates the potential of SSF with *Aspergillus niger* to enhance the bioactive content of DFPE. This approach offers a sustainable solution for waste valorization and opens avenues for the application of fermented DFPE in the food, cosmetic, and pharmaceutical industries.

Keywords: Optimization, Solid-state fermentation, extraction, *Hylocereus undatus* Peel, dragon fruit peels, polyphenols.

[MB-P02] Genomic Insights into *Ralstonia* Phages Uncovers 8 Clusters and 3 Singletons

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Abstract: *Ralstonia solanacearum*, a select agent in the United States and a quarantined pest in the European Union, threatens global food security by infecting economically important plants. The most abundant bacteria infecting viruses – bacteriophages, can infect this robust species complex. They can destroy and change the morphology and virulence of their host. Despite its importance in prokaryotic evolution and wide range of applications in combating antimicrobial resistance, research on bacteriophages infecting a single host is still limited. This study compared the genomes of 37 *R. solanacearum* infecting phages from the NCBI virus database. There is extensive genomic diversity despite originating from one specific host. The genome size ranged from 5.48 kb to 279.85 kb, the GC percentage ranged from 52.3% to 65.3%, and the number of Open Reading Frames (ORFs) ranged from 3 to 289. Based on the pairwise average nucleotide identity of each genome and synteny explored by dot plot analysis, 34 of the 37 genomes can be grouped into 8 clusters, 3 of which can be divided into subclusters remaining three phages are singletons. This study provided not just a digest of genome characteristics of each phage but also an opportunity to study specific proteins in each cluster for further understanding of *Ralstonia* phage evolution, diversity, and phage-host interaction.

Keywords: Genome synteny, *Ralstonia solanacearum*, bacteriophages

[MB-P03] Investigating the Antibacterial Activities of *Jatropha podagrica* Extracts Against Methicillin-Resistant *Staphylococcus aureus* in Dog's Pyoderma via *in vitro* and *in silico* Analysis

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Abstract: Previous studies have shown that *Jatropha podagrica*, a succulent shrub extensively available around the world in tropical and subtropical regions, possesses significant medicinal potential, namely antibacterial, antioxidant, cytoprotective, and antiproliferative effects. This scientific research studied the effects of the extracts of different parts of the plant on methicillin-resistant *Staphylococcus aureus* (MRSA), a common agent of pyoderma in dogs, thereby unveiling a potential prevention and treatment strategy for dogs with pyoderma. The process involved evaluating the antibacterial activities of the extracts of *J. podagrica* roots, stems, and leaves through conducting antimicrobial assays and performing molecular docking to model the interaction of the bioactive compounds with penicillin-binding protein 2a (PBP2a) of MRSA. The obtained results showed that the extracts of *J. podagrica* roots and stems exhibited good antibacterial activities against MRSA, with the n-hexane and ethyl acetate fractions having the greatest potential. The minimum inhibitory concentration against MRSA of the n-hexane fraction extract was 1.56 mg/mL, while that of the ethyl acetate fraction extract was 3.13 mg/mL. However, these extracts only had bacteriostatic effects against MRSA. Molecular docking analysis of the bioactive compounds extracted from *J. podagrica* roots showed that the compounds 16-hydroxyphorbol (7.9 Kcal/mol), jatrophone (-7.64 Kcal/mol), and 2-epihydroxyisojatrogrossidion (-7.48 Kcal/mol) showed a greater binding affinity toward PBP2a as compared to the standard drug Ceftobiprole (-6.99 Kcal/mol). From the results, the plant species could be a viable choice for *in vivo* testing in the future as inexpensive, herbal-based dermal creams for skin infections in dogs.

Keywords: *Jatropha podagrica*, antibacterial activity, methicillin-resistant *Staphylococcus aureus*, PBP2a, pyoderma.

[MB-P04] DNA Isolation and Identification of *Escherichia coli* O157:H7 Isolated from Fresh Vegetables in Phnom Penh

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Abstract: Fresh-eaten vegetables have become more popular in Cambodian diet. However, according to WHO, these vegetables should be one of the main sources of infection if contaminated with pathogenic microorganisms. The outbreaks of foodborne diseases related to fresh fruits and vegetables have been increasingly reported and raised concerns regarding the safety of these products. Therefore, it is very important to conduct determination virulence strain of *Escherichia coli* in fresh vegetables. This study aims to identify of *Escherichia coli* O157:H7 from fresh vegetables including cucumber (fruit vegetable), saw leaf (straight-leafy vegetable), and lettuce (curly-leafy vegetable) from different market and supermarket in Phnom Penh. Total of forty-two isolated bacteria from cucumber, lettuce, and saw leaf samples (fourteen for each type of vegetable) have been done for bacterial DNA isolation. Then, the conventional PCR method was used to detect virulence strain of *E. coli* (O157:H7) of each samples using stx primers. The results indicate that the virulence strain of *E. coli* has found most in the curl-leafy vegetables (lettuce) than straight-leafy vegetable and fruit vegetable (saw leaf and cucumber). The *E. coli* O157:H7 have not detected in all the tested cucumber samples, while the five of fourteen saw leaf samples have carried that virulent strain. Moreover, among fourteen of lettuce samples, there were ten samples that have been found the O157:H7 strain. This research may be used to raise public awareness of washing fresh vegetables with clean water more carefully to reduce adverse health impacts.

Keywords: DNA isolation, PCR, Virulence factor, *Escherichia coli*, *Salmonella*.

[MB-P05] Phenotypic changes of *Pseudomonas aeruginosa* in responding to Gentamicin

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Abstract: Gentamicin, an aminoglycoside antibiotic, is an important option to treat infections caused by *Pseudomonas aeruginosa*. This study aimed to evaluate the effects of serial exposure to sub-MIC levels of gentamicin on the bacterium's physiology and resistance. *Pseudomonas aeruginosa* ATCC 9027 was exposed to sub-MIC levels of gentamicin over 14 days, resulting in the resistant strain Ge-E1. This strain was then cultured in an antibiotic-free environment for 10 days, producing the strain Ge-E2. The susceptibility profiles, morphology, and key virulence factors—including protease activity, biofilm formation, pyocyanin, pyoverdine, elastase, rhamnolipid production, and swimming and swarming motility—of the gentamicin-exposed strains (Ge-E1 and Ge-E2) were analyzed in comparison to the original strain (*P. aeruginosa* ATCC 9027). The results showed that the original strain, with an MIC of 2 µg/mL, evolved into the resistant strain Ge-E1, with an MIC of 64 µg/mL. However, Ge-E2 showed a significant decrease in MIC to 4 µg/mL. Similar trends were observed in susceptibility profiles, with no cross-resistance to other antibiotic classes. Morphologically, Ge-E1 displayed significantly reduced cell size compared to the original strain, with this reduction reversed in Ge-E2. Regarding virulence factors, there were significant differences in protease, biofilm, and elastase production among the strains. Additionally, gentamicin treatment inhibited rhamnolipid secretion and decreased the production of pyocyanin and pyoverdine. This study provides valuable insights into the adaptive responses of *P. aeruginosa* to gentamicin exposure, identifying potential targets for combating antibiotic resistance.

Keywords: Antibiotic; gentamicin; resistance; virulence, *Pseudomonas aeruginosa*

[MB-P06] The effects of peanut oil on growth, development and cordycepin content of *Cordyceps militaris*

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Abstract: *Cordyceps militaris* is a valuable mushroom that has been widely used around the world. This study was conducted to investigate effects of peanut oil on the growth, development and cordycepin content of *C. militaris* fruiting bodies, aiming to enhance the quality of *C. militaris* for consumer needs. The study added peanut oil to the first, second propagation media and the fruiting body culture media. The results of the study showed that supplementing 3% peanut oil in the first medium, 2% in the secondary propagation medium, and 2.5% in the fruiting body medium was suitable for fruiting body formation. The mycelial growth rate increased by 1.22 times compared to the control, the number of fruiting bodies increased by 1.32 times, and the cordycepin content reached 156 mg/kg, which was 2.14 times higher than the control.

Keywords: *Cordyceps militaris*, peanut oil, culture, mycelium, culture conditions.

