Chula
Chulalongkorn University

TSB2025

Biotechnology in Action

Program & Abstracts

The 37th Annual Meeting of the Thai Society for Biotechnology and International Conference

29th– 31st October 2025

Mandarin Hotel Bangkok, Thailand

www.tsb2025.org

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Welcome Message

Welcome Message from the Conference Chair

Prof. Dr. Tanapat Palaga
Chair, TSB2025

On behalf of the Department of Microbiology, Faculty of Science Chulalongkorn University, it is my great honor to welcome you to the **37th Annual Meeting of the Thai Society for Biotechnology and International Conference (TSB2025)**, which will take place from **October 29–31, 2025, in the vibrant city of Bangkok, Thailand**.

This year's conference, held under the theme ***"Biotechnology in Action!"***, aims to showcase the power of biotechnology in driving innovation, addressing global challenges, and translating discoveries into real-world impact. The event will bring together a diverse and dynamic community of scientists, researchers, students, and industry professionals from around the world.

We are especially delighted to announce that **TSB2025** coincides with the **50th Anniversary of the Department of Microbiology, Faculty of Science, Chulalongkorn University**. In celebration of this milestone, we are proud to co-host the conference with the **Institute of Biotechnology and Genetic Engineering, Chulalongkorn University**.

The conference will feature keynote lectures by leading scientists, along with plenary sessions, oral and poster presentations, and interactive forums for academic and industry engagement.

We warmly invite you to join us in Bangkok to celebrate scientific excellence, strengthen collaborations, and explore how biotechnology continues to shape our future.

With warmest regards,

Prof. Dr. Tanapat Palaga
Chair, TSB2025

Welcome Message from Thai Society for Biotechnology

Associate Prof. Dr. Chuenchit Boonchird
President Thai Society for Biotechnology

Dear Friends and Colleagues,

On behalf of the **Thai Society for Biotechnology (TSB)**, and as Chair of the **37th Annual Meeting and International Conference of the Thai Society for Biotechnology (TSB2025)**, it is my great pleasure to welcome you to our flagship event, taking place from **29 to 31 October 2025**.

Since 1989, the TSB Conference has served as an active platform for sharing the latest advances in biotechnology and encourage collaboration among academic, industrial, and governmental sectors. I would like to express my sincere appreciation to the **Faculty of Science and the Institute of Biotechnology and Genetic Engineering, Chulalongkorn University**, for their efforts in hosting this year's conference.

The theme of TSB2025 is ***"Biotechnology in Action."*** This year's program highlights cutting-edge research from both international and Thai scientists, demonstrating how biotechnology can provide real-world solutions and drive industrial innovation. We are also showcase strong regional collaboration through the participation of networks including **the Asian Federation of Biotechnology (AFOB), the Society for Biotechnology Japan (SBJ), the Biotechnology and Biochemical Engineering Society of Taiwan (BEST), and the AFOB Malaysian Chapter (AFOB-MC)**. Together, we aim to strengthen scientific exchange and collaboration across Asia, bridging academia and industry.

As part of our tradition, we will honor excellence in the field through the **Taguchi Prizes and the Ajinomoto-TSB Award**. The Taguchi Prize, established in 1990, commemorates the remarkable contributions of Professor Dr. Hisaharu Taguchi of The University of Osaka to the advancement of biotechnology education in Thailand. This prize recognizes exceptional young researchers, as well as outstanding M.Sc. and Ph.D. theses, reflecting the next generation of leadership in our field. The Ajinomoto-TSB Award, formerly known as the Ajinomoto Lecture Award and awarded since 1991 by the Ajinomoto Foundation, honors innovative achievements in biotechnology. This year, the award will focus on innovative contributions in the fields of Health and Medicine.

I warmly welcome all participants to **TSB2025**. I hope the conference inspires new ideas, cultivates meaningful partnerships, and continues to drive the advancement of biotechnology in Thailand and beyond.

With kind regards,

Associate Prof. Dr. Chuenchit Boonchird
President Thai Society for Biotechnology

INTERNATIONAL SCIENTIFIC COMMITTEE

Prof. Dr. Kohsuke Honda — *Japan*
ICBiotech, The University of Osaka

Prof. Dr. Hiroshi Shimizu — *Japan*
Graduate School of Information Science and Technology, The University of Osaka

Prof. Dr. Randeep Rakwal — *Japan*
Institute of Health and Sport Sciences, University of Tsukuba

Prof. Dr. Takeharu Tsuge — *Japan*
Department of Materials Science and Engineering, Major in Human Centered Science and Biomedical Engineering, Institute of Science Tokyo

Prof. Dr. Beom Soo Kim — *Republic of Korea*
Department of Chemical Engineering, Chungbuk National University

Assoc. Prof. Dr. Rietie Venter — *Australia*
UniSA Clinical and Health Sciences, Health and Biomedical Innovation, University of South Australia

Assoc. Prof. Dr. Joy Scaria — *USA*
Veterinary Pathobiology, Oklahoma State University

Prof. Dr. Stephen Brian Pointing — *Singapore*
Yale-NUS College & Department of Biological Sciences, National University of Singapore

Prof. Dr. Sudesh Kumar — *Malaysia*
School of Biological Sciences, Universiti Sains Malaysia

Prof. Dr. Tuck Seng Wong — *UK*
Department of Chemical & Biological Engineering, The University of Sheffield

Assoc. Prof. Dr. Masaki Honda — *Japan*
Department of Chemistry, Meijo University

Prof. Dr. Hakuto Kageyama — *Japan*
Graduate School of Environmental and Human Sciences, Meijo University

Prof. Dr. Shinya Kodani *Japan*
Shizuoka University

Prof. Sheng-Fan Wang *Taiwan*
Kaohsiung Medical University

LOCAL ORGANIZING COMMITTEE

Prof. Dr. Tanapat Palaga
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Prof. Dr. Tavan Janvilisri
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Prof. Dr. Wanchai Assavalapsakul
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Prof. Dr. Chulee Yompakdee
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Panan Rerngsamran
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Rungaroon Waditee-Sirisattha
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Suchada Chanprateep Napathorn
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Ekawan Luepromchai
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Onruthai Pinyakong
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Cheewanun Dachoupakan Sirisomboon
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Naraporn Somboonna
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Asst. Prof. Dr. Kobchai Pattaragulwanit
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Asst. Prof. Dr. Supat Chareonpornwattana
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Asst. Prof. Dr. Chonchanok Muangnapoh
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Asst. Prof. Dr. Chompoonik Kanchanabanca
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Asst. Prof. Dr. Sita Virakul
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Asst. Prof. Dr. Nuttapon Pombubpa
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Dr. Jirasin Koonthongkaew
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Dr. Tatpong Boontawon
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

Prof. Dr. Nuttha Thongchul
Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Kittinan Komolpis
Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Aphichart Karnchanatat
Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Thailand

Assoc. Prof. Dr. Chuenchit Boonchird
Mahidol University

Prof. Dr. Vilai Rungsardthong
King Mongkut's University of Technology North

Assoc. Prof. Dr. Prakit Sukyai
Kasetsart University

Assoc. Prof. Dr. Ratchaneewan Aunpad
Thammasat University

Assoc. Prof. Dr. Sehanat Prasongsuk
Chulalongkorn University

Dr. Kuakoon Piyachomkwan
Poon Phol Company Limited

Dr. Korsak Towantakavanit
Mitr Phol Sugar Corp., Ltd.

Mr. Niwat Suriyakamon
Pharmafac plan technology Co.,Ltd.

Assoc. Prof. Dr. Tatsaporn Todhanakasem
King Mongkut's Institute of Technology Ladkrabang

Assoc. Prof. Dr. Theppanya Charoenrat
Thammasat University

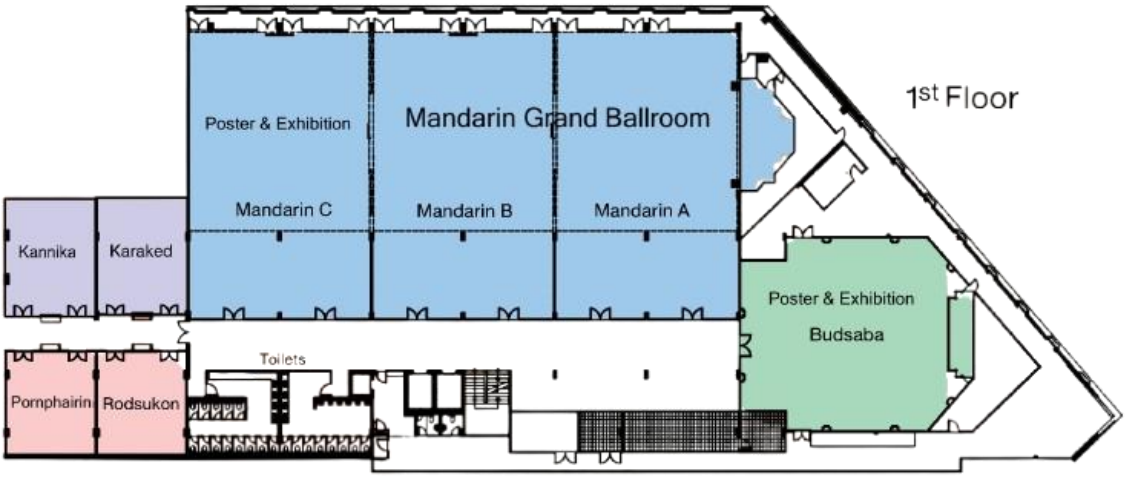
Asst. Prof. Dr. Adisak Romsang
Mahidol University

Assoc. Prof. Dr. Apichart Karnchanatat
Chulalongkorn University

Assoc. Prof. Dr. Rujikan Nasanit
Silpakorn University

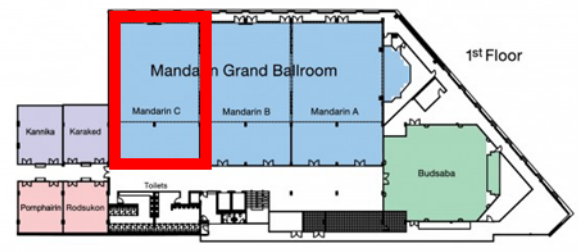
FLOOR PLAN

Map of Conference Rooms

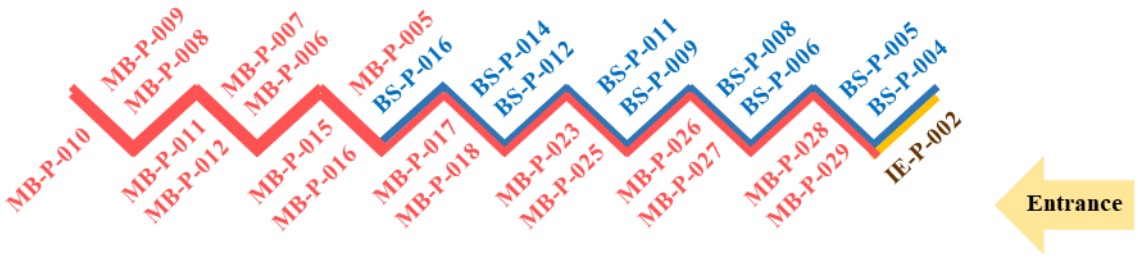


Conference Room:	Mandarin A, Mandarin B
File Uploading Point:	Rodsukon
Poster Room:	Mandarin C, Budsaba
Exhibition:	Mandarin C, Budsaba

Poster Zone: MANDARIN C



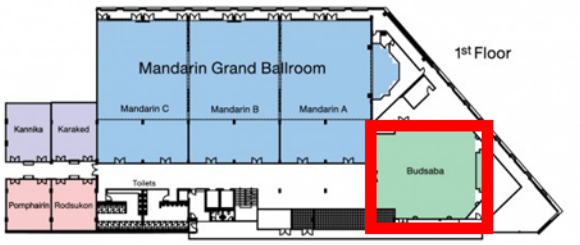
Session I. Bioinformatics and Systems Biology, Synthetic Biology (BS)



Session II. Medical Biotechnology & One health (MB)

Session III. Industrial & Environmental Biotechnology, & Alternative energy (IE)

Poster Zone: BUDSABA



Session IV. Biodiversity, Natural Products and Applications (BN)

AB-P-012 BN-P-003 BN-P-004
AB-P-011 AB-P-007 BN-P-008 BN-P-010
AB-P-004 AB-P-003 BN-P-011 BN-P-012
BN-P-031 BN-P-030 BN-P-014 BN-P-015
BN-P-029 BN-P-028 BN-P-016 BN-P-020
BN-P-027 BN-P-026 BN-P-021 BN-P-022
BN-P-025 BN-P-024 BN-P-023

Entrance

Session V. Agriculture Biotechnology (AB)

FB-P-019 AB-P-013 AB-P-014
FB-P-018 FB-P-015 AB-P-015 AB-P-017
FB-P-013 FB-P-010 AB-P-018 AB-P-019
FB-P-009 FB-P-006 AB-P-020 AB-P-026
FB-P-005 FB-P-004 AB-P-027 AB-P-029
FB-P-003 AB-P-040 AB-P-030 AB-P-033
AB-P-038 AB-P-037 AB-P-034 AB-P-035
AB-P-036

Session VI. Food Biotechnology & Food Security (FB)

PROGRAM AT A GLANCE

<table>
<tr><th colspan="5">29 October 2025 (Day 1); Mandarin Hotel Bangkok</th></tr>
<tr><td>8:00-8:45</td><td colspan="4">Open for Registration</td></tr>
<tr><td></td><td colspan="4">Mandarin Grand Ballroom</td></tr>
<tr><td>8:45-9:00</td><td colspan="4">Welcome Remarks</td></tr>
<tr><td>9:00-10:30</td><td colspan="4">Plenary Lecture I-III</td></tr>
<tr><td>10:30-11:00</td><td colspan="4">Refreshment (Mandarin C and Budsaba)</td></tr>
<tr><td></td><td colspan="4">Mandarin Grand Ballroom</td></tr>
<tr><td>11:00-11:30</td><td colspan="4">Plenary Lecture IV</td></tr>
<tr><td>11:30-12:20</td><td colspan="4">Taguchi Prize and Ajinomoto Award Announcement and Presentation</td></tr>
<tr><td>12:20-13:45</td><td colspan="4">Lunch</td></tr>
<tr><td>13:45-14:30</td><td colspan="4">Exhibition Talks (Mandarin A)</td></tr>
<tr><td>14:30–16:25</td><td>Mandarin A
Session I: Bioinformatics and Systems Biology, Synthetic Biology</td><td>Mandarin B
Session II: Medical Biotechnology & One Health</td><td>Karaked
Session III: Industrial & Environmental Biotechnology & Alternative Energy</td><td>Kannika
Session V: Agriculture Biotechnology</td></tr>
<tr><td>16:25-18:00</td><td colspan="2">Refreshment + Poster Presentation (Mandarin C and Budsaba)</td><td colspan="2">TSB Annual Meeting (Pornphairin)</td></tr>
<tr><td></td><td colspan="4">Mandarin Grand Ballroom</td></tr>
<tr><td>18:00-20:00</td><td colspan="4">Welcome Reception and Dinner
Flag-giving ceremony</td></tr>
</table>

30 October 2025 (Day 2); Mandarin Hotel Bangkok					
8:00-9:00	Open for Registration				
	Mandarin Grand Ballroom				
9:00-10:00	Plenary Lecture V and VI				
10:00-10:40	Business Talks				
10:40-11:00	**Refreshment (Mandarin C and Budsaba)**				
11:00-12:25	**Mandarin A** Session II: Medical Biotechnology & One Health	**Mandarin B** Session III: Industrial & Environmental Biotechnology & Alternative Energy	**Karaked** Session IV: Biodiversity, Natural Products and Applications	**Kannika** Session VI: Food Biotechnology & Food Security& Future Food	**Pornphairin** Special Symposium Marine Biotechnology and Bioprospecting
12:25-14:00	**Lunch** **Poster presentation (Mandarin C and Budsaba)**				
14:00-15:25	**Mandarin A** Session I: Bioinformatics and Systems Biology, Synthetic Biology	**Mandarin B** Session V: Agriculture Biotechnology	**Karaked** Session IV: Biodiversity, Natural Products and Applications	**Kannika** Session VI: Food Biotechnology & Food Security& Future Food	**Pornphairin** Special Symposium Marine Biotechnology and Bioprospecting
15:25-15:45	**Refreshment (Mandarin C and Budsaba)**				
	Mandarin Grand Ballroom				
15:45-17:00	Special plenary session				
17:00-17:15	Award announcement and Closing Ceremony by TSB President				

31 October 2025 (Day 3) Faculty of Science, Chulalongkorn University	
Option 1:	**Special Symposium to Commemorate the 50th Anniversary of Department of Microbiology, Faculty of Science, Chulalongkorn University** Banyen meeting room, Maha Vajirunhis Building
9:00-9:15	Welcome remarks
9:15-10:30	Microbiology and Biotechnology research in Japan
10:30-10:45	**Coffee Break**
10:45-12:15	Microbiology and Biotechnology research in Thailand
12:15-13:30	**Lunch**
13:30-15:00	Microbiology and Biotechnology Business in Thailand
15:00-15:15	**Coffee Break**
15:15-16:30	Microbiology and Biotechnology Business in Thailand (cont.)
16:30-16:45	Closing remarks
Option 2:	**Special Symposium: Tackling Antifungal Resistance Through a One Health Lens** Multipurpose Room, 2nd Floor, TAB Building
9:00-9:10	Opening Remarks
9:10-9:40	Keynote Address
9:40-10:10	Session 1: SEA-ARMI - Fungal AMR across southeast Asia
10:10-10:30	Session 2: Clinical insights on antifungal resistance in Thailand
10:30-10:45	**Coffee Break and Networking**
10:45-11:05	Session 3: Tackling antifungal resistance: bridging environmental and veterinary health through aquaculture insights
11:05-11:50	Session 4: Panel Discussion: Policy, Partnerships & Future Funding
11:50-12:00	Closing Remarks
12:00-13:00	**Lunch & Networking**

The 2025

Taguchi Prize

&

Ajinomoto – TSB Award

Awarded at

The 37th Annual Meeting of the Thai Society for Biotechnology and International Conference (TSB 2025)

“Biotechnology in Action”

29 October 2025

Mandarin Hotel

Bangkok

TAGUCHI FUND

Foundation for the Promotion of Biotechnology (FPB) in Thailand

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The “TAGUCHI FUND”, commemorating the contribution by Professor Dr. Hisaharu Taguchi to education and promotion of biotechnology in Thailand, was founded by his family and colleagues both in Japan and Thailand. The FUND awards the Taguchi Prize to young scientists conducting research in Thailand. Dr. Hisaharu Taguchi, Professor Emeritus of The University of Osaka, passed away on June 1, 1987 shortly after his retirement from the professorship at The University of Osaka. He made remarkable contributions to the biotechnology world, especially through “International Education.” Professor Taguchi contributed greatly to the operation of the International Post-Graduate University Course in Microbiology, which has benefitted more than 200 young researchers from various Asian countries. In addition, he trained more than 200 young researchers from various Asian Countries and directed a scientific exchange program in microbial engineering and biotechnology as part of a Southeast Asian exchange program sponsored by the Japan Society for the Promotion of Science. Through these and other activities in the region, Professor Taguchi developed close professional and personal relationships that promote excellence in biotechnology research and in education of young scientists in the field.

The “TAGUCHI FUND” has been awarding **“Taguchi Prize”** for outstanding researcher in biotechnology during the annual meeting of Thai Society for Biotechnology (TSB) since 1990. Initially, the prize was awarded only to young scientists who accomplished outstanding research in biotechnology. However, it has since been extended to recognize outstanding Master’s and Doctoral theses conducted in Thailand.

The 2025 Taguchi Prize

For

Outstanding Young Scientist Research Achievements

in the Field of Biotechnology

Awarded to

Assistant Professor Dr. Thanyaporn Wongnate

Vidyasirimedhi Institute of Science and Technology

Research Theme

Biotechnological Advancements in Enzyme and Microbial Systems for Renewable Energy and Circular Bioeconomy

BIOTECHNOLOGICAL ADVANCEMENTS IN ENZYME AND MICROBIAL SYSTEMS FOR RENEWABLE ENERGY AND CIRCULAR BIOECONOMY

Thanyaporn Wongnate[1,*]
[1] School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC), Rayong, 21210 Thailand
*e-mail: thanyaporn.w@vistec.ac.th

Abstract:
The Thanyaporn Wongnate Research team advances anaerobic microbial technology through the integration of biocatalysis, enzyme engineering, metabolic engineering, and synthetic microbiology to develop efficient, sustainable, and practical systems for bioenergy and bioproduct generation. The research encompasses microbial strain discovery, enzyme engineering, and microbial consortia design for organic waste degradation, alongside the optimization of anaerobic fermentation to produce hydrogen, methane, and organic acids, as well as the bioconversion of CH_4 and CO_2 into bio-based chemical precursors. A major achievement is the isolation of *Enterococcus faecalis* VT-H1 from palm oil mill effluent, which exhibits exceptional hydrogen-producing potential and has enabled the development of immobilized-cell technologies successfully applied to food waste management at laboratory and pilot scales. The team also promotes waste valorization through the utilization of digestate as biofertilizers and plant biostimulants, aligning with circular economy and bioeconomy principles. One flagship innovation is the SUZDEE (Sustainable Zero Waste Digestant for Well-Being) system, a community-scale platform that converts food waste into bioenergy and bioproducts, currently deployed in households, schools, and municipalities across Thailand, with demonstrated benefits for cultivating medicinal and economic crops. The team's industrial collaborations extend these technologies to factory-scale wastewater treatment and value-added waste processing. To bridge research and commercialization, innovations have been realized through GreenGen Biotechnology, a spin-off company providing scalable organic waste digestion and bioenergy solutions for both community and industrial applications. The team's excellence is reflected in 50 publications in high-impact journals, three registered petty patents, and over 20 patent applications in progress. With a long-term vision to integrate academia, industry, and community impact, the team remains dedicated to advancing biotechnological innovations that drive a sustainable bioenergy future.

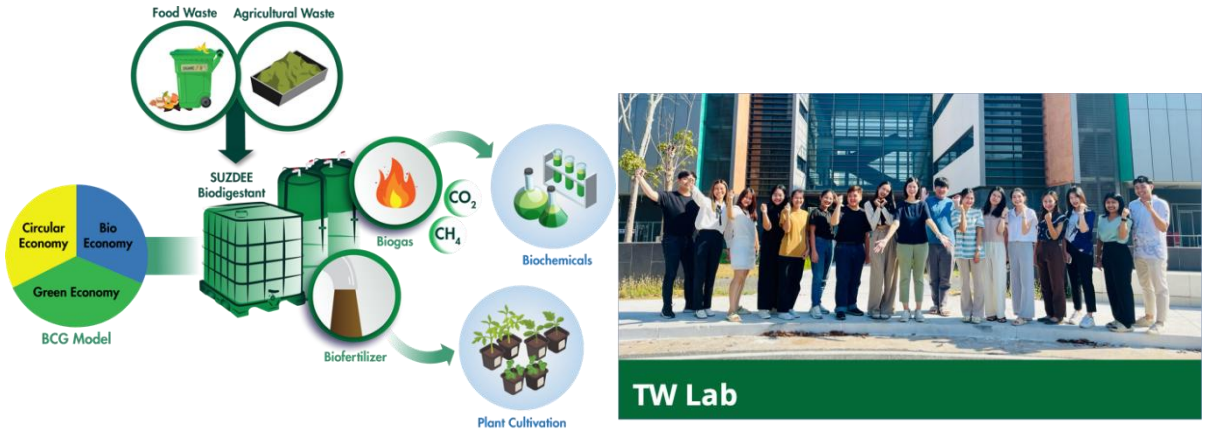

Figure 1.

Circular biotechnological platform converting organic waste into biofuel and biochemicals.

CITATION

Assistant Professor Dr. Thanyaporn Wongnate received her Ph.D. in Biochemistry from Mahidol University, Thailand, and conducted postdoctoral research at the University of Michigan, USA. She is currently an Assistant Professor at the School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC). Her research integrates enzymology, biocatalysis, metabolic engineering, and anaerobic microbial technology to develop sustainable bioenergy systems and green bioprocesses. Dr. Wongnate's pioneering work on enzyme mechanisms, including methyl-coenzyme M reductase and pyranose 2-oxidase, has contributed fundamental insights into biological methane synthesis and oxidative catalysis. Her recent research emphasizes microbial and enzymatic systems for waste-to-energy conversion, including the SUZDEE (Sustainable Zero Waste Digestant for Well-Being) platform for community-scale biogas and biofertilizer production.

Dr. Wongnate has published 50 international peer-reviewed papers, authored five book chapters, and holds three registered petty patents with more than 20 patent applications pending. Her research outputs bridge fundamental enzymology and industrial biotechnology, contributing to Thailand's circular bioeconomy and green innovation. She has received numerous honors, including the 2024 Professor M.R. Jisnuson Svasti Young Protein Scientist of Thailand Award, the ACES-CST Early Career Award for Green Chemistry, the Mahidol University Young Alumni Award, and national recognition for invention and innovation from the NRCT. She was also selected among the "Generation T Asia 100" and "The Future List Thailand 100" for her contributions to sustainability and scientific leadership.

Dr. Wongnate continues to lead interdisciplinary collaborations with academia and industry, advancing enzyme-based and microbial technologies toward practical biotechnological applications for renewable energy, environmental sustainability, and community well-being.

The 2025 Taguchi Prize

For

Outstanding Master's Thesis
in the Field of Biotechnology

Awarded to

Miss Vasita Lapee-e

Chulalongkorn University

Thesis Title

Electrochemical DNA Super-sandwich Biosensor for Porcine DNA Adulteration Detection in Foods

ELECTROCHEMICAL DNA SUPER-SANDWICH BIOSENSOR FOR PORCINE DNA ADULTERATION DETECTION IN FOODS

Vasita Lapee-e[1 2], Suphachai Nuanualsuwan[3 4], Sudkate Chaiyo[2 4], Abdulhadee Yakoh[2 4*]

[1] Program in Biotechnology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

[2] The Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok 10330, Thailand

[3] Department of Veterinary Public Health, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, 10330, Thailand

[4] Center of Excellence for Food and Water Risk Analysis (FAWRA), Department of Veterinary Public Health, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, 10330, Thailand

*e-mail: Abdulhadee.y@chula.ac.th

Abstract:

The increasing incidence of meat adulteration and mislabeling poses significant challenges in food safety, regulatory compliance, and consumer trust. This study presents a molecular biology-based electrochemical DNA biosensor for the specific detection of porcine mitochondrial DNA in tainted meat products. Unlike conventional nucleic acid amplification methods that rely on polymerase chain reaction (PCR), this PCR-free assay utilizes a molecularly amplified sandwich hybridization strategy with DNA tracers that bind to two regions of the target DNA. This configuration enables the formation of elongated hybridization structures tagged with multiple redox molecules, allowing autonomous signal amplification without enzymatic reactions. One-step probe immobilization via poly-adenine (poly-A) oligonucleotides enhances hybridization efficiency and eliminates the need for laborious DNA purification, thereby simplifying the detection workflow. The biosensor achieves a linear detection range of 10^1–10^6 pM with a low limit of detection (LOD) of 2.2 pM under optimized conditions. Furthermore, it successfully distinguishes pork contamination in beef samples with a LOD of 1% w/w. With operational stability exceeding 9 weeks and an estimated cost of less than 0.5 USD per test, the platform offers a sensitive, robust, and cost-effective molecular diagnostic solution. This innovation holds significant potential for on-site applications in food quality monitoring, halal verification, and point-of-need molecular testing across the meat industry.

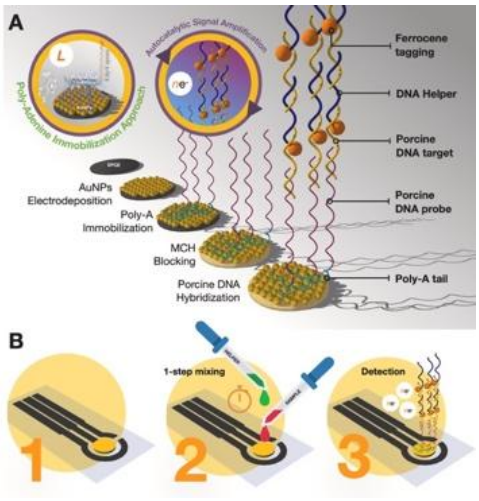

Figure 1.

(A) Schematic illustration of the preparation and (B) detection process in the MAD sandwich assay.

CITATION

Ms. Vasita Lapee-e is a research assistant at the Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Thailand. She obtained her B.Sc. in 2022 from Thammasat University and her M.Sc. in 2024 from Chulalongkorn University. And nowadays, she is currently pursuing a Ph.D. in biotechnology.