[MB-P07] Determination of antifungal activity against *Trichophyton rubrum* of *Piper betle* L. extract using ultrasound-assisted extraction method

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Abstract: Scalp fungus, caused by fungi like *Trichophyton rubrum*, is a common and persistent condition with symptoms such as itching, hair loss, and discomfort. Despite existing antifungal medications, there is a rising demand for natural alternatives. Betel leaves, a traditional medicinal plant, have shown potential therapeutic benefits. This study aims to investigate the antifungal properties of betel leaf extract against *Trichophyton rubrum*, using ultrasound technology to enhance its effectiveness. By combining natural and technological approaches, we hope to develop a promising solution for treating scalp fungus. In this study, *Piper betle* L. extracts were obtained using ultrasound-assisted extraction method with different solvents (96 ethanol, and water). The extracted solution was filtered through Whatman filter paper, the extracts were obtained after removing the solvent by water bath method. The biological compounds of the extracts were examined using different biochemical assays, namely total phenolic content, and total flavonoid content. DPPH (2,2- diphenyl-1-picrylhydrazyl) was used to determine the antioxidant activity. The extracts of *Piper betle* L. were evaluated *in vitro* for anti-fungal activity against *Trichophyton rubrum*, using the agar well diffusion and solid diffusion assays. The results showed that the ethanol 96 extract of *Piper betle* L. had better secondary metabolite content, antioxidant activity, and antifungal activity than the water extract of *Piper betle* L. The total phenolic and flavonoid content of ethanol 96 extract was 567.228 mg GAE/g extract and 21.926 mg QE/g extract compared to 84.4 mg GAE/g extract and 3.46 mg QE/g extract of water extract. IC₅₀ value of extracts from ethanol 96 and water solvents varied significantly and was found at 1 mg/mL và 3.46 mg/mL. Ethanol 96 extract of *Piper betle* L. inhibited 100% the growth of *T. rubrum* from concentrations of 1.25 mg/mL, water extract inhibited 100% at the concentration of 25 mg/mL. Initial results showed that ethanol 96 extract of *Piper betle* L. using ultrasound-assisted extraction method had strong fungicidal effects against *Trichophyton rubrum*.

Keywords: Antifungal activity, antioxidant activity, secondary metabolite, *Piper betle*, ultrasound method.

[MB-P08] Study on the cholesterol – lowering potential of *Lactobacillus plantarum* V3 combined with *Solanum procumbens* and *Gynostemma pentaphyllum* extracts

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Abstract: Lactic acid bacteria (LAB) are beneficial microorganisms crucial for human health and widely used in probiotics and lactic fermentation products. Recognized as "Generally Recognized as Safe" (GRAS), LAB have become essential in probiotic development due to their benefits, including improved digestion, enhanced immunity, and reduced blood cholesterol. Moreover, medicinal plants in Vietnam, like *Gynostemma pentaphyllum* and *Solanum procumbens*, are known for their cholesterol and blood glucose-lowering effects. The combining LAB with these plant extracts for health benefits has been understudied. This study examined the cholesterol-assimilating activity of *Lactobacillus plantarum* V3 combined with these extracts. The mixture of *Gynostemma pentaphyllum* extract and the bacterial strain at a ratio of 2:10 (v/v) resulted in a cholesterol assimilation rate of 51.65%. Similarly, the combination of *Solanum procumbens* extract with the bacterial strain at the same ratio led to a cholesterol assimilation rate of 48.92%. Furthermore, the combination of *L. plantarum* V3 with plant extracts at a concentration of 10 mg/mL in a 2:10 (v/v) ratio demonstrated inhibitory effects against the pathogenic bacterium *Salmonella typhimurium* ATCC 14028. Additionally, when combined with plant extracts at concentrations of 10 mg/mL, 20 mg/mL, 40 mg/mL, and 80 mg/mL, all in a 2:10 (v/v) ratio with the *L. plantarum* V3 strain exhibited antimicrobial activity against the pathogenic bacterium *Staphylococcus aureus* ATCC 25923.

Keywords: *Lactobacillus plantarum*, cholesterol – lowering potential, *Solanum procumbens* extract, *Gynostemma pentaphyllum* extract, antimicrobial.

[MB-P09] Investigation of *Bacillus* strain WS2 from marine water for use as probiotics

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Abstract: The existence of *Escherichia coli* and *Klebsiella pneumoniae*, both drug-resistant pathogens, poses a significant health threat, making standard treatments often ineffective. While current drugs have increased survival rates, they are not without adverse side effects. However, probiotics are increasingly recognized as safe for human consumption and offer a promising alternative. They can serve as a valuable adjunct in treatment, contributing to the achievement of the Sustainable Development Goals (SDGs), particularly SDG3, which emphasizes good health and well-being. Consequently, the study explores the probiotic potential of *Bacillus* strain WS2 in accordance with ICMR guidelines. Marine water samples from the coastal regions of the Andaman and Nicobar Islands were evaluated. The bacterial strain was identified by Polymerase Chain Reaction (PCR) targeting the 16S rRNA gene and assessed for their probiotic potential which included testing their resistance to gastric acidity and bile acid, bile salt hydrolase activity, antimicrobial activity against pathogenic bacteria like *Escherichia coli* and *Klebsiella pneumoniae* (Microbial Type Culture Collection strains) using crude extract from bacterial strain WS2, and their ability to adhere to HT-29 cell lines. Our findings highlight that *Bacillus* strain WS2 is gram-positive, motile, gamma hemolytic, and PCR-positive, with an approximate product size of 1500 bp. The strain WS2 demonstrated rapid growth in fluids simulating gastric and bile acids, subsequently producing high levels of bile salt hydrolase and exhibiting antimicrobial activity against *Klebsiella pneumoniae* with inhibition zones of 8 mm (40 µL). The strain WS2 did not show any activity against *Escherichia coli*. Additionally, results on the adherence of strain WS2 to HT-29 cells are pending. In conclusion, our investigation suggests that *Bacillus* strain WS2 possesses probiotic potential by reducing *Klebsiella pneumoniae* survival and supporting the maintenance of beneficial gut microbiota.

Keywords: *Bacillus* species, probiotics, antimicrobial potential, *Escherichia coli*, *Klebsiella pneumoniae*, gut health.

[MB-P10] A pilot study to analyze the composition and diversity of healthy gut microbiota of Vietnamese and other populations

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Abstract: Understanding the gut microbiome and the complex community of microorganisms is crucial for maintaining overall health. It is reported that healthy individuals often have different gut microbiota, and these differences can be partly influenced by their country of origin or their race. This pilot study aimed to compare the gut microbiota compositions of healthy Vietnamese and healthy individuals from other populations using shotgun metagenomics approach. Sequencing data of healthy Vietnamese cohort was generated in this study, while the data of healthy individuals from other population was extracted from public sources. Each cohort, comprising 30 samples, was analyzed for abundances of specific taxa, alpha and beta diversity. Preliminary results revealed consistently significant differences in gut microbial species between populations. We also observed microbial features associated with population and geography, which will inspire the need for additional research to establish correlations between specific microbial properties and individual health status.

Keywords: Gut microbiota, microbiome, Human gut microbiota, healthy gut of Vietnamese, Shotgun metagenomics

[MB-P11] Developing A Bioinformatics Pipeline for Compositional Analysis of the Human Gut Microbiome

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Abstract: The relationship between the gut microbiota and human health has been increasingly demonstrated. Currently, there is a growing interest in research to determine the composition of the gut microbiota, as the immune system, metabolism, and defense against infections are significantly influenced by intestinal microorganisms. Next-generation sequencing (NGS) methods for DNA have become the preferred approach for comprehensively identifying the complex and diverse microbial communities in the human gut. This project aims to develop a bioinformatics pipeline for analyzing the human gut microbiome composition. The proposed pipeline processes sequencing data through four key stages: assessing the sequencing quality of input data, preprocessing the data, removing host sequences present in the samples, and performing taxonomic profiling based on k-mer approach to identify the presence of microorganism.

By using both simulated and real datasets, the obtained results show that Bowtie2 is an effective tool for removing human genome sequences. Ganon outperforms two other k-mer based tools, Kraken2 and KMCP, in taxonomic classification. Collectively, this developed pipeline represents a valuable resource for gut microbiome research.

Keywords: Human gut microbiome, gut microbiome analysis, gut microbiota taxonomic profiling, metagenomic sequencing, bioinformatics pipeline.

[MB-P12] Identify *Lactobacillus acidophilus* in probiotic formulations using the real-time PCR technique

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Abstract: The Vietnamese market currently offers a variety of probiotic products containing *Lactobacillus acidophilus* in the form of functional foods and biological products. To ensure these products' quality and efficacy, it is crucial to establish reliable methods for both qualitative and quantitative analysis of this bacterium. Despite numerous global studies investigating techniques such as culturing, biochemical analysis, and molecular biology methods like PCR and real-time PCR, challenges with accuracy and specificity persist. Therefore, this study focused on developing a real-time PCR method with specific primers to quickly identify and quantify *L. acidophilus* in commercial products. This method involved designing primers for PCR and real-time PCR specifically targeting the *tilS* gene. The primers were thoroughly tested against 151 *L. acidophilus* strains in the NCBI database using Geneious Prime® software to confirm their binding capability. The results indicated that the primer pair LA.qPCR.F-R had high specificity, with all 19 negative reference samples yielding negative results. Positive reference strains produced fluorescence signals with Ct values ranging from 16 to 18. According to the standard curve generated for the *L. acidophilus* strain ATCC 4356, the assay's detection limit was 2.01×10^2 cells per μl . The standard curve also exhibited a strong correlation coefficient in linear regression analysis (0.9959), with a slope of -3.096 and a qPCR efficiency of 110.0%. Additionally, the qPCR method achieved an R^2 coefficient ≥ 0.99 , indicating high amplification efficiency.

Keywords: *Lactobacillus acidophilus*, real-time PCR, probiotics, microbial products.

[MB-P13] Applying real-time PCR in quantitative and qualitative analysis of *Lactiplantibacillus plantarum* in bio-products

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Abstract: *Lactiplantibacillus plantarum* is a versatile probiotic bacterium with significant applications in both human health and agriculture. In the context of probiotics, it plays a crucial role in promoting digestive health by balancing intestinal flora, enhancing immune responses, producing antimicrobial substances that inhibit pathogenic bacteria, and supporting cardiovascular health by lowering cholesterol levels. In agriculture, *L. plantarum* is used in biofertilizers to improve plant growth by enhancing soil health, increasing nutrient availability, and suppressing harmful pathogens. This dual functionality highlights its importance in both human wellness and sustainable farming practices. To ensure the quality control of bio-products that contain *L. plantarum*, our research group developed a sensitive and specific real-time PCR method for detecting this bacterium in marketed products. This method involves designing primers for PCR and real-time PCR, specifically targeting the *tilS* gene. The identification of *L. plantarum* was based on the sequences of the *tilS* and *16S rRNA* genes. Primers for the real-time PCR was rigorously tested against 238 *L. plantarum* taxa in the NCBI database using Geneious Prime[®] software to ensure its binding capability. Further specificity checks were conducted using the BLASTN application on NCBI, which confirmed that the selected primer pair was highly specific to *L. plantarum*. The real-time PCR method was then applied to gDNA from two positive controls (*L. plantarum* ATCC 14917 - ALp14 and *L. plantarum* VTCC 10936 - VLp10), 13 putative *L. plantarum* strains isolated from bio-products, and 30 reference bacterial species. The results confirmed the presence of *L. plantarum* through amplification curves and melting peaks, with Ct values ranging from 9.65 to 18.47 at Tm from 83.08-84.65 for DNA concentrations of 10⁷ cells per µl. The qPCR standard curve, constructed from a 10-fold dilution range of 10⁷ to 10⁰ cells per µl of positive controls, gave Ct values ranging from 9.65 to 36.48. This indicated a detection limit as low as one cell per µl at Ct values of 32.5 and 36.48 for Alp14 and VLp10 respectively, demonstrating a strong linear relationship with a correlation coefficient (R²) of approximately 0.99. The slope of the curve ranged from -3.36 to -3.21, with an amplification efficiency (e) greater than 98%. This linear relationship between Ct values and cell numbers allows for accurate quantification of *L. plantarum* in various samples.

Keywords: *Lactobacillus*, real-time PCR, plant growth-promoting rhizobacteria, microbial products, bio-fertilizers, probiotics, agricultural applications, *L. plantarum*.

[MB-P14] Specific quantitative detection of *Bacillus pumilus* in commercial products using real-time PCR

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Abstract: *Bacillus pumilus* is a bacterium known for its significant role in agriculture, where it is commonly used in bio-products. Notably, two products marketed by Bayer-YieldShield (GB34) and Sonata™ ASO (QST2808)-were originally reported to contain *B. pumilus* as the active ingredient. However, recent taxonomic re-evaluations revealed that the strains GB34 and QST2808 actually belong to *B. altitudinis*. Given the importance of quality and safety management in microbial products containing *B. pumilus*, there is a need for rapid and accurate methods to detect the target species. To address this, researchers have developed a qualitative identification method for *B. pumilus* using real-time PCR. This method is designed based on the genomic characteristics of the *B. pumilus* complex group. The binding capability of primers for real-time PCR reactions was confirmed by comparing nucleotide sequences from 113 *B. pumilus* complex reference genomes available on NCBI using Geneious Prime® software. Specificity checks performed using the BLASTN application on NCBI demonstrated that the selected primer pair was highly specific to *B. pumilus*. Real-time PCR reactions were conducted in triplicate on gDNA from positive controls (ATCC 7061 – ABp70, and ATCC 14884 – ABp14), four putative *B. pumilus* strains isolated from bio-products, and 30 reference bacterial species. The results showed Ct values for the positive control ABp70 and the tested *B. pumilus* samples ranging from 15.23 to 27.97, with melting temperatures (T_m) between 72°C and 75.13°C. The assay's detection limit was determined to be 8.86 x 10³ cells per µl, with a correlation coefficient of 0.9967 in the linear regression analysis. The slope for ABp70 was -2.6512, with a reaction efficiency (E) of 138.33%, indicating a strong correlation between Ct values and cell numbers, enabling precise detection and quantification of *B. pumilus* in marketed products.

Keywords: *Bacillus pumilus*, real-time PCR, plant growth-promoting rhizobacteria, microbial products, bio-fungicide, bio-fertilizers.

[MB-P15] Study on the prevalence of efflux pumps in clinical *Staphylococcus* spp. and their role on biocide resistance.

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Abstract: Efflux pumps represent a resistance mechanism employed by various bacteria against antimicrobial compounds. The presence of multiple bacterial strains carrying efflux pumps potentially diminishes the effectiveness of disinfection in hospitals, thereby heightening the risk of hospital-acquired infections. In this study, *Staphylococcus*, a genus frequently encountered in hospital-acquired infections, was isolated to assess its resistance to biocides such as benzalkonium chloride. Surface samples directly in contact with patients - were collected and incubated in a selective medium, followed by preliminary classification by Gram staining. Eighty-nine strains were isolated which exhibit Gram-positive staphylococci morphology. These strains were further tested for resistance against benzalkonium chloride and a range of antibiotics to determine resistance profiles. The presence of *qacA* and *qacC* genes was detected using polymerase chain reaction (PCR), followed by sequencing to identify potential genetic variations. The results indicate a significant prevalence of the *qacA* genes among the isolates, with strains SDH.b4 and SDH.b5 showing high-level resistance to both biocides and antibiotics. Phylogenetic analysis further revealed that strains SDH.b4 and SDH.b5 are closely related to *Staphylococcus ureilyticus* CK27 and *Staphylococcus haemolyticus* JCM 2416 respectively, while strain SDH.b1 shares similarities with *Staphylococcus arlettae* ATCC 43957 and *Staphylococcus nepalensis* CW1. These findings underscore the potential threat posed by efflux pump-mediated biocide resistance in clinical *Staphylococcus* spp., and highlight the need for ongoing surveillance of efflux pump prevalence and further research into the underlying mechanisms of resistance to develop more effective infection control strategies in healthcare settings.

Keywords: Efflux pumps, *qacA* gene, *qacC* gene, *Staphylococcus* spp., biocide resistance.

[MB-P16] Detection of *Salmonella* spp. in finishing pig feces using PCR method

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Abstract: Pig farming in Vietnam is a major agricultural sector, featuring a range of production systems from small-scale farms to large commercial operations. Recent challenges in this sector include disease outbreaks, fluctuating market prices, and the need for enhanced biosecurity and sustainable practices. One significant risk to swine health and food safety is *Salmonella* spp., which necessitates effective detection methods. The study aimed to detect and evaluate the infection rates of *Salmonella* spp. in finishing pigs across three regions of Vietnam - North, Central and South. Using the PCR method, samples were collected from 18 farms in these regions, totaling 108 samples from finishing pigs - 36 samples from each region, evenly split between the diarrhea and non-diarrhea groups. DNA was extracted from the samples, and the presence of *Salmonella* spp. was detected using PCR with universal primers targeting the 16S rRNA sequence of the species. The results indicated that no *Salmonella* spp. was detected in any of the fecal samples, regardless of region or health status of the pigs. This finding suggests that, at the time of sampling, *Salmonella* spp. was not a prevalent pathogen in the finishing pigs from these regions, regardless of their clinical symptoms. This study underscores the effectiveness of the PCR method as an accurate and reliable tool for pathogen detection in swine fecal samples and provides valuable insights into the prevalence of *Salmonella* spp., highlighting the need for ongoing surveillance in livestock to ensure food safety and animal health.

Keywords: *Salmonella* spp., finishing pigs, diarrhea, fecal sample, PCR, detection

[MB-P17] Detection of *Salmonella* spp. in weaned pig feces using PCR method

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Abstract: Diarrhea among weaned pigs presents a significant challenge for livestock producers. It not only hampers piglet growth and escalates veterinary expenses but also carries the potential for piglet mortality, which causes economic losses in the pig industry. Many previous studies have demonstrated that *Salmonella* spp. is one of the most common factors leading to post-weaning diarrhea (PWD) and is also a notable zoonotic risk to farmers, veterinarians, and consumers of pork products. This study aims to assess the presence of *Salmonella* spp. in 108 fecal samples from 18 farms across northern, central, and southern Viet Nam using PCR. Additionally, risk factor infections were compared through clinical symptoms, farm type, and geographical location. The result showed no presence of *Salmonella* spp. in fecal samples from non-diarrhea pigs while the infection rate of *Salmonella* spp. in fecal samples from diarrhea pigs was 27,78%. This rate was higher in northern farms (14,81%) compared to central farms (4,62%) and northern farms (8,33%). Fecal samples collected from closed houses showed a lower infection rate than opened houses, with 12% and 15,7%, respectively. This study contributed to the evaluation of *Salmonella* spp. in some provinces of Vietnam and reflected on the sanitary condition of farms, providing deeper insights into the appropriate management of pig feces and reducing the risk of zoonotic transmission.