Her work centers on DNA biosensors, with a specific focus on the miniaturization of DNA biosensing platforms for practical, point-of-need use. In her master thesis, she develops a PCR-free electrochemical DNA biosensor that selectively detects porcine mitochondrial DNA in complex meat matrices. By coupling sandwich hybridization with poly-adenine probe immobilization, the platform offers a linear range of 10^{1}–10^{6} pM, a limit of detection of 2.2 pM, ~30-minute turnaround, operational stability beyond nine weeks, and a per-test cost below USD 0.50. It reliably identifies pork contamination in beef at 1% w/w, supporting on-site quality control, halal verification, and regulatory screening. A prototype kit (PorkGuard) has been validated on real food samples, and a petty patent has been filed in Thailand (Application No. 01030; pending).

Ms. Vasita is first author of recent publications in *Sensors International* and *Microchemical Journal*, and she has presented her work at national and international conferences. To date, she has received seven awards, including Best Oral (PACCON 2024), Best Poster (RSC–JAIMA 2024), Merck Young Scientist Award 2025 in Chemistry, the Outstanding Graduate Student Research Award, the Takuchi Award for Outstanding Master's Thesis, and two innovation prizes (Gold Medal and First Runner-up) at the NRCT I–New Gen Award 2025. Her portfolio demonstrates originality, technical rigor, and a clear pathway to affordable, impactful diagnostics for a wide range of sectors. She brings a forward-looking vision and a commitment to keeping the technology responsive to global needs and emerging challenges.

The 2025 Taguchi Prize

For

Outstanding Doctoral Thesis

in the Field of Biotechnology

Awarded to

Acting Sub Lt. Dr. Sakonwat Kuepethkaew

Thaksin University

Thesis Title

Production and Use of Gelatin Hydrolysate from Fish Skin as Cryoprotectant for Improving Surimi Quality

PRODUCTION AND USE OF GELATIN HYDROLYSATE FROM FISH SKIN AS CRYOPROTECTANT FOR IMPROVING SURIMI QUALITY

Sakonwat Kuepethkaew,[1,*] Sappasith Klomklao,[2] Benjamin Kofi Simpson[3]
[1] Division of Food Science and Technology, Faculty of Agricultural Technology, Rajamangala University of Technology Thanyaburi, Pathum Thani, 12120, Thailand
[2] Food Science and Nutrition Program, Faculty of Agro and Bio Industry, Thaksin University, Phatthalung Campus, Pa-Phayom, Phatthalung, 93210, Thailand
[3] Department of Food Science & Agricultural Chemistry, McGill University, 21111 Lakeshore Road, Ste-Anne-de-Bellevue, QC, Canada H9X 3V9
* e-mail: Sakonwat@outlook.com, sakonwat_k@rmutt.ac.th

Abstract:
Surimi is a wet concentrate of myofibrillar proteins from fish muscle that is mechanically deboned, water-washed, and frozen. It serves as an intermediate material for surimi-based products such as fish balls and crab sticks. During frozen storage, surimi may lose its functional properties as a result of the denaturation and/or aggregation of myofibrillar proteins. Therefore, the addition of commercial cryoprotectants (sucrose/sorbitol) is required to retain these properties. However, such additives can impart an excessively sweet taste and increase the caloric value of the final surimi products. Processing wastes generated during surimi production, particularly skin and viscera, can be used as raw materials for gelatin production and as sources of proteases, respectively. Gelatin hydrolysates, especially those derived from fish skin, have gained increasing interest as multifunctional additives. Protein hydrolysates and peptides have been shown to exhibit cryoprotective effects and antioxidant activity. Therefore, gelatin hydrolysates could be used as alternative cryoprotectants in surimi to mitigate these deteriorative processes. Given the abundance of fish viscera, particularly stomachs, the recovery of pepsin from fish stomachs should be considered. Furthermore, to maximize the utilization of fish skin, the production of gelatin hydrolysate using recovered fish pepsin as a cryoprotectant in surimi should be explored to develop a novel product with increased market value. As a result, full utilization of fishery resources can be achieved, and the knowledge gained will be beneficial for surimi processing plants as well as the food industry.

CITATION

Dr. Sakonwat Kuepethkaew obtained his B. Sc. degree in Food Science and Technology from Thaksin University and both his M. Sc. and Ph. D. degrees in the Biotechnology program from Thaksin University. During his Ph. D. studies, he received the financial supported outstanding academic performance scholarship from National Research Council of Thailand and Thailand Research Fund under the Research and Researchers for Industries.

He has published his research results in five high-quality journals (ISI Web of Science) such as Food Chemistry, International Journal of Refrigeration, and Journal of Food Science and Technology. In addition, he has six manuscripts that have been submitted to international journals. He has also contributed 17 conference proceedings and received 10 awards for his presentations. His research findings have further led to the publication of an international book chapter and the registration of a petty patent in Thailand.

Currently, Dr. Sakonwat Kuepethkaew is a lecturer in the Division of Food Technology, Faculty of Agricultural Technology, Rajamangala University of Technology Thanyaburi, Thailand. His current research focuses on the utilization of agro-industrial waste materials and the functional properties of food ingredients.

AJINOMOTO FOUNDATION

Ajinomoto Co., (Thailand) Ltd., has been conducting business in Thailand since 1960 and has received wide support and recognition from Thai people and society. The company has always realized its responsibility towards the Thai community, which inspired the establishment of the "AJINOMOTO FOUNDATION" in July 1976. The foundation's primary objective is to promote and support education at all levels.

The socially beneficial projects carried out by the foundation include scholarships, school lunch programs, educational and medical aid equipment, technical lectures for the interested public, assistance for sufferers from natural disasters, and contributions to various Royal projects.

The **Ajinomoto Lecture Award** is one of the Foundation's activities. The Award has been organized by the Foundation and operated by the Thai Society for Biotechnology since **1990** to promote outstanding research in the biotechnology field. The awarded researcher must have made research achievements that contributed to the betterment of Thai society in this field.

Starting in **2023**, the Foundation and the Executive Board of the Thai Society for Biotechnology have agreed to rename the Award to the **"Ajinomoto – TSB Award" for Outstanding Innovative Biotechnologist**. This new title reflects the award's focus on biotechnologists who have successfully engaged in innovation and application. The Award theme for this year is focused on the fields of **Health and Medicine**.

The 2025 Ajinomoto - TSB Award

For

Outstanding Innovative Biotechnologist

Awarded to

Dr. Sissades Tongsima

National Center for Genetic Engineering and Biotechnology

Innovation Theme

From Innovation to Implementation: Developing Computational Genomics Infrastructure for Thailand's Precision Medicine Future

FROM INNOVATION TO IMPLEMENTATION: DEVELOPING COMPUTATIONAL GENOMICS INFRASTRUCTURE FOR THAILAND'S PRECISION MEDICINE FUTURE

Sissades Tongsima[1*]
[1]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Thailand
*e-mail: sissades.ton@biotec.or.th

Abstract:
Genomics is redefining the future of healthcare, offering the ability to diagnose, prevent, and treat disease with unprecedented precision. Yet the field is constrained by the enormous complexity of genomic data and the high cost of computational resources, which often limit access to only the most well-funded institutions. To overcome these barriers, Thailand has invested in a national innovation that integrates high-performance computing, advanced bioinformatic pipelines, a Thai reference genome database, and user-friendly web applications into a single, comprehensive ecosystem.

Developed as part of the country's 50,000-genome reference initiative, the Genomics Thailand project, this ecosystem is more than a collection of tools—it is a shared national infrastructure that enables researchers, clinicians, and innovators to work together on a common foundation. At its heart is a Trusted Research Environment, a secure digital space that ensures compliance with the Personal Data Protection Act (PDPA) while allowing sensitive genomic data to be analyzed collaboratively. By pooling resources at the national level, the system prevents redundant investments by individual hospitals or companies, ensuring that even resource-limited institutions can access world-class genomic capabilities.

The impact is already visible. In regional hospitals, where advanced diagnostics were once out of reach, genomic analysis through this infrastructure has raised rare disease diagnosis rates to 39–52%, providing families with long-sought answers and guiding more effective care. Beyond healthcare, the platform also opens new opportunities for Thailand's businesses in health and wellness, nutrigenomics, microbiome research, and other omics-driven frontier industries, positioning the country as a regional leader in precision health innovation.

This award-winning achievement represents a turning point: by democratizing access to genomics, Thailand is transforming complexity into opportunity, ensuring that the benefits of precision medicine and omics research are shared equitably across the nation.

CITATION

Dr. Sissades Tongsima
Director, Medical Molecular Biotechnology Research Group
National Center for Genetic Engineering and Biotechnology (BIOTEC), NSTDA, Thailand

Dr. Sissades Tongsima earned a B.Eng. in Electrical Engineering from King Mongkut's Institute of Technology Ladkrabang and an M.S. and Ph.D. in Computer Science and Engineering (parallel & distributed computing) from the University of Notre Dame, USA, on a Royal Thai Government scholarship.

He began his career building national computational infrastructure at NECTEC and joined BIOTEC in 2002 to focus on genomics and bioinformatics. After postdoctoral training in France, he helped establish Thailand's early national SNP resources and contributed to regional population genomics work published by the HUGO Pan-Asian SNP Consortium in Science (2009).

As Principal Researcher and Head of the Biostatistics & Bioinformatics Laboratory at the Genome Institute, he led the development of Thailand's national computational genomics infrastructure — including the national genetic-variant resource derived from the Genomics Thailand initiative (50,000 whole-genome sequences) used for research and clinical interpretation.

From 2019 until July 2025 he served as Director of the National Biobank of Thailand, advancing national sample and data governance. On 1 August 2025 he was appointed Director of the Medical Molecular Biotechnology Research Group at BIOTEC, where he continues to drive efforts in genomic data platforms, variant interpretation, and precision medicine services.

Dr. Tongsima's work bridges computation and medicine and has supported national programs for genomic diagnostics and public-health research. He is active in regional collaborations and, following the Pan-Asian work, was invited to serve as an Associate Editor of the Journal of Human Genetics.

CONFERENCE PROGRAM

<table>
<tr><th colspan="5">29 October 2025 (Day 1); Mandarin Hotel Bangkok</th></tr>
<tr><td>8:00-8:45</td><td colspan="4">Open for Registration</td></tr>
<tr><td>8:45-9:00</td><td colspan="4">Welcome Remarks
1. Assoc. Prof. Dr. Chuenchit Boonchird, the President of Thai Society for Biotechnology (TSB)
2. Prof. Dr. Wilert Puriwat, the President of Chulalongkorn University</td></tr>
<tr><td>9:00-9:30</td><td colspan="4">Plenary Lecture I: Prof. Dr. Hiroshi Takagi, Nara Institute of Science and Technology, Japan
Title: Functional amino acids engineering in yeast: From metabolic regulations to biotechnological applications</td></tr>
<tr><td>9:30-10:00</td><td colspan="4">Plenary Lecture II: Prof. Dr. Stephen B. Pointing, Yale-NUS College, Singapore
Title: Intertidal microbial dynamics in response to the 2024 Pasir Panjang oil spill in Singapore</td></tr>
<tr><td>10:00-10:30</td><td colspan="4">Plenary Lecture III: Prof. Dr. Hideaki Nojiri, The University of Tokyo, Japan
Title: Application of a novel screening method for degrading bacteria reveals unknown microbial functions and interactions</td></tr>
<tr><td>10:30-11:00</td><td colspan="4">Refreshment</td></tr>
<tr><td>11:00-11:30</td><td colspan="4">Plenary Lecture IV: Dr. Natphasuth Patthirasinsiri, Chairman of Biotech Industry Club, The Federation of Thai Industries (FTI), Thailand
Title: Biotechnology business in Thailand</td></tr>
<tr><td>11:30-12:20</td><td colspan="4">Taguchi Prize and Ajinomoto Award Announcement and Presentation</td></tr>
<tr><td>12:20-13:45</td><td colspan="4">Lunch</td></tr>
<tr><td>13:45-14:30</td><td colspan="4">Exhibition Talks
1. S.K. POWERABLE Co., Ltd., Mr. Purin Kiatrasmee, Title: Laboratory safety
2. Ward Medic Ltd. Ms. Supamard Chooyim, Title: Seamless research solutions for modern life sciences</td></tr>
<tr><td></td><td>Session I:
Bioinformatics and Systems Biology, Synthetic Biology</td><td>Session II:
Medical Biotechnology & One Health</td><td>Session III:
Industrial & Environmental Biotechnology & Alternative Energy</td><td>Session V:
Agriculture Biotechnology</td></tr>
<tr><td>14:30–14:50</td><td>Prof. Dr. Hiroshi Shimizu</td><td>Prof. Dr. Michiya Matsusaki</td><td>Prof. Dr. Robert Duran</td><td>Prof. Dr. Hakuto Kageyama</td></tr>
<tr><td>14:50-15:10</td><td>Prof. Dr. Tuck Seng Wong</td><td>Assoc. Prof. Dr. Salvador Almagro-Moreno</td><td>Prof. Dr. Beom Soo Kim</td><td>Prof. Dr. Timothy Mahony</td></tr>
<tr><td>15:10-16:25</td><td>Oral Presentation (5 topics)</td><td>Oral Presentation (5 topics)</td><td>Oral Presentation (5 topics)</td><td>Oral Presentation (5 topics)</td></tr>
<tr><td>16:25-18:00</td><td colspan="2">Refreshment + Poster Presentation (Presentations with odd number)</td><td colspan="2">TSB Annual Meeting</td></tr>
<tr><td>18:00-20:00</td><td colspan="4">Welcome Reception, flag-giving ceremony, and dinner</td></tr>
</table>

30 October 2025 Mandarin Hotel Bangkok					
8:00-9:00	Open for Registration				
9:00-9:30	**Plenary Lecture V: Prof. Dr. Fitnat Yildiz, University of California, Santa Cruz, USA** Title: Mechanisms and regulation of biofilm formation in *Vibrio cholerae*				
9:30-10:00	**Plenary Lecture VI: Prof. Dr. Kohsuke Honda, The University of Osaka, Japan** Title: Design and implementation of synthetic metabolic pathways outside the cells				
10:00-10:40	**Business Talk: The startup mindset from a venture creator** Mr. Phusith Jitjaruek and Mr. Teeratat Bunsantrakul, Origgin Ventures CO., LTD. Moderator: Prof. Dr. Tavan Janvilisri				
10:40-11:00	**Refreshment**				
	Session II: Medical Biotechnology & One Health	**Session III:** Industrial & Environmental Biotechnology & Alternative Energy	**Session IV:** Biodiversity, Natural Products and Applications	**Session VI:** Food Biotechnology & Food Security& Future Food	**Special Symposium** Marine Biotechnology and Bioprospecting
11:00-11:20	Assoc. Prof. Dr. Noorjahan Banu Alitheen	Prof. Dr. Si-Yu Li	Prof. Dr. Masaki Mizunuma	Dr. Nitsara Karoonuthaisiri	1. Assoc. Prof. Dr. Kustiariyah Tarman 2. Asst. Prof. Dr. Rath Pichyangkura, 3. Prof. Iriani Setyaningsih 4. Dr. Sorawit Paotongsook 5. Dr. Heti Mulyati 6. Dr. Dimas Andrianto (11:00 -12:30)
11:20-11:40	Assoc. Prof. Dr. Yi-Chen Ethan Li	Prof. Dr. Kumar Sudesh	Prof. Dr. Shinya Kodani	Assoc. Prof. Dr. Inthawoot Suppavorasatit	
11:40-12:25	Oral Presentation (3 topics)	Oral Presentation (3 topics)	Oral Presentation (3 topics)	Oral Presentation (3 topics)	

<table>
<tr><td>12:25-14:00</td><td colspan="5">Lunch + Poster presentation (Presenters with even number)</td></tr>
<tr><td></td><td>Session I: Bioinformatics and Systems Biology, Synthetic Biology</td><td>Session V: Agriculture Biotechnology</td><td>Session IV: Biodiversity, Natural Products and Applications</td><td>Session VI: Food Biotechnology & Food Security & Future Food</td><td>Special Symposium Marine Biotechnology and Bioprospecting</td></tr>
<tr><td>14:00-14:20</td><td>Prof. Dr. Shen-Long Tsai</td><td>Prof. Dr. Yoichi Honda</td><td>Assoc. Prof. Dr. Hui-min Neoh</td><td>Dr. Nobuyuki Kijima</td><td rowspan="3">1. Prof. Dr. Sri Suharti
2. Prof. Dr. Wanchai Assavalapsakul
3. Prof. Asadatun Abdullah
4. Assoc. Prof. Dr. Hoàng Anh Hoàng
5. Asst. Prof. Dr. Novriyandi Hanif
6. Dr. Eng. Safrina Dyah Hardiningtyas
(14:00 -15:30)</td></tr>
<tr><td>14:20-14:40</td><td>Prof. Dr. Takeharu Tsuge</td><td>Assoc. Prof. Dr. Masaki Honda</td><td>Dr. Nurzila Ab Latif</td><td>Assoc. Prof. Dr. Soraya Chaturongakul</td></tr>
<tr><td>14:40-15:25</td><td>Oral Presentation (3 topics)</td><td>Oral Presentation (3 topics)</td><td>Oral Presentation (3 topics)</td><td>Oral Presentation (3 topics)</td></tr>
<tr><td>15:25-15:45</td><td colspan="5">Refreshment</td></tr>
<tr><td>15:45-17:00</td><td colspan="5">Special plenary session
Job opportunities and research fundings for microbiologists/ biotechnologists
1. Prof. Dr. Nuttha Thongchul, Director Institute of Biotechnology and Genetic Engineering, Chulalongkorn University
Title: Job opportunities + research fundings for microbiologists/ biotechnologists
2. Dr. Jittima Phonbuppha, Researcher - Innovation Growth Platforms, PTT Global Chemical Public Company Limited
Title: Opportunities for industrial biotechnology in Thailand
3. Dr. Prakaipetch Kitiyanan, Director - Specialty Business, Thai Wah Public Company Limited
Title: Job opportunities and research funding for microbiologists/ biotechnologists at Thai Wah PLC
Moderator: Prof. Dr. Nuttha Thongchul</td></tr>
<tr><td>17:00-17:15</td><td colspan="5">Award Announcement and Closing Ceremony by the TSB President</td></tr>
</table>

31 October 2025

Option 1: Special Symposium to Commemorate the 50th Anniversary of Department of Microbiology, Faculty of Science, Chulalongkorn University
Banyen meeting room, Maha Vajirunhis Building, Chulalongkorn University*

Co-organized by The Society for Biotechnology, Japan

9:00-9:15	**Welcome remarks** 1. Prof. Dr. Tanapat Palaga, Head of Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand 2. Prof. Dr. Hiroshi Shimizu, President of The Society for Biotechnology (SBJ), Japan
9:15-10:30	**Microbiology and Biotechnology Research in Japan** 1. Prof. Dr. Hiroshi Shimizu, The University of Osaka, Japan Title: Metabolic engineering for microbial bioproduction 2. Prof. Dr. Hiroshi Takagi, Nara Institute of Science and Technology, Japan Title: Development of yeast-based sustainable proteins using functional amino acid engineering 3. Prof. Dr. Kohsuke Honda, The University of Osaka, Japan Title: *In vitro* reconstitution of non-oxidative glycolysis with thermophilic enzymes Moderator: Asst. Prof. Dr. Chonchanok Muangnapoh
10:30-10:45	**Coffee Break**
10:45-12:15	**Microbiology and Biotechnology Research in Thailand** 1. Prof. Dr. Arinthip Thamchaipenet, Kasetsart University, Thailand Title: *Wolffia globosa* microbiome benefits vitamin B12 production 2. Prof. Dr. Tavan Janvilisri, Chulalongkorn University, Thailand Title: We gotta start somewhere, right? A small step of cultured meat research in Thailand 3. Dr. Supattra Treerattrakool, Mahidol University, Thailand Title: Biologics and its application in shrimp Moderator: Prof. Dr. Tavan Janvilisri
12:15-13:30	**Lunch**
13:30-15:00	**Microbiology and Biotechnology Business in Thailand** 1. Dr. Worawan Watthanathadakit, Senior CVC Analyst, Bangchak Initiative and Innovation Center (BiiC), Thailand Title: Why startups need more than capital: Scaling SynBio with strategic corporate partnerships 2. Assoc. Prof. Dr. Naraporn Somboonna, Chulalongkorn University and AL-DNA Co. Ltd., Thailand Title: AL-DNA and THANARA skin microbiome products 3. Asst. Prof. Dr. Jomkhwan Meerak, Chiang Mai University and BIRTH 2022 Co. Ltd., Thailand Title: Immune boosting cold brew coffee: Future beverage trends but more sustainable Moderator: Dr. Ritu Ningthoujam

15:00-15:15	**Coffee Break**
15:15-16:30	**Microbiology and Biotechnology Business in Thailand (cont.)** 1. Dr. Pinidphon Prombutara, Modgut Co. Ltd., Thailand Title: Microbiome-based business opportunities: What are the next steps following a decade of research on the human gut microbiome? 2. Dr. Jirasin Koonthongkaew, Chulalongkorn University, Thailand Title: Development of *Saccharomyces cerevisiae* strain for isobutanol production from an osmotolerant and ethanol-producing yeast Moderator: Dr. Ritu Ningthoujam
16:30-16:45	**Closing Remarks**

*Banyen meeting room, Maha Vajirunhis Building, Chulalongkorn University
https://maps.app.goo.gl/2KcVmCtqefWLxAXd6

31 October 2025 **Option 2: Special Symposium: Tackling Antifungal Resistance Through a One Health Lens** Multipurpose Room, 2nd Floor, TAB Building, Faculty of Science, Chulalongkorn University** Hosted by SEA-ARMi: Southeast Asia Antifungal Resistance Monitoring Initiative	
8:30–9:00	**Registration and Welcome Coffee**
9:00-9:10	**Opening Remarks** Prof. Dr. Pranut Potiyaraj Dean of Faculty of Science, Chulalongkorn University, Thailand
9:10-9:40	**Keynote Address "Antifungal Resistance in a One Health Context: Global Challenges and Opportunities"** Prof. Dr. Neil Gow, FAILSAFE representative, University of Exeter, UK
9:40-10:10	**Session 1: SEA-ARMI - Fungal AMR across southeast Asia** Asst. Prof. Dr. Nuttapon Pombubpa, Faculty of Science, Chulalongkorn University, Thailand
10:10-10:30	**Session 2: Clinical insights on antifungal resistance in Thailand** Assoc. Prof. Dr. Ariya Chindamporn, Faculty of Medicine, Chulalongkorn University, Thailand
10:30-10:45	**Coffee Break and Networking**
10:45-11:05	**Session 3: Tackling antifungal resistance: bridging environmental and veterinary health through aquaculture insights** Assoc. Prof. Dr. Saharuetai Jeamsripong Faculty of Veterinary, Chulalongkorn University, Thailand
11:05-11:50	**Session 4: Panel Discussion: Policy, Partnerships & Future Funding** 1. Professor Neil Gow, University of Exeter, UK 2. Assoc. Prof. Jiruth Sriratanaban, Dean of Faculty of Medicine, Chulalongkorn University, Thailand 3. Mr. Chavit (Bank) Uttamachai, Science and Innovation Advisor, British Embassy Bangkok, Thailand
11:50-12:00	**Closing Remarks**
12:00-13:00	**Lunch & networking**

**Multipurpose Room, 2nd Floor, TAB Building, Faculty of Science, Chulalongkorn University
https://maps.app.goo.gl/9w9BAm9HGachRMf86

SESSION SYNOPSIS

I. Bioinformatics and Systems Biology, Synthetic Biology
This session showcases advanced in silico metabolic modeling, enzyme engineering, and synthetic biology strategies to optimize microbial cell factories. Talks highlight directed evolution, biopolyester biosynthesis, synthetic microbial consortia, and biological CO_2 capture for sustainable bioproduction and biocatalysis innovations.

II. Medical Biotechnology & One Health
Gain insights into emerging biomedical frontiers, including Lactobacillus-mediated cognitive enhancement, stem cell-on-a-chip systems, and evolutionary mechanisms behind pandemic *Vibrio cholerae*. This session also features functional polymers and biomaterials shaping the future of tissue engineering and regenerative medicine.

III. Industrial & Environmental Biotechnology & Alternative Energy
Explore microbial platforms for bio-based chemical production, including high-yield nicotinamide mononucleotide synthesis. Talks cover microbial diversity from extreme environments, marine oil bioremediation, metal biotransformations, and innovative biodegradable materials sourced from agro-industrial waste such as oil palm residues.

IV. Biodiversity, Natural Products and Applications
Delve into microbial pathogenesis, natural compound discovery, and functional peptide biosynthesis. Speakers address MRSA virulence, sepsis diagnostics, and the gut microbiome's role in colorectal cancer, alongside genome-guided mining for phytochemicals and heterologous production of novel bioactive peptides.

V. Agricultural Biotechnology
This session presents advances in microbial and fungal biotechnology for agricultural resilience. Topics include UV-protective compounds from cyanobacteria, genetic enhancement of edible mushrooms, biofunctional carotenoids, and novel strategies in molecular virology to mitigate viral diseases in livestock.

VI. Food Biotechnology, Food Security & Future Food
Addressing global food challenges, this session explores aquaculture innovations, flavor science, and the rise of multidrug-resistant foodborne pathogens. Talks highlight antimicrobial resistance surveillance in food systems and strategies for safer, more sustainable food production.

SPECIAL SYMPOSIUMS

1. Marine Biotechnology and Bioprospecting
Co-organized with IPB University, Indonesia, the session explores marine resources including macro and microorganisms, such as seaweeds, invertebrates, microalgae and marine fungi. Marine resources are rich in bioactive compounds and enzymes. This session highlights their potential uses in foods, animal sciences, pharmaceuticals, environment and industrial biotechnology.

2. Special Symposium Commemorating the 50th Anniversary of the Department of Microbiology, Chulalongkorn University.
Co-organized with The Society for Biotechnology, Japan, this event covers cutting-edge microbiology and biotechnology advancements, from microbiome benefits to cultured meat and biologics. Explore the thriving biotech business landscape in Thailand, including insights on startups, skin microbiome products, and innovative beverages.

3. Tackling Antifungal Resistance Through a One Health Lens
Hosted by SEA-ARMi, this event delves into the critical issue of antifungal resistance. Gain insights from leading experts like Professor Dr. Neil Gow on global challenges, and explore regional and clinical perspectives with Chulalongkorn University's Dr. Nuttapon Pombubpa and Dr. Ariya Chindamporn. Discover how aquaculture research is bridging environmental and veterinary health with Dr. Saharuetai Jeamsripong. Conclude with a dynamic panel discussion on policy, partnerships, and funding.

CONFERENCE PROGRAM

29 October 2025			
Session I. Bioinformatics and Systems Biology, Synthetic Biology			
Meeting room: Mandarin A			
Chairperson: Prof. Dr. Tavan Janvilisri, Chulalongkorn University **Co-chairperson:** Asst. Prof. Dr. Nuttapon Pombubpa, Chulalongkorn University			
14:30-14:50	*In silico* design and experimental analysis of metabolic pathways for microbial bioproduction	Prof. Dr. Hiroshi Shimizu, The University of Osaka, Japan	Invited Speaker #1
14:50-15:10	Advancing industrial biotechnology through adaptive laboratory evolution	Prof. Dr. Tuck Seng Wong, The University of Sheffield, UK	Invited Speaker #2
15:10-15:25	Upcycling of chicken manure fertilizer into proline by engineered halophilic *Halomonas elongata* cell factory	Prof. Hideki Nakayama, Nagasaki University, Japan	BS-O-013
15:25-15:40	Tailoring phosphite dehydrogenase for a highly efficient and robust NAD(P)H cofactor regeneration system	Dr. Gamal Abdel-Hady, Hiroshima university, Japan	BS-O-015
15:40-15:55	Impact of HOG1 deletion on glucose fermentation and redox stress response in *Saccharomyces cerevisiae*	Dr. Nunthaphan Vikromvarasiri, RIKEN, Japan	BS-O-001
15:55-16:10	Capturing viral diversity and adaptation through metagenomics	Dr. Worakorn Phumiphanjarphak, Mahidol University, Thailand	BS-O-018
16:10-16:25	High-temperature upcycling of poly(3-hydroxybutyrate-co-3-hydroxyvalerate) by a novel *Actinomadura* sp. SCN-SB	Dr. Natthaphat Phothong, Chulalongkorn University, Thailand	BS-O-017

30 October 2025			
Session I. Bioinformatics and Systems Biology, Synthetic Biology			
Meeting room: Mandarin A			
Chairperson: Asst. Prof. Dr. Adisak Romsang, Mahidol University **Co-chairperson:** Asst. Prof. Dr. Nuttapon Pombubpa, Chulalongkorn University			
14:00-14:20	Harnessing synthetic microbial consortia for advanced bioprocessing applications	Prof. Dr. Shen-Long Tsai, National Taiwan University of Science and Technology, Taiwan	Invited Speaker #1
14:20-14:40	Polyhydroxyalkanoates production by recombinant *Ralstonia eutropha* from CO_2 as sole carbon source	Prof. Dr. Takeharu Tsuge, Institute of Science Tokyo, Japan	Invited Speaker #2
14:40-14:55	Recombinant arsenite oxidase (aioA & aioB) from *Thiomonas cuprina*: comparative insights into native and synthetic gene constructs	Dr. Mahesh Mannacharaju, Kyushu University, Japan	BS-O-010
14:55-15:10	Knowledge graphs to predict bioactivity of natural products	Assoc. Prof. Dr. Natapol Pornputtapong, Chulalongkorn University, Thailand	BS-O-019
15:10-15:25	Transcriptomics analysis of *Starmerella riodocensis* GT-SL1R under high carbon to nitrogen ratio condition for enhanced sophorolipid production	Mr. Sirawich Sapsirisuk, King Mongkut's University of Technology Thonburi	BS-O-002