Keywords: weaned pigs, post-weaning-diarrhea, *Salmonella*, zoonotic risk, fecal sample, PCR, detection.

[MB-P18] Film from Agricultural By-Products for Fruit Preservation

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Abstract: Among commonly used foods, fruits stand out for their high nutritional and economic value, but they are also highly susceptible to spoilage due to oxidation and pathogen attack. Traditional preservation methods raise concerns regarding environmental impact, health risks, and associated costs while failing to fully protect the post-harvest fruits. Besides, the large-scale agricultural production results in significant amounts of agricultural by-products being discarded, without fully utilizing their potential. This study aims to integrate available agricultural by-products into biodegradable films, leveraging their antimicrobial and antioxidant properties, and then applying these films to selected fresh fruit samples. Initially, agricultural by-products are processed to obtain extracts using organic solvents, then applied for antimicrobial and antioxidant activity evaluation. Among the 18 extracts derived from Vietnamese agricultural by-products, antioxidant assays demonstrated robust efficacy in most samples with IC₅₀ less than 300 µg/mL. Besides, antimicrobial activity assessments against common ATTC strains and bacteria isolated from spoiled fruit revealed strong effectiveness across some extracts. During antimicrobial testing using a 96-well microplate, several challenges were encountered: While using a single solvent for extraction often led to suboptimal activity, the varied solubility of extracts in activity assessment required concentration adjustments to accurately measure bioactivity. Limitations of the microplate reader, such as non-uniform light scattering, overlapping extract colors, and microbial metabolic activity, caused measurement fluctuations, complicating the assessment of extract activity. Despite these challenges, bioactive extracts were successfully incorporated into food wrap films, with some exhibiting expected bioactivity, pending further evaluation on fresh fruit.

Keywords: biodegradable food wraps, agricultural byproducts, fruit preservation, antioxidant, antimicrobial testing challenges.

[MB-P19] Genome Mining and Gene Expression of Cryptic Antimicrobial Compounds from rare Actinobacteria Strains

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Abstract: The escalating threat of antibiotic resistance highlights the urgent need for the discovery of novel antimicrobial agents. Traditionally, many antibiotics have been discovered through the isolation and cultivation of environmental bacteria, followed by screening for natural product production and antimicrobial activity - this approach is known as the top-down approach. However, its limitations include the frequent rediscovery of known compounds and a bias toward certain natural products, often due to the restricted diversity of laboratory culture conditions.

This study adopted a bottom-up approach to discover antimicrobial compounds. Using the genomic sequenced data and leveraging bioinformatic tools: SPAdes, antiSMASH, and ARTS on four *Streptosporangium* strains. Potential antibiotic-producing genes were identified. The focus was shifted to two putative biosynthetic gene clusters (BGCs) in *Streptosporangium roseum* NRRL 2505 and *Streptosporangium fragile* B16437. These BGCs, associated with Ribosomally Synthesized and Post-Translationally Modified Peptides (RiPPs), were selected based on their genomic proximity to putative resistant genes. The identified BGCs, both more than 10 kilobases, were successfully cloned into expression vectors and transformed into *Streptomyces* hosts, followed by the cultivation in four distinct media types (A1F, ISP2, NZSG, TY), both in solid and liquid media. High-Performance Liquid Chromatography (HPLC) analyses of extracts from these transgenic *Streptomyces* strains revealed successful compound expression of the cloned gene in *Streptosporangium roseum* NRRL 2505 and *Streptosporangium fragile* B16437 when cultured on A1F agar, as well as from the *Streptosporangium roseum* NRRL 2505's BGC on TY agar. This study contributes to the development of new antibiotics and understanding on drug discovery.

Keywords: Antibiotics, Nature products, bottom-up, genome mining, bioinformatics, biosynthetic gene clusters (BGCs), cloning, *Streptosporangium*, Ribosomally Synthesized and Post-Translationally Modified Peptide (RiPP), *Streptomyces*, HPLC.

[MB-P20] Isolation, Characterization, and Diversity of Endophytic Fungi in Different Senescent Stages of *Rhizophora apiculata* Blume Leaves

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Abstract: The diversity of endophytic fungi isolated from healthy leaves of different mangrove species has been a subject of investigation in the Philippines for the past years. However, their diversity in senescent mangrove leaves remains to be underexplored in the country. Hence, this study primarily aimed to answer this gap. Fungal endophytes were isolated from *Rhizophora apiculata* leaves at different stages of senescence (green, yellow, and brown leaves). The leaves were collected from two mangrove sites in San Fernando City, La Union, Philippines: Barangays Carlatan and Catbangan. The highest rate of endophyte colonization (96.7%) was recorded in brown leaves collected from Carlatan. In contrast, green leaves from Catbangan recorded the lowest colonization rate (20%). Morphocultural characterization and molecular analysis using ITS genes classified the fungal isolates as belonging to the genera *Colletotrichum*, *Diaporthe*, *Fusarium*, *Aspergillus*, *Lasiodiplodia*, *Penicillium*, *Pestalotiopsis*, *Phomopsis*, and *Trichoderma*. Species accumulation curve for leaf senescence revealed that all senescence-specific samplings were exhaustive with yellow leaves exhibiting the highest species richness. Similarly, all site-specific samplings were also exhaustive with Barangay Catbangan having higher species richness than Barangay Carlatan. Alpha diversity analyses showed that yellow senescence is significantly more species-rich than green leaves and significantly more species-diverse than brown leaves. All site-specific samples have negligible differences in terms of their species richness and species diversity. Non-metric multidimensional scale (NMDS) showed that the two sampling sites have similar endophytic fungi composition. Furthermore, the isolated fungal endophytes were subjected to an indole-3-acetic acid colorimetric assay. Results revealed varying concentrations of the phytohormone, indicating their potential to assimilate nutrients. These results also demonstrate that the isolated mangrove fungal endophytes may be potential sources of substances that may have biotechnological applications.

Keywords: Diversity, Endophytic Fungi, *Rhizophora apiculata*, Senescence, indole-3-acetic acid

[HB-P21] Effect of isosorbide-based poly(β -amino ester) on gene transformation in *Escherichia coli*

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Abstract: Deoxyribonucleic acid (DNA) or gene transformation is extensively utilized in biotechnology for gene cloning, protein expression, and genetic engineering. This study assessed the gene transformation efficiency of a cationic poly(β -amino ester) polymer, synthesized via an aza-Michael addition reaction between piperazine and isosorbide diacrylate. Competent *Escherichia coli* DH5 α cells were prepared using optimized methods with Ca²⁺ and Mg²⁺ ions. The polymer was mixed with the plasmid pRSET-EmGFP at varying concentrations before being introduced into the competent cells through the heat shock method. Transformed cells were screened on ampicillin-containing media and analyzed using colony PCR, after which transformation efficiency was calculated. The results demonstrated the successful transformation of the EmGFP gene in the presence of the polymer. Moreover, isosorbide-based poly(β -amino ester) at a concentration of 20 ng/ μ L increased transformation efficiency more than twice as compared to the control without the polymer. In conclusion, isosorbide-based poly(β -amino ester) effectively enhances transformation efficiency.

Keywords: Ca²⁺; DH5 α ; gene transformation; isosorbide; Mg²⁺; poly(β -amino ester); pRSET-EmGFP.

[HB-P22] Alterations in proteomic profiles of piperacillin/tazobactam-exposed *Pseudomonas aeruginosa*

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Abstract: Understanding the adaptive response to antibiotic stress is important to the prevention and treatment of drug-resistant bacteria. In this work, we investigate the alterations in *Pseudomonas aeruginosa* under sub-MIC piperacillin-tazobactam (Pt) exposure. Antibiotic susceptible *P.aeruginosa* ATCC9027 (MIC=4 µg/mL) was serially exposed to a sub-MIC level of Pt for 14 days to generate Pt-E1 strains, then cultured in an antibiotic-free environment for 10 days to generate Pt-E2 strains. Changes in MIC values, susceptibility profiles, and proteomic profiles were evaluated. After antibiotic exposure, Pt-E1 developed resistance with MIC= 512 µg/mL, which did not revert in Pt-E2. In addition, both strains had reduced sensitivity against other beta-lactam antibiotics, namely cefazidime and cefepime. Proteomic analysis identified 890 proteins, of which 20-35% were up or down-regulated in E1 and E2 strains. Approximately 28% was irreversibly up- and 18% irreversibly down-regulated in both E1 and E2, corresponding to the persistent change in MIC value. Both exposed stains had expected increased beta-lactamase expression. Interestingly, porins such as oprD was downregulated, indicating an adaptive response to reduce the cellular concentration of antibiotics. Analysis of protein functions also showed alterations in ribosome machinery, metabolism, and pathway regulators. In summary, sub-MICs antibiotic exposure provided a positive selection for antibiotic-resistant phenotypes and resulted in irreversible alterations in antibiotic susceptibility and proteomes, which might be relevant to the development of multidrug-resistant phenotypes.

Keywords: antibiotic resistance, iTRAQ, proteomic, *Pseudomonas aeruginosa*, sub-MIC

[HB-P23] Inhibition of chitin synthase (*chs*) encoding genes exhibited a reduction of sporulation and hyphal morphogenesis in pathogenic fungi

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Abstract: Mucormycosis, also known as 'black fungus,' is a rare but highly lethal invasive fungal infection caused by fungi from the order Mucorales. It primarily affects immunocompromised patients and has an extremely high mortality rate. The incidence of this deadly infection has been rising rapidly due to increasing risk factors and has recently been identified as one of the most common fungal infections among severe COVID-19 patients. A major challenge in managing mucormycosis is the limited understanding of its pathogenesis. Chitin is a fundamental component of the fungal cell wall and plays a critical role in maintaining cell wall structure, morphogenesis, and virulence in pathogenic fungi. Chitin, a polymer of N-acetyl-D-glucosamine, is highly abundant not only in the cell walls of fungi but also in the exoskeletons of insects and various other organisms, including mollusks, coelenterates, nematodes, and protozoa. Many enzymes are involved in the biosynthesis and degradation of chitin. Through transcriptomic data analysis, we identified several genes in *Mucor lusitanicus* that encode chitin synthase, chitinase, and chitin deacetylase—enzymes involved in chitin synthesis and degradation. These genes were selected for further study based on their significant differences in expression under aerobic and anaerobic conditions.

In this study, we used RNA interference (RNAi) to inhibit the expression of two candidate genes encoding chitin synthase (*chs1* - ID 151786 and *chs2* - ID 85917) to explore their biological functions. Specific RNAi plasmids were constructed by cloning ~1 kb fragments of each gene into the pMAT1812 vector. The resulting gene-silenced strains exhibited a significant reduction in growth rate (~67%) compared to the control strain. The sporulation of the *chs1* and *chs2* silenced strains was also reduced by approximately 35% and 52%, respectively, compared to the control. Additionally, the morphology of the silenced fungal strains was altered, producing abnormal hyphae with fewer branches but increased branch width, leading to a substantial reduction in colony diameters. These changes in hyphal growth, sporulation, and morphology highlight the important roles of *chs1* and *chs2* in the growth and virulence of the human pathogenic fungus *M. lusitanicus*.

Keywords: cell wall, chitin, chitin biosynthesis, chitin synthase, mucormycosis, *Mucor lusitanicus*.

POSTER PRESENTATIONS

Human Biology



[HB-P01] Retrospective Analysis of the SARS-CoV-2 Infection Profile in COVID-19 Positive Patients in Kazakhstan 2023

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Abstract: The COVID-19 pandemic posed significant challenges to Kazakhstan's healthcare system and economy, particularly during the multiple waves of infections from 2021 to 2023. This study provides a retrospective analysis of the SARS-CoV-2 infection profile in Kazakhstan during this period, focusing on the trends and characteristics of the virus and evaluating the effectiveness of public health measures and vaccination campaigns. Our findings indicate that the third wave of COVID-19, driven by the emergence of the B.1.617.2 variant, was the most severe. The analysis also highlights the regional variations in infection rates, with certain areas experiencing higher transmission rates. The study involved 881 patients across 16 regions of Kazakhstan, including 152 children hospitalized with COVID-19. Clinical-epidemiological data were analyzed using descriptive statistics and multivariate logistic regression. The results provide crucial insights into the dynamics of the virus in Kazakhstan, contributing to informed decision-making for future public health strategies.

Keywords: Covid-19, SARS-CoV-2, Kazakhstan, Pandemic waves, Public health measures, Vaccination campaign, Clinical-epidemiological analysis, Infection trends

[HB-P02] One-pot synthesis of injectable and biodegradable poly(beta-amino ester) hydrogel for curcumin delivery

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Abstract: The biodegradable poly(beta-amino ester) hydrogel is a promising material for several applications such as gene transfer, wound dressing, and as a carrier for anti-cancer or anti-inflammatory medications. In this study, the new poly(beta-amino ester) hydrogels were synthesized *via* aza-Michael addition reaction. The reaction involved combining two primary components, poly(ethylene glycol) diacrylate and cystamine, and incubating them at a constant temperature of 37 °C. In addition, curcumin was selected as the active component to examine its dispersal capability within the material. The chemical structure of the hydrogel containing curcumin was analyzed using FT-IR and ¹³C CP/MAS solid state NMR spectroscopies. The surface characteristics of the hydrogel were further examined using scanning electron microscopy (SEM). The hydrogel's typical features, such as water content, swelling ratio, and biodegradability, were also assessed. In addition, we examined the release of curcumin in simulated biological conditions, namely at pH levels of 7.4 and 5.0. The antioxidant, antibacterial, and cytotoxic properties of both free curcumin and curcumin loaded in hydrogel were finally evaluated. The results indicate that curcumin in the gel decomposition fluid exhibits more activity compared to free curcumin, while also preserving the original features of the hydrogel. This study emphasized the possible use of injectable poly(beta-amino ester) hydrogels as biomaterials for wound dressings.

Keywords: poly(beta-amino ester), curcumin, hydrogel, cystamine, wound dressings

[HB-P03] Synthesis and evaluation of drug delivery properties of poly(beta-amino ester) nanoparticles

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Abstract: Nanomedicine-based drug delivery system is the newest and most potential development in drug delivery system. This system is applied to increase the bioavailability of drugs, increase absorption time and targeting ability. Ionosilica nanoparticle (INP) is a promising direction in drug delivery and disease treatment. In this study, INPs were synthesized based on two silica-sourced precursors. The amino ester precursor was synthesized by an aza-Michael addition reaction between poly(ethylene glycol) diacrylate (PEGDA) and bis[(3-triethoxysilyl)propyl]amine. The amino ester precursor is methylated with iodomethane to form the ammonium ester precursor. The chemical structure of the precursors and nanoparticles was confirmed using spectrometric methods such as FT-IR, ¹H NMR, ¹³C CP/MAS NMR, and ²⁹Si CP/MAS NMR. The size and surface morphology of resulting nanoparticles were determined by SEM, TEM and DLS. The antioxidant activity of curcumin was determined by the ABTS free radical method. In addition, evaluation of the in vitro cytotoxicity of curcumin was carried out by MTT experiment using colon carcinoma cells (CT-26). Analytical results show that INP was synthesized from ammonium ester precursor has the smallest particle size (198.6 ± 3.1 nm). The cytotoxic ability showed curcumin in INP was improved seventeenth times compared to free curcumin, IC₅₀ of curcumin decreased from 112.7 ± 8.10 $\mu\text{g mL}^{-1}$ to 6.602 ± 0.367 $\mu\text{g mL}^{-1}$. Furthermore, testing on INP without curcumin also showed the safety of the material, with the concentration of 562.5 $\mu\text{g mL}^{-1}$ only inhibiting 35% of cells. The above results showed that INP has potential biological properties for developing nanomedicine drug delivery systems.

Keywords: Ionosilica nanoparticle, nanomedicine, drug delivery system, curcumin, cytotoxicity.

[HB-P04] The Impact of *Helicobacter pylori* infection on transcriptional profile of AGS Cells

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Abstract: *Helicobacter pylori* (*H. pylori*) is one of major causes of gastric cancer (GC). Upon infection, the bacteria induce inflammatory responses, and triggers DNA damages in infected cells. Previous studies have also reported an increased genomic instability that resulted from inappropriate DNA damage repair capacity in gastric epithelial cells infected with *H. pylori*. The mechanisms by which *H. pylori* affects signaling pathways and activities of DNA repair systems are still elucidating. In this study, we investigated the effects of *H. pylori* infection on transcriptional profile of the human gastric adenocarcinoma cell line AGS using RNA sequencing approach. The preliminary data analysis showed that *H. pylori* NCTC 11637 strain deregulates the expression of signaling, and inflammatory response proteins, as well as DNA repair factors. These results provide insights into the molecular mechanism of *H. pylori*-induced GC.

Keywords: *Helicobacter pylori*, RNA sequencing, transcriptional profile

[HB-P05] *In silico* comparing low-pass sequencing and genotyping array for imputation performance in diverse human populations

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Abstract: Recently, low-coverage whole-genome sequencing combined with imputation has emerged as a competitive approach to traditional array-based technologies, particularly for large-scale genetic studies such as GWAS. Considering the vast number of arrays designed for different populations and purposes, as well as the flexibility of performing low-coverage sequencing at various depths, evaluating their performance has become crucial in determining the most suitable approach for each experimental circumstances.

In this study, we conducted a large-scale *in silico* assessment of imputation performance across five major population groups for six different low-coverage sequencing depths (ranging from 0.5X to 2X) and eight high-performance arrays. The results indicate that at a sequencing depth of 1X or higher, low-coverage whole-genome sequencing combined with imputation consistently achieves greater imputation accuracy than any of the arrays tested. Notably, the performance gains are more pronounced for rare variants and underrepresented populations, such as AFR, EAS, and SAS. Overall, our study supports a paradigm shift from array-based genotyping to low-coverage whole-genome sequencing.