29 October 2025			
Session II. Medical Biotechnology & One Health			
Meeting room: Mandarin B			
Chairperson: Assoc. Prof. Dr. Chuenchit Boonchird, Mahidol University **Co-Chairperson:** Prof. Dr. Fitnat Yildiz, The University of California, Santa Cruz, USA			
14:30-14:50	Dynamic regulation of cells and extracellular matrix for tissue engineering	Prof. Dr. Michiya Matsusaki, The University of Osaka, Japan	Invited Speaker #1
14:50-15:10	Emergence of pandemic *Vibrio cholerae*: Molecular drivers and evolutionary bottlenecks	Assoc. Prof. Dr. Salvador Almagro-Moreno, St. Jude Children's Research Hospital, USA	Invited Speaker #2
15:10-15:25	Distribution of *Vibrio* spp. in relation to water quality in the Songkhla lake basin, Thailand	Ms. Jutamas Manit, Prince of Songkla University, Thailand	MB-O-024
15:25-15:40	Functional analysis of aromatic amino acid transporter gene aaaT on antimicrobial resistance in *Pseudomonas aeruginosa*	Ms. Pacharapon Phoopanish, Mahidol University, Thailand	MB-O-022
15:40-15:55	Suppression of *Pseudomonas aeruginosa* virulence and biofilm formation by ciprofloxacin-loaded ZnO@lignin@chitosan nanoparticles	Dr. Nadia Fattahi, Pukyong National University, Republic of Korea	MB-O-021
15:55-16:10	Phycocyanin-loaded hierarchical micro/nanofibrous membrane for guided bone regeneration	Ms. Da-Bin Kim, Pukyong National University, Republic of Korea	MB-O-019
16:10-16:25	Therapeutic efficacy of fucoidan-loaded gelatin/oxidized carboxymethyl cellulose hydrogels in accelerating wound healing	Ms. Yu-Jin Ahn, Pukyong National University, Republic of Korea	MB-O-020

30 October 2025			
Session II. Medical Biotechnology & One Health			
Meeting room: Mandarin A			
Chairperson: Asst. Prof. Sita Virakul, Chulalongkorn University, Thailand **Co-Chairperson:** Dr. Phawinee Subsomwong, Chulalongkorn University, Thailand			
11:00-11:20	Ameliorative effect of *Lactobacillus paracasei* HBUAS52231 on spatial learning and memory of D-Galactose-induced aging mice	Assoc. Prof. Dr. Noorjahan Banu Alitheen, Universiti Putra Malaysia, Malaysia	Invited Speaker #1
11:20-11:40	Automated centrifugal microfluidic platform for drug screening	Assoc. Prof. Dr. Yi-Chen Ethan Li, Feng Chia University, Taiwan	Invited Speaker #2
11:40-11:55	Towards rapid biosensing of invasive fungal diseases: a PCR-enhanced lateral flow assay for clinical application	Dr. Jasper Elvin James, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, Malaysia	MB-O-031
11:55-12:10	Adaptive quorum sensing rewiring in *Vibrio campbellii* suppressor mutants: implications for aquaculture and one health	Assoc. Prof. Dr. Pimonsri Mittraparp-arthorn, Prince of Songkla University, Thailand	MB-O-013
12:10-12:25	*Staphylococcus aureus*-derived extracellular vesicles promote pathogenicity of *Pseudomonas aeruginosa*	Dr. Phawinee Subsomwong, Chulalongkorn University, Thailand	MB-O-033

29 October 2025			
Session III: Industrial & Environmental Biotechnology & Alternative Energy			
Meeting room: Karaked			
Chairperson: Assoc. Prof. Dr. Onruthai Pinyakong, Chulalongkorn University **Co-Chairperson:** Dr. Panaya Kotchaplai, Chulalongkorn University			
14:30-14:50	Microbial ecology of contaminated environments	Prof. Dr. Robert Duran, University of Pau, France	Invited Speaker #1
14:50-15:10	Production of nicotinamide mononucleotide by high cell density culture of metabolically engineered *Escherichia coli*	Prof. Dr. Beom Soo Kim, Chungbuk National, Republic of Korea	Invited Speaker #2
15:10-15:25	Sorghum stem juice valorization to produce bioethanol: Process simulation and life cycle assessment	Ms. Jutima Tantrakool, Kasetsart University, Thailand	IE-O-005
15:25-15:40	A novel design of intermittent waterwheel carbon fixation bioreactor	Ms. Mei-Chen Ko, National Chung Hsing University, Taiwan	IE-O-007
15:40-15:55	Bacterial cellulose: genome analysis of strains producing cellulose from sucrose	Dr. Naoto Tonouchi Bio-Polymer Research, Co., Ltd., Japan	IE-O-008
15:55-16:10	Biofilm structural differences in *Mycolicibacterium parafortuitum* impact on cell colonization and pyrene degradation	Dr. Kallayanee Naloka, Chulalongkorn University, Thailand	IE-O-043

30 October 2025			
Session III: Industrial & Environmental Biotechnology & Alternative Energy			
Meeting room: Mandarin B			
Chairperson: Assoc. Prof. Dr. Suchada Chanprateep Napathorn, Chulalongkorn University **Co-Chairperson:** Assoc. Prof. Dr. Ekawan Luepromchai, Chulalongkorn University			
11:00-11:20	Towards sustainable solutions: advancing biodegradable materials in Asia	Prof. Dr. Si-Yu Li, National Chung Hsing University, Taiwan	Invited Speaker #1
11:20-11:40	Efficient production and characteristics of biobased and biodegradable polyhydroxyalkanoates from oil palm wastes	Prof. Dr. Kumar Sudesh, Universiti Sains Malaysia, Malaysia	Invited Speaker #2
11:40-11:55	Enhancing biotransformation of cassava pulp to biomethane with liquid hot water and microbial pretreatments	Mr. Saengmany Phommakod, King Mongkut's University of Technology Thonburi, Thailand	IE-O-011
11:55-12:10	Effects of Thai herbal extracts on mitigating alachlor-induced oxidative stress in *Saccharomyces cerevisiae*	Ms. Pham Ngoc Nhi Huynh, Mahidol University, Thailand	IE-O-022
12:10-12:25	Glutamate-independent production of poly-γ-glutamic acid by *Bacillus subtilis* FSO3: Medium optimization and biomass valorization potential	Dr. Panaya Kotchaplai, Chulalongkorn University, Thailand	IE-O-054

30 October 2025			
Session IV. Biodiversity, Natural Products and Applications			
Meeting room: Karaked			
Chairperson: Prof. Dr. Chulee Yompakdee, Chulalongkorn University **Co-Chairperson:** Asst. Prof. Dr. Chompoonik Kanchanabanca, Chulalongkorn University			
11:00-11:20	Lifespan extension mediated by methionine metabolite	Prof. Dr. Masaki Mizunuma, Hiroshima University, Japan	Invited Speaker #1
11:20-11:40	Strategy for heterologous production of new peptides based on genome mining	Prof. Dr. Shinya Kodani, Shizuoka University, Japan	Invited Speaker #2
11:40-11:55	Biological activities and mechanisms of DMC derivatives in human colon cancer cell lines	Ms. Atchara Janthong, Chiang Mai University, Thailand	BN-O-009
11:55-12:10	Bacterial community structure and diversity in agricultural soils across Northeast Thailand	Ms. Pakkawan Kamolklang, Chulalongkorn University, Thailand	BN-O-032
12:10-12:25	Targeted genome editing in *Pleurotus ostreatus* using pre-assembled CAS9 ribonucleoprotein and split-marker donor DNA template	Dr. Tatpong Boontawon, Chulalongkorn University, Thailand	BN-O-033

30 October 2025			
Session IV. Biodiversity, Natural Products and Applications			
Meeting room: Karaked			
Chairperson: Assoc. Prof. Dr. Naraporn Somboonna, Chulalongkorn University **Co-Chairperson:** Asst. Prof. Dr. Chanya Chaicharoenpong, Chulalongkorn University			
14:00-14:20	Harnessing biotechnology for antimicrobial resistance surveillance and detection: patient to environment; genotyping to genome sequencing	Assoc. Prof. Dr. Hui-min Neoh, Universiti Kebangsaan Malaysia, Malaysia	Invited Speaker #1
14:20-14:40	GC-MS profiling of *Piper sarmentosum*: Impact of solvent selection on phytochemical extraction	Dr. Nurzila Ab Latif, Universiti Teknologi Malaysia, Malaysia	Invited Speaker #2
14:40-14:55	*Ecklonia cava* extract-incorporated silver nanoparticles: Dual therapeutic potential as biofunctional agents with *in vivo* insights in zebrafish model	Ms. Tri Purwa Ningrum Pukyong National University, Republic of Korea	BN-O-017
14:55-15:10	Investigation of the antioxidant activity of a selected compound derived from *Curcuma comosa* Roxb. in *Saccharomyces cerevisiae*	Mr. Trin Tangnararatchakit Chulalongkorn University, Thailand	BN-O-018
15:10-15:25	Scalable and green bioprocesses for zwitterionic biosurfactant production using mixed lignocellulosic residues under alkaline fermentation	Asst. Prof. Dr. Nichakorn Khondee, Naresuan University, Thailand	BN-O-034

29 October 2025			
Session V. Agriculture Biotechnology			
Meeting room: Kannika			
Chairperson: Dr. Ruengwit Sawangkeaw, Chulalongkorn University **Co-Chairperson:** Dr.Wannapawn Watsuntorn, Chulalongkorn University			
14:30-14:50	Biosynthetic regulation and biological activities of UV-absorbing compounds in cyanobacteria	Prof. Dr. Hakuto Kageyama, Meijo University, Japan	Invited Speaker #1
14:50-15:10	The application of RNA technologies to drive innovations in animal health	Prof. Dr. Timothy Mahony, The University of Queensland, Australia	Invited Speaker #2
15:10-15:25	Microbial-based bioinsecticides, bioherbicides and biofungicides: a sustainable approach to pest, weed and disease control	Dr. Alongkorn Amnuaykanjanasin, National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand	AB-O-005
15:25-15:40	Biomass production of *in vitro Microchirita involucrata* roots and evaluation of biological activity of root culture extracts elicited with elicitors	Mr. Adsadayu Thonnondang, Naresuan University, Thailand	AB-O-008
15:40-15:55	Extremophilic cyanobacteria and their photoprotective compounds	Dr. Sasiprapa Samsri, Chulalongkorn University, Thailand	AB-O-009
15:55-16:10	Antifungal activity of *Priestia aryabhattai* ptku-123 crude extract against *Fusarium* spp. associated with durian die-back disease	Mr. James Konkov, Kasetsart University, Thailand	AB-O-021
16:10-16:25	Functional study of *Litopenaeus vannamei* alpha-2-macroglobulin and white spot syndrome viral protein targets in response to white spot syndrome	Mr. Kittisak Chawichan Chulalongkorn University, Thailand	AB-O-031

30 October 2025			
Session V. Agriculture Biotechnology			
Meeting room: Mandarin B			
Chairperson: Dr. Piroonporn Srimongkol, Chulalongkorn University **Co-Chairperson:** Prof. Dr. Wanchai Assavalapsakul, Chulalongkorn University			
14:00–14:20	Recent progress and prospects in molecular genetics and application of mushroom-forming fungus, *Pleurotus ostreatus*	Prof. Dr. Yoichi Honda, Kyoto University, Japan	Invited Speaker #1
14:20-14:40	Potential applications of Z-isomer-enriched carotenoids in the food, cosmetic, and feed industries	Assoc. Prof. Dr. Masaki Honda, Meijo University, Japan	Invited Speaker #2
14:40-14:55	Variaton of growth and yield plasiticity to drought in high-yielding thai cassava varieties	Ms. Monica Adu-Gyamfi, King Mongkut's University of Technology Thonburi, Thailand	AB-O-006
14:55-15:10	Gelling agent-free temporary immersion micropropagation of *Labisia pumila*: a cost-effective approach	Dr. Nurnadiah Roslan, Forest Research Institute Malaysia (FRIM), Malaysia	AB-O-016
15:10-15:25	Biological properties of alkali lignin extract from longan peel for cosmetic application	Ms. Kittiya Phiguntong, Chiangmai University, Thailand	AB-O-024

30 October 2025			
Session VI. Food Biotechnology & Food Security & Future Food			
Meeting room: Kannika			
Chairperson: Dr. Nobuyuki Kijima, National Agriculture and Food Research Organization, Japan **Co-Chairperson:** Dr. Piroonporn Srimongkol, Chulalongkorn University			
11:00-11:20	mycoSMART: a portable device for multiplex detection of mycotoxins	Dr. Nitsara Karoonuthaisiri, The National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand	Invited Speaker #1
11:20-11:40	Flavor formation during food fermentation	Assoc. Prof. Dr. Inthawoot Suppavorasatit, Chulalongkorn University, Thailand	Invited Speaker #2
11:40-11:55	Lateral flow dipstick assay for dna-based detection of ochratoxin a producing fungi in coffee	Dr. Amorn Owatworakit, Mae Fah Luang University, Thailand	FB-O-016
11:55-12:10	Process optimization of liquefaction in enzymatic hydrolysis of waste bread using response surface methodology	Ms. Hsu Yadanar Htun, King Mongkut's University of Technology Thonburi, Thailand	FB-O-008
12:10-12:25	Characterization and screening of flavor-producing non-*Saccharomyces* yeasts for fermentation applications	Ms. Manatsanun Boonyanuwat, Chulalongkorn University, Thailand	FB-O-017

30 October 2025			
Session VI. Food Biotechnology & Food Security & Future Food			
Meeting room: Kannika			
Chairperson: Assoc Prof Dr.Pimonsri Mittraparp-Arthorn, Prince of Songkla University **Co-Chairperson:** Dr. Wannapawn Watsuntorn, Chulalongkorn University			
14:00-14:20	AMR in the agricultural environment	Dr. Nobuyuki Kijima, National Agriculture and Food Research Organization (NARO), Japan	Invited Speaker #1
14:20-14:40	Diversity of MDR *Enterobacteriaceae* in Thai meat products	Assoc. Prof. Dr. Soraya Chaturongakul, Mahidol University, Thailand	Invited Speaker #2
14:40-14:55	Discrepancies of antimicrobial resistant genotypes and phenotypes in foodborne bacteria *Vibrio parahaemolyticus* from aquatic bird feces in Thailand	Ms. Wijitra Khaosoong, Chulalongkorn University, Thailand	FB-O-012
14:55-15:10	Development and characterization of cellulose acetate/chitosan films incorporated with piper betel extract for antimicrobial food packaging	Mr. Prapot Kumhang, King Mongkut's University of Technology Thonburi, Thailand	FB-O-011
15:10-15:25	Impact of bacteriophage contamination from silage on yogurt fermentation	Mr. Noppakorn Thadasawate, Silpakorn University, Thailand	FB-O-014