[HB-P06] Anti-osteoclastogenic Effect of Astilbin on RANKL-induced RAW264.7 murine macrophage cells

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Abstract: Osteoclast-mediated bone loss is a significant health concern associated with conditions such as osteoporosis and rheumatoid arthritis. Astilbin, a naturally occurring bioactive flavonoid, has been reported to possess various biological activities such as anti-inflammation and antioxidants. Previous data also showed that this compound had an anti-osteoporotic impact using the bone marrow mouse (BMM) cell and ovariectomize mice model. In this study, we continued to investigate the anti-osteoclastogenic effect of astilbin using RANKL-induced RAW 264.7 murine macrophage cells, a typical model for osteoclast differentiation. Our data indicated that astilbin compound was non-toxic to RAW 264.7 cells at concentrations $\leq 100\mu\text{g/mL}$, and hence, these concentrations could be used for next experiments. Astilbin exhibited an inhibition on the differentiation of osteoclasts from RANKL-induced RAW 264.7 cells. This inhibition followed a dose-dependent manner, with concentrations ranging from 25 to $100\mu\text{g/mL}$ resulting in a remarkable reduction in the number of the osteoclasts formed from $69.2\% \pm 19.8$ to $30.7\% \pm 17.7$, respectively. Further, our conventional PCR data showed that astilbin could suppress the expression of key bone resorption-related genes, including NFATc1, TRAP, DC-STAMP and MMP-9 at concentrations 50 and $100\mu\text{g/mL}$, thereby confirming its anti-osteoclastogenic ability. In conclusion, astilbin demonstrates dose-dependent inhibition of the osteoclast formation and suppression of key osteoclast-related genes in RANKL-induced RAW 264.7 cells at concentrations 50 and $100\mu\text{g/mL}$. Further experiments need to be carried out to comprehend the signalling pathways of astilbin's anti-osteoclastogenesis on RANKL-induced RAW 264.7 model.

Keywords: Osteoporosis, anti-osteoclastogenesis, Astilbin, RAW264.7, bone resorption-related genes.

[HB-P07] Preliminary study on faeces metabolomics comparison between Vietnamese healthy controls and patients with colorectal cancer using mass spectrometry high resolution

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Abstract: A faeces metabolomic analysis was conducted to identify potential biomarkers between 49 colorectal cancer (CRC) patients and 9 healthy controls (HC) using an UPLC-QToF-MS method. Despite limitations related to computer configurations, a trial model was implemented. Initial PCA results indicated overlapping metabolic profiles between the two groups. However, further analysis using PLS-DA revealed distinct metabolic signatures for CRC and healthy groups. K-means clustering confirmed two optimal clusters, supported by silhouette scores above 0.5, though no correlation was found among individuals within the same clusters. The Random Forest approach showed promising classification results, with significant metabolites classified with errors of 2.04% for CRC and 33.33% for healthy controls, suggesting a need for proper model operation. Statistical analysis identified 22 metabolites with significant differences ($p\text{-value} \leq 0.05$, fold change ≥ 1.5 , CV $< 30\%$) between the two investigated groups. Notably, five biomarkers, including 17-hydroxypregnenolone, squalene, retinol, progesterone, and D-sorbitol, showed potential for CRC diagnosis. This study highlights the innovative use of metabolomic profiling in CRC diagnosis and underscores the need for future research to validate these biomarkers.

Keywords: Metabolomics, Colorectal Cancer (CRC), UPLC-QToF-MS, Faeces, Human biomarkers.

[HB-P08] Non-invasive preimplantation genetic testing for aneuploidy (NiPGT-A) using cell-free DNA in blastocyte culture medium

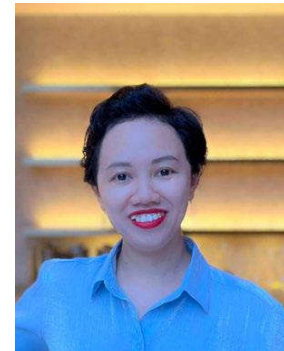
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Abstract: Preimplantation genetic testing for aneuploidy (PGT-A) using trophectoderm (TE) biopsy samples is commonly performed, but it still faces certain limitations, including invasive, complex manipulation, and susceptibility to sampling bias. Recent attention has been given to NiPGT-A non-invasive preimplantation genetic testing for aneuploidy using cell-free DNA in a spent blastocyst culture medium (SCM). To develop a non-invasive technique for application in routine clinical assays, a prospective longitudinal validation study was conducted at IVFMD from August 2020 to December 2020 to assess the concordance of the chromosome analysis results of NiPGT-A via SCM and PGT-A via TE biopsy. Forty-four couples eligible for PGT-A cycles were included in the study, with 100 trophectoderm PGT-A biopsies and their corresponding SCM evaluated. TE biopsy and SCM analyses were carried out using Veriseq (Illumina). The amplification success rate of SCM was 80% (79.3% of day 5 group and 100% of day 6 group). In the evaluation of 77 SCM samples with clear NGS results, the total concordance rate with TE biopsy was 63.6% (49/77), respectively; in which, the total concordance rate of day 5 group was 59.4% (38/64) and day 6 group was 84.6% (11/13). The use of SCM from blastocysts on day 5 and day 6 for aneuploidy detection resulted in a sensitivity of 57.1%, specificity of 67.3%, a positive predictive value (PPV) of 50.0%, and a negative predictive value (NPV) of 73.3%. Of the identified euploid embryos, 35 were used in single euploid transfer cycles, resulting in 18 live births, representing a 51.4% success rate. Of these, 21 showed euploidy in NiPGT-A, and 6 showed aneuploidy. In particular, 4 out of 6 aneuploid embryos (66.7%) resulted in live births, while the live birth rate for euploid embryos in noninvasive PGT was 47.6% (10/21). 4 live births from NiPGT-A aneuploid embryo transfer showed a high false-positive rate. Therefore, the current process of NiPGT-A is still not dependable enough to substitute the traditional PGT-A via TE biopsy.

Keywords: Aneuploidy, Cell-free DNA, Spent culture medium, NiPGT-A, PGT-A, TE biopsy

POSTER PRESENTATIONS

Session 4 – Animal Biology



[AB-P01] Phytochemical evaluation, embryotoxic, and teratogenic effects of Buwakan (*Decalobanthus peltatus* (L.) A.R.Simões & Staples) leaf extracts on duck embryo

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Abstract: *Decalobanthus peltatus* is a woody vine that is commonly utilized in traditional Southeast Asian medicinal preparations. Despite the documented therapeutic uses of *D. peltatus*, there is hardly any information regarding its toxic effects on its consumers. In this study, crude leaf extracts (aqueous, methanol, ethyl acetate, and hexane) from *D. peltatus* were prepared and evaluated for their embryotoxicity and teratogenic effects. Phytochemical screening of bioactive compounds from the plants showed the presence of alkaloids, flavonoids, saponins, steroids, and tannins. In addition, investigations on the toxicity of the crude leaf extracts were determined using brine shrimp lethality assay, in which the LC₅₀ was calculated. Results showed that the ethyl acetate leaf extract was the most toxic among the crude leaf extracts, with an LC₅₀ of 14.54 ppm. Based on this result, ethyl acetate leaf extract was treated on duck embryos, and the alteration of vascular branching patterns in the chorioallantoic membrane was quantified. Gross morphological and histological analysis of the skin tissues from the treated duck embryos were also examined. We found significant reduction of primary and tertiary vessel diameters in the duck embryos treated with ethyl acetate leaf extracts in both concentrations compared to the control group. Treated duck embryos exhibited gross malformations, growth retardation, and hemorrhages on the external body surfaces at 1000 ppm. Histopathological analysis of the skin tissues from the 14-day-old treated duck embryos showed a reduced number of feather follicles compared to the control group. These results suggest that *D. peltatus* crude leaf extracts present risks when taken in significant dosages and comprehensive toxicity testing on therapeutic herbs should be performed to ensure their safety on the consumers.

Keywords: CAM assay, *Decalobanthus peltatus*, embryo malformations, embryotoxic, medicinal plants, teratogenic

[AB-P02] The Weevils (Coleoptera: Curculionidae) of Lanao del Sur Province, Bangsamoro Region, Philippines: Diversity and Habitat Distribution

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Abstract: More than 400 weevil species were identified in the Philippines constituting 0.78% of the estimated total weevil population across the globe. Despite this low diversity in the Philippines, weevil species are still understudied in the country. In the Bangsamoro region, in fact only few data are known. This study aimed to record the diversity and habitat distribution of weevil species in the Bangsamoro region. Opportunistic samplings were conducted on seven (7) sites in Lanao del Sur province from 25 February to 26 March 2024. Adult species were collected using beating sheet, tree bark net, and hand grabbing. A total of 142 individual belonging to fifteen species of weevils were documented, all of which are new record in the province. Interestingly, *Sp7* and *Sp12* are the most encountered genus whereas *Sp14* had higher species abundance. Among the surveyed sites, S4 (agroforest) had higher species richness with seven (7) species. Although *Sp13* was recorded in montane forest, *Sp2* was found in both montane and agroforest ecosystem. *Sp1* and *Sp15* are commonly found in both university campus area and agroforest site whereas *Sp3* is common to both agroforest and agriculture area. All other studied species are common in the agroforest ecosystems. Studied species are actually found on elevation between 716-943 masl. Some of which are observed copulating and hiding in abaxial part of leaves. Some are active during night time whereas others are noted perching on the leaves and active during day time. Despite their ecological significance, Curculionid species in Lanao del Sur, Bangsamoro region are vulnerable to anthropogenic disturbances such as agricultural activities, cutting of trees, and commercialization. Therefore, this study suggests to protect the natural habitats of weevils in the region.

Keywords: *Abundance, Agroforest, Curculionid, Richness, Understudied*

[AB-P03] Isolation, semi-synthesis and anti-osteoporosis activity of xanthenes from the *Guttiferae* family: *in silico* and *in vivo* study

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Abstract: Xanthenes, a class of secondary metabolites found in higher plants, fungi, and lichens, have attracted significant attention due to their diverse biological and pharmacological properties. This study aims to isolate xanthenes from plants belonging to the *Guttiferae* family, particularly *Cratoxylum cochinchinense*, *Garcinia oblongifolia*, and *Garcinia mangostana*, followed by their semi-synthesis and evaluation of their anti-osteoporosis activity. Four xanthenes were successfully isolated from these species, and additional 10 derivatives were produced chemical modifications through substitution reactions, ozonolysis, and acetylation. The structures of all isolated and synthesized compounds were determined using FT-IR, HRMS, and NMR spectroscopies. *In silico* studies, including molecular docking of over 400 xanthenes, were performed to screen for anti-osteoporosis activity, resulted in the selection of cowanol as promising compounds for molecular dynamic simulations. These candidates were further evaluated *in vivo* using rankl:HSE:CFP transgenic medaka larvae models for osteoporosis, induced by heat-shock-driven Rankl overexpression. Notably, *in vivo* experiments demonstrated that these xanthenes significantly reduced bone damage in the fish model ($p < 0.0001$) and achieved a bone protection index (I_p) of up to 62.9% in the case of 3,6-diacethoxymangostin. The findings of this study provide compelling evidence that xanthenes possess the potential to favorably influence bone health and maintain bone integrity.

Keywords: xanthone, anti-osteoporosis, Rankl fish, medaka, *Guttiferae*

[AB-P04] Acute toxicity of xanthone compounds in medaka fish (*Oryzias latipes*)

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Abstract: Xanthone compounds, which are secondary metabolites found in various plants, have garnered considerable interest due to their wide range of biological and pharmacological properties. However, their toxicity has not been thoroughly studied. In this study, we isolated three xanthone compounds including cowanol, cochinchinone A, and ζ -mangostin from plants of the *Garcinia* genus and synthesized 3,6-di-*O*-acetyl- ζ -mangostin, a derivative of ζ -mangostin. We assessed their acute toxicity using medaka, a standardized fish model for toxicity research. Acute toxicity was evaluated by exposing medaka embryos (24-120 hours post-fertilization) and larvae (7-11 days post-fertilization) to a series of concentrations of each compound over a 96-hour period. We observed and recorded the daily number of dead fish and any abnormalities in surviving animals. Among the four xanthenes and their derivative, cochinchinone A and 3,6-di-*O*-acetyl- ζ -mangostin were non-toxic to both medaka embryos and larvae, even at doses up to 75 μ M, as they neither caused mortality nor induced abnormalities. ζ -Mangostin exhibited the highest toxicity to larvae, with an LC₅₀ of 3.44 μ M after 96 hours and observable deformities in survivors. Cowanol was non-toxic to embryos but showed dose- and time-dependent toxicity to larvae, with an LC₅₀ of 11.4 μ M. At doses of 2 μ M or lower, cowanol was safe for larvae. These results provide valuable data for further studies on xanthone compounds and their potential therapeutic applications.

Keywords: acute toxicology, medaka, xanthone, *Garcinia*

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[AB-P05] Molecular identification of freshwater crabs in northern ecological regions

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Abstract: Freshwater crabs are a diverse group of aquatic animals, with over 1,280 species described worldwide, primarily inhabiting freshwater ecosystems in tropical and subtropical regions. In Vietnam, molecular identification of freshwater crab species is essential for understanding biodiversity and supporting conservation efforts. In this study, 14 freshwater crab samples were collected from northern provinces such as Ha Giang and Cao Bang and were molecularly identified using PCR with the COI gene from mitochondrial DNA. After DNA extraction, the COI gene segment was amplified by PCR. The amplified COI sequences were then sequenced and compared with existing databases to identify the species present in each sample. The results indicated that the crab samples were genetically related to *Indochinamon ou* as confirmed by BLAST sequence comparisons with NCBI reference sequences. However, the Taxonomy and GenBank databases currently have limited reference sequences for the *Indochinamon* genus. Consequently, it is tentatively concluded that the crab samples belong to the *Indochinamon* genus. Further genetic studies are needed to complete the genetic database for crab species within the *Indochinamon* genus.

Keywords: Freshwater crabs, *Indochinamon ou*, *Indochinamon*, molecular identification, PCR approach

[AB-P06] Identification of *Bactrocera correcta* in guava using morphological and molecular analyses

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Abstract: Guava (*Psidium guajava* L.), a member of the Myrtaceae family, is a popular tropical fruit cultivated in many tropical and subtropical regions. It is widely grown for commercial purposes, contributing significantly to the national economy. However, guava trees are also susceptible to insect pests with the guava fruit fly, *Bactrocera correcta* (Bezzi) (Diptera: Tephritidae), being a major threat. These insects have a destructive impact on agriculture worldwide. Damage caused by fruit flies results in young fruits becoming wrinkled and falling off prematurely, while mature fruits around the damaged ones show slight concavity. Given this threat, it is crucial to develop a rapid, accurate, and reliable method for identifying *B. correcta* in quarantine settings to provide early warnings and prevent widespread invasion. This study aims to identify *B. correcta* using both morphological and molecular methods to distinguish it from other species within the genus *Bactrocera*. The study will discuss the process of detecting *B. correcta* through these two identification methods. The results are expected to serve as an effective tool for evaluating and checking guava quality before export. Additionally, this research will lay the groundwork for developing methods to quickly detect *B. correcta* in the future.

Keywords: Guava, fruit fly, *Bactrocera correcta*, morphological identification, molecular identification

[AB-P07] Identification of *Bactrocera dorsalis* in mango orchards in Dong Nai and Tien Giang province using morphological and molecular analyses

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Abstract: Mango (*Mangifera indica* L.), a member of the Anacardiaceae family, is a fruit tree widely cultivated in tropical and subtropical regions, including Vietnam. This plant not only provides significant nutritional benefits but also holds substantial economic potential. However, the fruit fly *Bactrocera dorsalis* has compromised the quality and yield of mangoes, causing considerable losses for farmers. To manage, control, and prevent the spread of this pest, it is essential to accurately identify *B. dorsalis*. This study focuses on identifying *B. dorsalis* in mango orchards in Dong Nai and Tien Giang provinces using two methods: morphological and molecular identification. A total of 24 fruit fly samples collected from 24 mango orchards were morphologically identified using a stereo microscope. Following this, DNA was extracted, and molecular identification was performed through PCR with specific primers. The results indicate that *B. dorsalis* exhibits distinct morphological characteristics particularly in wings and body color, compared to other species within the genus *Bactrocera*. In addition, molecular identification through PCR revealed target bands of less than 200 bp in size. These findings provide valuable information about the *B. dorsalis* species in mango orchards in Dong Nai and Tien Giang provinces, laying the groundwork for future research on the diversity and genetic relationships of this species in the region.