30 October 2025			
Special Symposium: Marine Biotechnology and Bioprospecting I			
Meeting room: Pornphairin			
Chairperson: Dr. Chawalit Charoenpong, Chulalongkorn University, Thailand			
11:00-11:15	Antibacterial activity and fatty acid content of mangrove-derived *Thraustochytrids*	Assoc. Prof. Dr. Kustiariyah Tarman, IPB University, Indonesia	Invited Speaker #1
11:15-11:30	Applications of marine chitin and chitosan in Thailand	Asst. Prof. Dr. Rath Pichyangkura, Chulalongkorn University, Thailand	Invited Speaker #2
11:30-11:45	Productivity and bioactivity of *Spirulina* cultivated in inclined plastic column photobioreactor	Prof. Iriani Setyaningsih, IPB University, Indonesia	Invited Speaker #3
11:45-12:00	Cultivation and application of cyclopoid copepod in fish and shrimp hatcheries	Dr. Sorawit Powtongsook, The National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand	Invited Speaker #4
12:00-12:15	Supply chain of seaweed and its impact on bioprospecting	Dr. Heti Mulyati, IPB University, Indonesia	Invited Speaker #5
12:15-12:30	Effect of NPK fertilization on water physicochemical properties and the nutritional composition of *Ulva lactuca*	Dr. Dimas Andrianto, IPB University, Indonesia	Invited Speaker #6

30 October 2025			
Special Symposium: Marine Biotechnology and Bioprospecting II			
Meeting room: Pornphairin			
Chairperson: Assoc. Prof. Dr. Kustiariyah Tarman, IPB University, Indonesia **Co-chair:** Dr. Dimas Andianto, IPB University, Indonesia			
14:00-14:15	Fiber digestibility in the *In Vitro* rumen fermentation with the presence of marine endophytic fungi	Prof. Dr. Sri Suharti, IPB University, Indonesia	Invited Speaker #1
14:15-14:30	Recombinant proteins for aquatic science in Thailand: Challenges and opportunities	Prof. Dr. Wanchai Assavalapsakul, Chulalongkorn University, Thailand	Invited Speaker #2
14:30-14:45	Amorphous cellulose nanofiber from green seaweed *Ulva lactuca* prepared with hydrophobic deep eutectic solvent and in silico characterization	Dr. Rizfi Fariz Pari IPB University, Indonesia	Invited Speaker #3
14:45-15:00	Phage therapy for a sustainable striped catfish industry in Vietnam	Assoc. Prof. Dr. Hoàng Anh Hoàng, Ho Chi Minh City University of Technology, Vietnam	Invited Speaker #4
15:00-15:15	The next generation of integrated eco-friendly anti-biofouling and anti-biocorrosion marine natural products	Asst. Prof. Dr. Novriyandi Hanif, IPB University, Indonesia	Invited Speaker #5
15:15-15:30	Phycocyanin from *Spirulina platensis*: A green-derived bioactive for skin protection and nanocosmetic innovation	Dr. Eng. Safrina Dyah Hardiningtyas, IPB University, Indonesia	Invited Speaker #6

POSTER PRESENTATION

Session I. Bioinformatics and Systems Biology, Synthetic Biology

Submission number	Abstract title	Presenter
BS-P-004	Biodegradation pathways of phthalate esters in *Gordonia polyisoprenivorans* SPK-13	Ms. Pimdao Theerasin, Mahidol University, Thailand
BS-P-005	Identification of genetic markers to aid the distinction of *Bacillus subtilis* from other closely related species	Mr. Teerapat Khatkanta, King Mongkut's University of Technology Thonburi, Thailand
BS-P-006	Probiogenomic analysis and anti-proliferative activity of probiotic and postbiotics *Lactococcus lactis* BKKT-1: an *in silico* therapeutic prediction	Mr. Papinwit Busayaboriboonchot, King Mongkut's Institute of Technology Ladkrabang, Thailand
BS-P-008	Impact of heterologous *Beta Carotene Ketolase* (*bkt*) gene expression from *Hematococcus pluvialis* in *Synechocystis* sp. PCC 6803 on carotenoid production under salt stress	Ms. Benjamat Sukkokee, Chulalongkorn University, Thailand
BS-P-009	Development of beta-class carbonic anhydrases from *Roseateles terrae* HL11 for CO_2 capture	Ms. Benjarat Bunterngsook, National Center for Genetic Engineering and Biotechnology, Thailand
BS-P-011	Discovery and functional characterization of recombinant alpha-class carbonic anhydrase derived from anaerobic uncultured microbial consortium	Mr. Nattachai Kasipan, Suankularb Wittayalai Rangsit, Thailand
BS-P-012	Structural and functional insights into a novel aldehyde deformylating oxygenase for biofuel applications	Dr. Nidar Treesukkasem, Vidyasirimedhi Institute of Science and Technology, Thailand
BS-P-014	Complete genome insights into a *Bacillus cereus* group isolates from food	Ms. Sawanya Potirungsee, Mae Fah Luang University, Thailand
BS-P-016	Microbiome biomarkers for colorectal cancer diagnosis via metagenomic analysis	Mr. Kasidet Taweepon, Mahidol University, Thailand

Session II. Medical Biotechnology & One Health

Submission number	Abstract title	Presenter
MB-P-005	Performance testing of a urine microalbumin dip test strips developed for preliminary kidney disease screening	Ms. Umaporn Pimpitak, Chulalongkorn University, Thailand
MB-P-006	Mechanisms of SSG1-mediated lifespan extension that appear to be involved in transport of *S*-adenosylmethionine in budding yeast	Ms. Sayaka Kawasaki, Hiroshima University, Japan
MB-P-007	Analysis of the oxidative stress resistance induced by *S*-adenosyl-L-homocysteine in *Saccharomyces cerevisiae* and *Caenorhabditis elegans*	Ms. Miyuko Kanaji, Hiroshima University, Japan
MB-P-008	*Terminalia catappa* leaf extract-incorporated sodium alginate/carboxymethyl chitosan hydrogel with antibacterial, antioxidant, and anti-inflammatory properties for burn wound healing applications	Mr. Tudchaphong Tim Chongsubthum, Bangkok Christian College, Thailand
MB-P-009	PCL/collagen/alginate 3D scaffold incorporating phlorotannin for bone tissue regeneration: assessment of sub-chronic toxicity	Assoc. Prof. Tae-Hee Kim, Pukyong National University, Republic of Korea
MB-P-010	ITS-based identification of common poaceae species found around bangkok	Ms. Lilian Haidvogl, Mahidol University, Thailand
MB-P-011	Microfluidic bacteria-nose chip employing *Corynebacterium accolens* for breath VOC diagnostics	Mr. Po-Hui Wu, National Chung Hsing University, Taiwan
MB-P-012	Enhancing scoliosis detection using ai: integrating deep learning into the medical field	Mr. Pittayud Aursukitwattana, Denla British School, Thailand
MB-P-015	Evaluation of chondrocyte culture formats for enhancing early cartilage matrix formation	Ms. Matthuros Sonthisathapron, Kasetsart University, Thailand
MB-P-016	UV-responsive gallic acid conjugated chitosan methacryloyl hydrogel: synthesis and application for diabetic wound treatment	Ms. Dong-Joo Park Pukyong National University, Republic of Korea
MB-P-017	Optimizing a split lentiviral delivery system for CRISPR/Cas9-based gene knockout in mesenchymal stem cells	Ms. Lanlalit Pongsasakulchot, Naresuan University, Thailand
MB-P-018	Exploring fish gelatin bioactive hydrogel for enhanced diabetic wound healing	Ms. Nayab Pukyong National University, Republic of Korea

Submission number	Abstract title	Presenter
MB-P-023	Screening, purification and whole-genome analysis of bacteriocin produced by *Lactococcus lactis* www1-2 with potentials against *Aeromonas hydrophila*	Mr. Woratep Jumi, King Mongkut's Institute of Technology Ladkrabang, Thailand
MB-P-025	OCT-4 activating compound 1 enhances developmental competence and pluripotency of porcine SCNT embryos	Ms. Thida Praeksamut, Suranaree University of Technology, Thailand
MB-P-026	Assessment of the antioxidant and anti-inflammatory properties of human placental extract in human mesenchymal stem cells	Ms. Kanda Rungboon, Suranaree University of Technology, Thailand
MB-P-027	Novel insights into the role of vesicle- and monolayer-derived extracellular vesicles from bovine oviduct epithelial cells in enhancing embryo quality *in vitro*	Mr. Apisit Polrachom, Suranaree University of Technology, Thailand
MB-P-028	Development of digital droplet PCR (ddPCR) assay for rapid detection of G6PD viangchan mutation in Thai population	Mr. Akawich Wangsiriwech, Concordian International School, Thailand
MB-P-029	Establishment of the glycoprotein CD147 knockout in a human leukemia cell line (K562) using lentivirus-based CRISPR/Cas9 system	Ms. Wannakan Jaikamlue, Chiang Mai University, Thailand

Session III: Industrial & Environmental Biotechnology & Alternative Energy

Submission number	Abstract title	Presenter
IE-P-002	Fluorometric detection of iron (III) ions and hemoglobin using o-toluidine based carbon dots	Prof. Hyun Kyoung Yang, Pukyong National University, Republic of Korea
IE-P-003	CRISPR/Cas9-driven gene ko of β-glucan synthase gene *fkss* in selective lignin-degrading fungus, *Gelatoporia subvermispora*	Dr. Junko Sugano, Kyoto University, Japan
IE-P-004	Synergistic n-caproic acid production via co-culture of *Enterococcus faecalis* isolate VT-H1 and *Clostridium kluyveri*	Ms. Suttavadee Junyakul, Vidyasirimedhi Institute of Science and Technology, Thailand
IE-P-006	Evaluating *Chlorella* sp. Growth in solar panel shaded greenhouses	Mr. Nien-Hua Chen-Tai, National Chung Hsing University, Taiwan
IE-P-009	Evaluation of moss growth and its effectivenss in carbon dioxide uptake	Mr. Jyun-Yan Kuo, National Chung Hsing University, Taiwan
IE-P-012	Unlocking the potential of anaerobic digestion for tropical communities: the SUZDEE system's approach to biogas and biofertilizer production	Asst. Prof. Dr. Thanyaporn Wongnate, Vidyasirimedhi Institute of Science and Technology, Thailand
IE-P-013	Enhanced biohydrogen production form food waste using immobilized *Enterococcus faecalis* isolate VT-H1	Ms. Sasithorn Rungjaroenchaiwat, Vidyasirimedhi Institute of Science and Technology, Thailand
IE-P-014	Integrated approaches for LDPE biodegradation in soil using microbial and physicochemical strategies	Dr. Chanokporn Muangchinda, Chulalongkorn University, Thailand
IE-P-017	Isolation and characterization of *Enterococcus faecalis* VT-H2 for enhanced biohydrogen enhanced biohydrogen production from palm oil mill effluent	Ms. Cheerapat Supawatkon, Vidyasirimedhi Institute of Science and Technology, Thailand
IE-P-020	Biodegradation of co-occurring polyethylene microplastics and di(2-ethylhexyl) phthalate by *Ancylobacter* sp. PD-4	Dr. Sakaoduoen Bunsangiam, Chulalongkorn University, Thailand
IE-P-024	Enhancement of phosphite-dependent biocontainment strategy through engineering of the substrate specificity of a phosphorus transporter	Ms. Akari Miwa, Hiroshima University, Japan
IE-P-025	A sustainable conversion platform for bio-based α-hydroxyacetic acid: from recycled ethylene glycol to green cleaning and etching applications	Mr. Subhankar Dhar, Ming Chi University of Technology, Taiwan

Submission number	Abstract title	Presenter
IE-P-026	Efficient azeotropic condensation strategy for sustainable production of poly(glycolic acid) from glycolic acid	Mr. Maroof Ali, Ming Chi University of Technology, Taiwan
IE-P-027	Consolidated bioprocessing for the production of valuable chemicals from seaweed processing residues – Development of mannan-utilizing *Halomonas elongata*	Ms. Sae Tanaka, Mie University, Japan
IE-P-030	Tropical intertidal microbiome response to the *'2024 Marine Honour Oil Spill'*	Dr. Christaline George, National University of Singapore, Singapore
IE-P-031	Sugarcane leaf derived-biochar acid catalyst for efficient isosorbide production from sorbitol	Ms. Chonthicha Nilapornkul, Mahidol University, Thailand
IE-P-032	Distribution and diversity of chemolithoautotrophic phosphite-oxidizing bacteria in coastal and marine environments	Mr. Takafumi Yamanaka, Hiroshima University, Japan
IE-P-035	Value-added production of biosurfactant by an alkaliphilic consortium using mixed agro-industrial residues	Mr. Anawin Junsawang, Naresuan University, Thailand
IE-P-036	Upcycling of soy sauce industry byproduct into ectoine by the moderately halophilic bacterium, *Halomonas elongata*	Ms. Hanna Mitsunaga, Nagasaki University, Japan
IE-P-039	Effects of redox mediators on the removal of phenolics and color from palm oil mill effluent by ligninolytic peroxidase producing white-rot fungi	Ms. Wanitchaya Bunkoed, Prince of Songkla University, Thailand
IE-P-040	Isolation and screening of bacteria for biosurfactant production and oily sludge degradation in petroleum wastewater	Mr. Natcha Ruamyat, Naresuan University, Thailand
IE-P-041	Genetic improvement and chitinolytic enzyme production of *Stenotrophomonas maltophilia* Mc_E05 isolated from termite exoskeleton	Mr. Chinnaphat Meeto, Kasetsart University, Thailand
IE-P-042	Circular production of bacterial cellulose through valorization of palm oil mill effluent by *Komagataeibacter* sp. CV06	Ms. Naruemon Bunkaew, Prince of Songkla University, Thailand