Keywords: Mango, *Mangifera indica* L., fruit fly, *Bactrocera dorsalis*, morphological identification, molecular identification, Dong Nai, Tien Giang

[AB-P08] A study on the bioactivity of methanol extracts obtained from the *Lithocarpus* species

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Abstract: The *Lithocarpus* genus, one of the largest within the *Fagaceae* family, is traditionally recognized for its diverse therapeutic applications, including anti-inflammatory, antioxidant, and anticancer properties. Despite its extensive use in traditional medicine, scientific literature on the biological activities and chemical constituents of *Lithocarpus* species remains limited. Recent studies have highlighted the potential of this genus, yet comprehensive evaluations of its bioactive compounds and mechanisms of action are still needed. This study focuses on the bioactivities of five methanol extracts from three *Lithocarpus* species: *L. bonnetii* (Hickel & A. Camus) A. Camus, *L. bacgiangensis* (Hickel & A. Camus) A. Camus, and *L. cryptocarpus* (Darke) A. Camus. The extracts were analyzed for total phenolic content (TPC) and total flavonoid content (TFC), antioxidant activity using DPPH and ABTS radical scavenging assays, anti-inflammatory effects on LPS-activated RAW 264.7 macrophages, and anticancer activity against human liver cancer cells (HepG2). The results showed that *L. bonnetii* (L4) had the highest TPC at 457.53 ± 46.13 μg GAE/mg extract, while *L. cryptocarpus* (L2) demonstrated the highest TFC at 579.31 ± 48.69 μg QE/mg extract. *L. cryptocarpus* fruit extract (L3) exhibited the strongest antioxidant activity with an IC_{50} of 1.73 ± 0.01 $\mu\text{g/mL}$ in the ABTS assay, and an IC_{50} of 9.79 ± 0.53 $\mu\text{g/mL}$ in the DPPH assay. This extract also displayed cytotoxic effects against HepG2 cells, with an IC_{50} of 52.85 ± 1.68 $\mu\text{g/mL}$. Notably, the fruit extract from *L. bonnetii* demonstrated potent anti-inflammatory activity by significantly inhibiting NO production in LPS-stimulated RAW 264.7 cells, with an IC_{50} of 16.54 ± 2.11 $\mu\text{g/mL}$. These findings highlight the therapeutic potential of *Lithocarpus* extracts, supporting their use in the development of treatments for inflammatory and oxidative stress-related diseases.

Keywords: *Lithocarpus*, Anti-inflammatory, Antioxidant, Anticancer, TPC, TFC, DPPH, ABTS, MTT assay, NO assay.

[AB-P09] Minimizing misidentification of common snakes of Vietnam in the hospital setting

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Abstract: The global incidence of snakebites is a serious issue affecting the health and lives of thousands of people each year. Vietnam currently hosts 246 snake species, of which 79 species have been identified as venomous and potentially dangerous to humans, even capable of causing death. These venomous snakes belong to three families: Colubridae, Elapidae, and Viperidae. However, the process of identifying venomous snake species still faces some significant challenges. One of the main obstacles is the existence of many non-venomous snake species that appear venomous. This similarity often leads to confusion, especially among individuals lacking specialized knowledge of snakes. In this research, the differences between some common venomous snakes in Vietnam and several non-venomous snakes are shown and highlighted with emphasis on species resembling in appearance. Correctly identifying these snakes not only helps avoid unfortunate incidents but also aids in protecting and maintaining the natural ecological balance.

Keywords: Snakebites, identification, venomous snakes, non-venomous snakes, public health.

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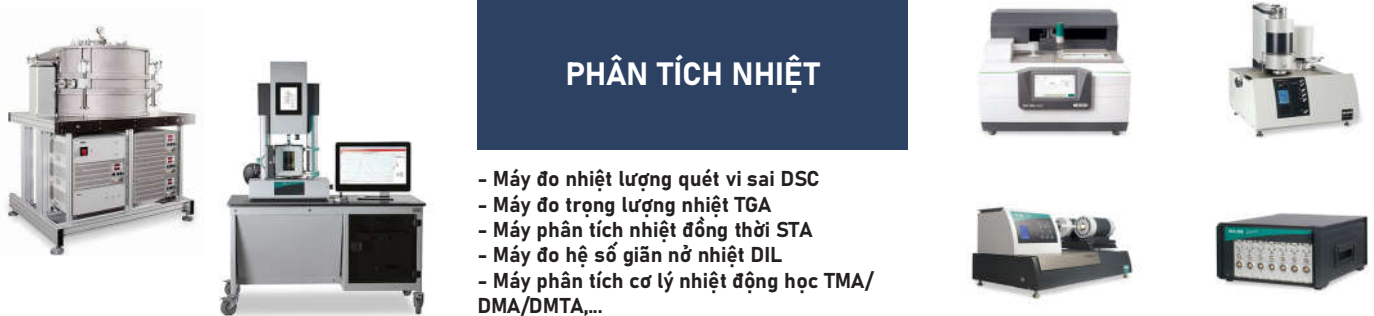
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abm không ngừng phát triển và các sản phẩm của chúng tôi cũng vậy. Việc theo đuổi các enzyme PCR thế hệ mới và không ngừng nghiên cứu, phát triển đã giúp nâng cấp đáng kể cho các sản phẩm PCR của chúng tôi. Kết quả là đã tạo nên một bộ sưu tập mới các enzyme PCR cùng các công thức hàng đầu thế giới với hiệu suất vượt trội so với các thương hiệu hàng đầu hiện tại. Đặc biệt, chúng tôi vẫn cung cấp mức giá chiết khấu cho các nhu cầu đặt hàng lớn



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Tỷ lệ lỗi thấp hơn 2000 lần so với Taq thông thường.



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Chạy nhanh chóng một chu trình PCR thông thường trong 2 giờ chỉ trong 20 phút.



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Bảng so sánh các loại Polymerase

Đặc điểm nổi bật	MegaFi™ Pro	BlasTaq™	BlasTaq™ hot-start	Taq
Proofreading	Có	Không	Không	Không
Độ tin cậy (so vs Taq)	2000X	1X	1X	1X
Độ đặc hiệu		...		...
Tốc độ kéo dài	20-30 giây/kb	15 giây/kb	15 giây/kb	60 giây/kb
Chiều dài tối đa	15-20 kb	10-15 kb	10-15 kb	6,5 kb
Phù hợp cho tạo dòng TA	Không	Có	Có	Có
Các đặc điểm khác	Độ chính xác và độ nhạy	Nhanh chóng và Mạnh mẽ	Độ đặc hiệu cao	PCR thông thường



Chứng nhận ISO 13485:2016 MDSAP

Các sản phẩm PCR của chúng tôi được sản xuất theo Hệ thống quản lý chất lượng tuân thủ tiêu chuẩn ISO 13485:2016, được chứng nhận bởi Intertek, một tổ chức kiểm toán được MDSAP công nhận.

Nhuộm DNA SafeView™

Thuốc nhuộm không độc hại để quan sát gel DNA/RNA

TÍNH NĂNG NỔI BẬT



Nhuộm axit nucleic trong gel an toàn mà không cần Ethidium Bromide độc hại



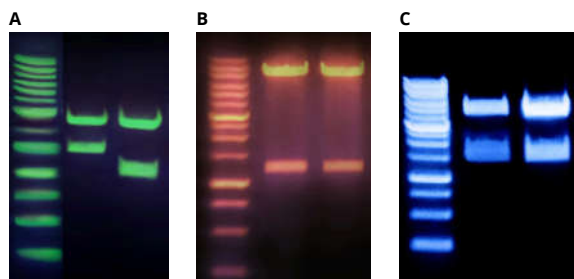
Dễ sử dụng và quan sát bằng đèn UV hoặc ánh sáng xanh



Độ nhạy đến 0,02 pg DNA trên mỗi vạch



Giảm thiểu hư hại DNA do phương pháp EtBr gây ra, mang lại tỷ lệ chuyển đổi cao hơn và tỷ lệ gây đột biến thấp hơn



D Thuốc nhuộm kèm dung dịch nạp mẫu

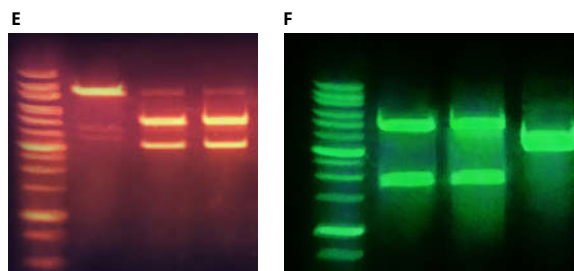


Các cấu trúc DNA được chạy trên gel agarose và nhuộm bằng thuốc nhuộm DNA Safe-Green™ (A), Safe-Red™ (B) hoặc Safe-White™ (C) và quan sát dưới ánh sáng UV. Quy trình nhuộm lấy ví dụ khi sử dụng Thuốc nhuộm DNA SafeView™ (D).

Thuốc nhuộm kèm dung dịch nạp mẫu

Tên sản phẩm	Quy cách	Mã ĐH
Safe-Green™	1ml	G108-G
Safe-Red™	1ml	G108-R
Safe-White™	1ml	G108-W
Safe-Pack™	1 gói	G108-P

Chứa một trong số Safe-Green™, Safe-Red™ và Safe-White™



Thuốc nhuộm khi đổ gel

Tên sản phẩm	Quy cách	Mã ĐH
SafeView™ Cổ điển	1ml	G108
SafeView™ FireRed	1ml	G926

G Quy trình nhuộm khi đổ gel



Thuốc nhuộm sau khi điện di

Tên sản phẩm	Quy cách	Mã ĐH
SafeView™ Plus	1ml	G468

H Quá trình nhuộm màu sau điện di



Các cấu trúc DNA được chạy trên gel agarose và nhuộm bằng Thuốc nhuộm DNA SafeView™ FireRed (E) hoặc SafeView™ Plus (F) và được quan sát dưới ánh sáng UV. Quy trình nhuộm gel thông thường sử dụng Thuốc nhuộm DNA SafeView™ (G, H)