Submission number	Abstract title	Presenter
IE-P-044	Reducing sugar extraction from over-roasted coffee beans and coffee silverskins	Asst. Prof. Dr. Sukon Tantipaibulvut, King Mongkut's Institute of Technology Ladkrabang, Thailand
IE-P-046	Characterization of UV-mutated *Kluyveromyces marxianus*: isobutanol tolerance and xylose utilization	Ms. Krittaporn Thungmuthaswade, Chulalongkorn University, Thailand
IE-P-048	Factors influencing on development of trehalose production by *Saccharomyces cerevisiae*	Ms. Warissara Chotiwanee, Chulalongkorn University, Thailand
IE-P-050	Liquid nitrogen-assisted lyophilization of *Saccharomyces cerevisiae* and spores of *Penicillium* sp.	Ms. Nanthorn Paorach, Chulalongkorn University, Thailand
IE-P-052	Nitrate reducing bacteria from oil sludge and their potential roles on metal corrosion inhibition	Mr. Luxnapol Marturunkakul, Chulalongkorn University, Thailand
IE-P-053	Effect of potentially pathogenic and plastic-degrading bacterial co-culture on polylactic acid microplastics	Ms. Nutthamon Boonlum, Chulalongkorn University, Thailand

Session IV. Biodiversity, Natural Products and Applications

Submission number	Abstract title	Presenter
BN-P-003	Culturable endophytic fungi from *Rhodomyrtus tomentosa* leaves in southern Thailand: diversity, distribution, and antimicrobial potential	Asst. Prof. Dr. Lakkhana Kanhayuwa Wingfield, Prince of Songkla University, Thailand
BN-P-004	Compartmental modelling for optimal fermentation of *Perilla frutescens* (L.) Britt.	Prof. Dr. Bor-Yann Chen, National I-Lan University, Taiwan
BN-P-008	Analysis of the concentration-dependent effects of the antibiotic rifampicin on actinomycetes	Ms. Miran Hasegawa, Shinshu University, Japan
BN-P-010	Assessment of heavy metal and fungicide tolerance in the plant growth-promoting strain *Daldinia eschscholtzii* mflucc20-0215 and three fungal strains isolated from *Litsea cubeba* (Lours.) Pers.	Assoc. Prof. Dr. Siraprapa Mahanil, Mae Fah Luang University, Thailand
BN-P-011	Biotransformations of white tea by *Lactococcus lactis* PKC-1: enhanced antimicrobial and antioxidant activities	Mr. Pasit Phatcharachaitas, King Mongkut's Institute of Technology Ladkrabang, Thailand
BN-P-012	*Cratoxylum formosum* extract attenuates inflammation in LPS-activated macrophages by reducing IL-6 expression	Dr. Tuangtong Vongpipatana, Kasetsart University, Thailand
BN-P-014	Functional charcterization of PlyCYU endolysin against *Streptococcus agalactiae*	Ms. Sakunrat Ubonprasert, National Science and Technology Development Agency, Thailand
BN-P-015	Metabolomics-based comparative study and evaluation of biological activities in two brown algae	Mr. Jun Hyung Lee Pukyong National University, Republic of Korea
BN-P-016	Chitinase production by *Aeromonas caviae* EW02 newly isolated from giant mud crab pond and potential to degrade chironomid egg masses (*Chironomus plumosus*)	Mr. Chirath Pitakkhuamdee, Kasetsart University, Thailand
BN-P-020	Biosynthesis and statistical optimization of polyhydroxyalkanoate (PHA) production by a newly isolated marine bacterium NF3-3	Ms. Piyawan Kunriya, Kasetsart University, Thailand
BN-P-021	Coffee silverskin as a biorefinery feedstock: integrated production of phenolics, bioactive peptides, and prebiotic xylooligosaccharides	Assoc. Prof. Dr. Thanongsak Chaiyaso, Chiang Mai University, Thailand
BN-P-022	Endolysin plyCYU: characterization and antimicrobial potential against *Streptococcus agalactiae* causing bovine mastitis	Ms. Wachiraporn Wachiradusit, National Science and Technology Development Agency, Thailand

Submission number	Abstract title	Presenter
BN-P-023	*Phyllosticta capitalensis*, an endophytic fungus isolated from *Ocimum sanctum* with antibacterial activity	Mrs. Pattaranan Ounjai, Silpakorn University, Thailand
BN-P-024	Cultivation of actinomycetes and their antimicrobial production on solid media using sterilized humus	Assoc. Prof. Dr. Takeshi Hosaka, Shinshu University, Japan
BN-P-025	Improvement of retinal production in *Escherichia coli*	Ms. Sae Amemiya, University of Shizuoka, Japan
BN-P-026	Screening of potent flavor compounds produced by non-*Saccharomyces* yeast	Mr. Naphattarachon Thamapanyaphong, Chulalongkorn University, Thailand
BN-P-027	Antimicrobial activity against *Cutibacterium acnes* of corn agro-residues extract as waste utilization for cosmetic application	Ms. Prinyaporn Pradmeeteekul, Mae Fah Luang University, Thailand
BN-P-028	Utilizing of *Spirulina* wastewater as a biofertilizer: effects on green cos lettuce growth and the soil microbiome	Ms. Julalak Mungmart, King Mongkut's Institute of Technology Ladkrabang, Thailand
BN-P-029	Study of diversity and metalaxyl resistance in *Phytophthora* spp. Causing black rot disease in orchids	Ms. Muthita Singsakulrat, Kasetsart University, Kamphaeng Saen Campus, Thailand
BN-P-030	Optimization of pectin yield from *Cyclea barbata* Miers leaves using response surface methodology	Mr. Witayapan Nantitanon, Mae Fah Luang University, Thailand
BN-P-031	Isolation and characterization of indole-3-acetic acid (IAA)-producing rhizobacteria from white butterfly pea (*Clitoria ternatea* L.)	Ms. Rattiya Padungpol, Kasetsart University, Kamphaeng Saen Campus, Thailand

Session V. Agriculture Biotechnology

Submission number	Abstract title	Presenter
AB-P-003	SSR-based marker-trait associations for the selection of drought-tolerant maize S1 genotypes	Mr. Theerawut Wongwarat, Khon Kaen Field Crops Research Center, Thailand
AB-P-004	Reemergence and characterization of snakehead rhabdovirus in Thai aquaculture	Dr. Kitipong Angsujinda, Chulalongkorn University, Thailand
AB-P-007	A novel *Azospirillum vistecanum* strain isolated from methane digestate enhances plant growth through high-efficiency indole-3-acetic acid (IAA) biosynthesis	Ms. Surat Moomthong, Vidyasirimedhi Institute of Science and Technology, Thailand
AB-P-011	Novel antiseptic consisting of an iodine-polysorbate 80 complex with long-term retention and a broad antimicrobial spectrum	Mr. Shingo Shimada, Yamagata University, Japan
AB-P-012	Encapsulated freeze-dried lactic acid bacteria modulate gut microbiota, health, and growth of *Penaeus monodon*	Asst. Prof. Narongchai Chupoon, Rajamangala University of Technology Srivijaya, Thailand
AB-P-013	Effect of salinity on poly-γ-glutamic acid production in *bacillus subtilis* FSO3	Ms. Thanaporn Wichai, Chulalongkorn University, Thailand
AB-P-014	Expression of chitinase encoding gene from *Serratia marcescens* Mc_G07 and termiticidal activity against the wood-feeding termite *Microcerotermes* sp.	Mr. Kittipong Chanworawit, Kasetsart University, Thailand
AB-P-015	Proof of concept for external protein immobilization on lactic acid bacteria: a non-GMO approach	Dr. Pinpunya Riangrungroj, National Science and Technology Development Agency, Thailand
AB-P-017	Comparative analysis of glutathione S-transferase gene family in extremophilic cyanobacteria	Mr. Thanawat Leknawin, Chulalongkorn University, Thailand
AB-P-018	Genome-based discovery of novel cyanobacterial natural products derived from *Gloeocapsa* sp. strain BRSZ	Mr. Hari Winanda, Chulalongkorn University, Thailand
AB-P-019	Exploring cyanobacterial diversity from a neutral-alkaline hot spring in Thailand and their photoprotective compound productions	Ms. Chatchadarat Anantasophon, Chulalongkorn University, Thailand
AB-P-020	Phenotypic variation and plasticity of root hair traits in Australian durum wheat (*Triticum turgidum* subsp. Durum) under phosphorus deficiency	Ms. Sukrita Majak, Mahidol University, Thailand

Submission number	Abstract title	Presenter
AB-P-026	Unveiling the quantitative landscape of gingerol and its derivatives in Thai ginger (*Zingiber officinale* Roscoe)	Asst. Prof. Dr. Kronsirinut Rothjanawan, Princess of Naradhiwas University, Thailand
AB-P-027	Identification of potential genes invovled in swarming activities-related virulence of *Vibrio parahaemolyticus* AHPND	Assoc. Prof. Dr. Ponsit Sathapondecha, Prince of Songkla University, Thailand
AB-P-029	Evaluation of antifungal activity of *Streptomyces* sp. against *Agroathelia rolfsii*	Ms. Rungnapa Pichaikarn, Prince of Songkla University, Thailand
AB-P-030	Characterization of multi-stress tolerant PGPR from orchard soils in Chanthaburi province, Thailand	Ms. Jirapat Chanthamalee, Rambhai Barni Rajabhat University, Thailand
AB-P-033	Effect of skim milk supplementation on the production of air-dried lactic acid bacterial starter culture immobilized on corn husk and its antagonistic activity against *Aspergillus flavus*	Mr. Possawee Boonyong, Chulalongkorn University, Thailand
AB-P-034	Bioelectricity from palm oil mill effluent: the role of the pentose phosphate pathway in *Choricystis parasitica* SW-03	Asst. Prof. Dr. Pimprapa Chaijak, Thaksin University, Thailand
AB-P-035	Isolation and characterization of fungi from organic rice cultivation soil for enhancing rice seed germination	Mr. Anuruk Seeka, Chulalongkorn University, Thailand
AB-P-036	Identification and functional characterization of small heat shock proteins in shrimp immune responses to *Ecytonucleospora hepatopenaei* (EHP) infection	Mr. Pithiwat Maiket, Chulalongkorn University, Thailand
AB-P-037	Probiotic potential of gut-derived lactic acid bacteria from *Heterotrigona itama*: towards functional starter cultures for pollen fermentation	Asst. Prof. Dr. Wankuson Chanasit, Thaksin University, Thailand
AB-P-038	Identification of signaling pathways controlling antimicrobial peptide gene expression in black tiger shrimp *Penaeus monodon*	Ms. Chayanit Khunrit, Chulalongkorn University, Thailand
AB-P-040	The efficacy of in straw dilution method on survival rates of vitrified bovine embryos	Ms. Chanyada Angchuan, Suranaree University of Technology, Thailand

Session VI. Food Biotechnology & Food Security & Future Food

Submission number	Abstract title	Presenter
FB-P-003	Impact of controlled postharvest conditions on enhancement of aroma-active profiles and sensory preference in Thai cocoa nibs	Dr. Pakavit Mathatheeranan, National Taiwan University of Science and Technology, Thailand
FB-P-004	Comparative effects of petroleum-based and biodegradable microplastics on the growth and stress responses of *Capsicum annuum* L.	Ms. Pariyapath Eiamtrakul, Mahidol University, Thailand
FB-P-005	Structural insights into the EXO-mode of action of *Bc*Xyn26a, a novel EXO-β-1,3-xylanase from a human gut bacterium	Ms. Kotone Yamamoto, Mie University, Japan
FB-P-006	Human gut bacteria possess a polysaccharide utilization locus that includes a novel EXO-β-1,3-xylanase for metabolizing β-1,3-xylan, a macroalgal polysaccharide	Prof. Dr. Fumiyoshi Okazaki, Mie University, Japan
FB-P-009	Isolation and characterization of *Chlorella* sp. AARLG049N mutants with high protein and low chlorophyll content	Ms. Kitkarn Veeraphisitt, King Mongkut's University of Technology Thonburi, Thailand
FB-P-010	Isolation, morphological identification and growth of thraustochytrid isolated from mangrove habitats in the gulf of Thailand	Ms. Sasiwimol Duangvichai, King Mongkut's Institute of Technology Ladkrabang, Thailand
FB-P-013	Ultrasound-assisted extraction, evaluation of interfacial properties and *in vitro* digestibility of tamarind seed protein	Ms. Pitchayapak Wipakul, Mahidol University, Thailand
FB-P-015	Assessment of antimicrobial constituents in FEST^{TM} food service paper packaging using spores of *Bacillus subtilis* ATCC 6633 and *Aspergillus niger* ATCC 6275	Ms. Charanyarut Sukphattanaudomchoke, Innovation and Product Development Center, Thailand
FB-P-018	Stabilization of fresh coffee pulp and effect on bioactive compounds	Dr. Sirirung Wongsakul, Mae Fah Luang University, Thailand
FB-P-019	Influence of ethanol desolvation ratio on lutein encapsulation in whey protein isolate particles	Ms. Panadda Nonthanum, Khon Kaen University, Thailand

Plenary Lecture

FUNCTIONAL AMINO ACIDS ENGINEERING IN YEAST: FROM METABOLIC REGULATIONS TO BIOTECHNOLOGICAL APPLICATIONS

Hiroshi Takagi
Nara Institute of Science and Technology, Nara, Japan

Abstract:
Amino acids are important not only as protein components of living organisms, but also as nutrients and energy sources. In recent years, many amino acids exist in free form and play important roles in cells, and thus, their physiological functions have been attracting attention. Various foods, beverages, nutritional supplements, and cosmetics, containing these amino acids have been commercialized worldwide. In yeast, amino acid metabolism vary under different growth environments and metabolic modes by regulating anabolic and catabolic processes, including uptake and export. Controlling the amino acid content is expected to contribute to improved productivity and value-added fermented foods and alcoholic beverages. The development of industrial yeast strains that overproduce "functional amino acids" could lead to improvement of fermentation ability, diversity of product taste and flavour, addition of healthy images, or increase of nutritional value. To emphasize these advantages, I named this breeding technology 'functional amino acids engineering' (*Biosci. Biotech. Biochem.*, **83**, 1449, 2019; *SIMB News*, 7**1**, 8, 2021). The yeast Saccharomyces cerevisiae, which is widely used in the fermentation industry, has been certified as 'Generally Recognized as Safe (GRAS)' by the US Food and Drug Administration (FDA), demonstrating its high safety, but unlike bacteria, there are few examples of industrialized production of amino acids by fermentation. In this lecture, I will introduce several topics of "functional amino acids engineering" with successful commercialization of alcoholic beverages, focused on the metabolic regulatory mechanisms and physiological functions of amino acids, such as proline, ornithine, leucine, isoleucine, valine, phenylalanine, and lysine, in *S. cerevisiae*.

MICROBIAL RESPONSE TO THE 2024 MARINE HONOUR OIL SPILL IN SINGAPORE

Stephen Pointing[1,2,*]
[1] Department of Biological Sciences, National University of Singapore, Singapore
[2] Tropical Marine Science Institute, National University of Singapore, Singapore
*e-mail: stephen.pointing@nus.edu.sg

Abstract:
The 2024 *Marine Honour* heavy fuel oil spill along Singapore's southern coast provided a rare opportunity to observe in real time how tropical marine microbiomes respond to acute petroleum contamination. This study integrates field surveys, controlled microcosm experiments, and genomic analyses to elucidate microbial mechanisms underpinning oil degradation and ecosystem recovery, with implications for bioremediation. Real-time metagenomic profiling revealed rapid selection for hydrocarbon-degrading taxa distinct from those in temperate or deep-sea spills. Genes for alkane and aromatic degradation, detoxification, and biosurfactant production proliferated post-spill and persisted for six months and after hydrocarbons became undetectable, indicating long-term functional priming. Field data suggest that redistribution of oil to offshore sinks contributed substantially to beach clearance. Laboratory microcosms showed first-order biodegradation kinetics under both aerobic and anaerobic conditions, though aerobic degradation proceeded four-fold faster, suggesting enhanced microbial activity during low tide exposure. Biodegradation rates exceeded abiotic loss by an order of magnitude. Ongoing metagenomic and transcriptomic analyses are resolving complete hydrocarbon catabolic pathways, including thermotolerant and halotolerant enzymes. By integrating these with metabolic network modelling, we aim to identify enzymatic bottlenecks and ecological interactions that can be optimized for accelerated bioremediation. Collectively, this work advances understanding of tropical marine microbial resilience and informs ecosystem-based responses to future oil spills.

APPLICATION OF A NOVEL SCREENING METHOD FOR DEGRADING BACTERIA REVEALS UNKNOWN MICROBIAL FUNCTIONS AND INTERACTIONS

Hideaki Nojiri[1]*
[1]Agro-Biotechnology Research Center, Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan
*e-mail: anojiri@g.ecc.u-tokyo.ac.jp

Abstract:
The enrichment culture is gold standard to isolate pollutant degraders. However, it has become clear that similar (e.g. taxonomically related or same genus) strains have been isolated as degraders for some pollutants and that it is difficult to obtain the "diverse" degraders. Obtaining a diverse degrader is important because there is no guarantee that isolated degraders will be able to clean up polluted environment, and having a variety of degradation tools is important for effective bioremediation.

We employed single cell sorting by flow cytometer (FCM) to make single cell culture or artificial two-cell consortia to isolate pyrene degraders. "Pyrene crystal plate culture system" is developed as a culture and monitoring method of pyrene degradation. This can be used to measure pyrene depletion in the liquid culture of 96-well plates in a non-destructive manner, by measuring the fluorescence of pyrene crystals deposited on the bottom of the well with a fluorescence microscope. Single or two bacterial cells was inoculated to each well using FCM. In total, the pyrene-degrading capability of 1,152 cultures, each one contained within a well of a 96-well pyrene crystal plate, was quantified. 17 strains were isolated as putative pyrene degraders, four of which were stably maintained as two-strain consortia during the screening procedure. The sensitivity of the system allows for its application without enrichment cultures, favoring the preservation of the environmental diversity of potentially novel pyrene-degrading strains.

We also employed the same system to screen environmental bacteria that affect the pyrene degradation ability of *Mycolicibacterium parafortuitum* PO1. In detail, we evaluated the pyrene degradation ability of an artificial microbial community created by inoculating one cell of PO1 and one cell of an environmental bacterium in pyrene crystal plate culture and screened for bacteria that altered the degradation ability of PO1. As the results, 30 bacterial strains were obtained from 756 independent cultures, including 25 strains of *Dermacoccus nishinomiyaensis*, by which, interestingly, both enhanced and inhibited pyrene degradation were observed. Microscopic observation of their growth on pyrene crystals revealed that, when the initial inoculation volume was high, *Dermacoccus* strains formed a flat biofilm well mixed with PO1, resulting in lower PO1 abundance and inhibited degradation compared to PO1 alone. On the other hand, when the initial inoculum size was small, the aggregates of only *Dermacoccus* strains were formed, attracting PO1 around them to form larger biofilms on the pyrene crystals. Compared to PO1 alone, inhibiting strain formed smaller nuclei and attracted fewer PO1 around them, while enhancing strain formed larger cell aggregates and attracted more PO1 around them to form biofilms. The results suggest that subtle differences in cell density-dependent aggregate formation ability could be determining factors for the positive or negative effect on the degradation ability of PO1.

MECHANISM AND REGULATION OF BIOFILM FORMATION IN *Vibrio cholerae*

Prof. Dr. Fitnat Yildiz
Microbiology & Environmental Toxicology Department, Institute of Marine Sciences, University of California, Santa Cruz, USA
*e-mail: fyildiz@ucsc.edu

Abstract:
Biofilms are surface-attached microbial communities composed of microorganisms and a matrix of extrapolymeric substances, such as exopolysaccharides, proteins, and nucleic acids. The ability to form biofilms enhances the environmental survival and infectivity of *Vibrio cholerae,* the bacterium that causes the disease. I will discuss the molecular mechanism of biofilm formation and its regulation in *V. cholerae*. A better understanding of matrix biosynthesis and elucidation of the regulatory mechanisms that enable biofilm formation will provide a foundation for the development of inhibitors that specifically alter biofilm matrix properties and regulatory components, thereby enabling novel treatments and prevention strategies against cholera.

DESIGN AND IMPLEMENTATION OF SYNTHETIC METABOLIC PATHWAYS OUTSIDE THE CELLS

Kohsuke HONDA*
International Center for Biotechnology, The University of Osaka, Japan
*e-mail: honda.kohsuke.icb@osaka-u.ac.jp

Abstract:
Metabolic engineering has been widely recognized as a robust technology for the design and implementation of synthetic pathways in living (micro)organisms. However, the introduction of such synthetic pathways into cells often perturbs native metabolic networks, resulting in compromised cell growth and diminished production of target compounds.

To overcome this limitation, our group has developed an alternative approach that involves constructing enzyme cascades—mimicking both natural and synthetic metabolic pathways—outside of living cells, using recombinant thermophilic enzymes.

Thanks to their remarkable thermal stability, thermophilic enzymes can be readily semi-purified through simple heat treatment of lysates from recombinant mesophilic hosts (e.g., Escherichia coli), making them practical and effective building blocks for assembling multi-step enzymatic cascades (FIG).

By employing this cell-free system, we have established a variety of synthetic cascades and successfully demonstrated the one-pot synthesis of valuable chemicals. Furthermore, we have developed several complementary technologies, including cofactor regeneration systems, to improve the overall feasibility of these cascades.

In this lecture, the author will present representative examples from our research and discuss their impact, along with the challenges that remain.

Keywords: thermophile, enzyme cascade, cell-free system

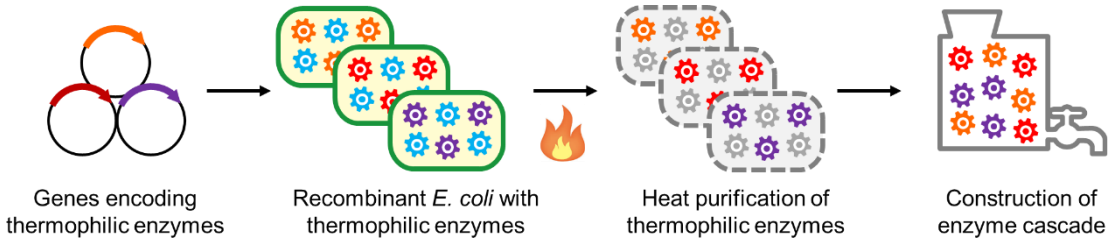

Figure 1.
Procedure of cascade construction with recombinant thermophilic enzymes

JOB OPPORTUNITIES AND RESEARCH FUNDING FOR MICROBIOLOGISTS/BIOTECHNOLOGISTS AT THAI WAH PLC

Prakaipetch Kitiyanan
Thai Wah Public Co.Ltd, Thailand
e-mail: prakaipetch.k@thaiwah.com

Abstract:
Thai Wah PLC, a leading Asian food and agribusiness conglomerate, offers exciting career and research opportunities for microbiologists and biotechnologists. Through its integrated biotechnology initiatives, the company is driving sustainable innovation across multiple sectors. Cassava Plantation Biotechnology**:** Professionals can develop microbial soil enhancers, plant growth-promoting rhizobacteria, and biocontrol agents to support sustainable cassava cultivation. Research focuses on improving yields and creating disease-resistant varieties. Waste Management Solution: Microbiologists contribute to advanced biological treatment systems and waste management solution as value added to support environmental improvement and regulatory compliance. Animal Feed Innovation: Biotechnologists work on probiotic supplements, enzyme production, and fermentation processes to enhance feed digestibility and nutritional value. Research includes gut microbiome optimization and novel feed additives. Bioplastic Development & Compostability: Opportunities include microbial polymer synthesis, fermentation optimization, and biodegradable packaging from cassava-based feedstocks. Research targets accelerated decomposition, microbial consortium development, and compostability certification.

Thai Wah's strategic commitment to sustainable biotechnological solutions provides dynamic cross-sector collaboration opportunities, and the unique chance to drive innovation while making meaningful contributions to global sustainability challenges.

Oral Presentation

Session I.
Bioinformatics and Systems Biology, Synthetic Biology

*In silico D*ESIGN AND EXPERIMENTAL ANALYSIS OF METABOLIC PATHWAYS FOR MICROBIAL BIOPRODUCTION

Hiroshi Shimizu
Department of Bioinformatic Engineering, Graduate School of Information Science and Technology, The University of Osaka, 1-5 Yamadaoka, Suita, Osaka 565-0817, Japan
TEL: +81-6-6879-7446

Abstract:
For bioproduction, microorganisms have been industrially utilized. Because the thousands of metabolic reactions simultaneously occur and many metabolic reactions are related to the target production and cell growth, development of the rational design method of metabolic pathway modification to optimize production of the target products are needed. In order to efficiently produce targets, carbon flow from a raw material to target compounds and well-coupling with cofactors balancing of ATP and NADPH should be considered.

In my presentation, recent advances in metabolic flux analyses are introduced, especially in terms of computational pathway modification design by flux balance analysis (FBA) and experimental evaluation of metabolic fluxes by ^{13}C-metabolic flux analysis (^{13}C-MFA). Computational tools of searching for effective gene deletion targets and recruitment of heterologous genes are introduced in FBA. AI and data science-based approaches for process monitoring and control are discussed to maximize the performance of the engineered cells in the bioproduction processes. Finally, recent results of opt-metabolic engineering for metabolic flux monitoring and control are also introduced.

Keywords: Metabolic Engineering, bioproduction, FBA, ALE, AI

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ADVANCING INDUSTRIAL BIOTECHNOLOGY THROUGH ADAPTIVE LABORATORY EVOLUTION

Tuck Seng Wong
School of Chemical, Materials and Biological Engineering, University of Sheffield, Sir Robert Hadfield Building, Mappin Street, Sheffield S1 3JD, United Kingdom.
e-mail: t.wong@sheffield.ac.uk

Abstract:
Microbes lie at the heart of modern biomanufacturing. As living cell factories, they transform raw materials into valuable bioproducts, and their catalytic efficiency, production yield, stability, and robustness are critical determinants of bioprocess viability and economic feasibility. However, most microbes are not naturally equipped for industrial-scale production. Their performance often requires significant optimisation to meet the demands of fit-for-purpose applications.

Given the inherent biological complexity of many microbial systems, even extensively studied chassis such as Escherichia coli, a purely rational engineering approach can be extremely challenging. It demands substantial resources and time, and often yields limited success. Adaptive Laboratory Evolution (ALE), when designed and executed intelligently, offers a powerful and often faster alternative for enhancing microbial traits. Crucially, when ALE is integrated with whole genome sequencing and omics technologies, it not only improves performance but also provides deep insights into the underlying biology, revealing how genetic networks are wired and how genotype translates into phenotype.

In this presentation, I will illustrate the power and versatility of ALE through three case studies: Cupriavidus necator, a natural producer of bioplastics [1]; Rhodotorula toruloides, an oleaginous yeast with great potential for lipid-based bioproducts [2]; and Escherichia coli, a widely used workhorse in both biomanufacturing and synthetic biology. Each case explores distinct microbial properties and demonstrates how ALE can be leveraged to optimise different traits, reflecting its broad applicability.

I will also share recent innovations developed by our laboratory in Sheffield that advance the field of ALE. These include an accelerated ALE platform using divalent metal ions [3], and the Protein-Infinity tool, which enables enhanced protein production and has been commercialised through Evolutor Ltd [4], a University of Sheffield spinout. Together, these tools exemplify how we are moving towards faster, more insightful, and more industrially relevant microbial optimisation.

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HARNESSING SYNTHETIC MICROBIAL CONSORTIA FOR ADVANCED BIOPROCESSING APPLICATIONS

Shen-Long Tsai*
Department of Chemical Engineering, National Taiwan University of Science and Technology, Taipei 10607, Taiwan
*e-mail: stsai@mail.ntust.edu.tw

Abstract:
Synthetic biology has advanced beyond single-strain engineering to the design of synthetic microbial consortia, in which engineered organisms cooperate through metabolic division of labor. Such systems provide enhanced robustness, modularity, and efficiency, enabling the sustainable conversion of renewable biomass and plastic waste into valuable fuels and chemicals. Here, we showcase several representative strategies from our laboratory that demonstrate the transformative potential of consortium-based engineering. We first established a synthetic yeast consortium for cellulose hydrolysis and ethanol production, where four engineered *Saccharomyces cerevisiae* strains each supplied distinct minicellulosome components: a surface-displayed scaffoldin and three dockerin-tagged cellulases. Optimizing the population ratio nearly doubled ethanol production compared to uniform cultures, achieving yields close to the theoretical maximum. To broaden substrate utilization, we constructed a hemicellulose-degrading yeast consortium. Complementary hemicellulases from *Trichoderma reesei* were secreted or displayed by engineered *S. cerevisiae* strains, which were also equipped with xylose-utilization pathways. This enabled efficient xylan hydrolysis and direct ethanol production from hemicellulose-derived sugars. Building on this concept, a phage-assisted supramolecular assembly strategy was proposed, using M13 phage coat proteins to recruit multiple cellulases onto yeast surfaces. This dense, modular organization further enhanced synergistic cellulose hydrolysis and fermentation efficiency. Beyond ethanol, a syntrophic cyanobacteria–bacteria consortium was developed to produce the platform chemical 2,5-furandicarboxylic acid (FDCA). *Synechococcus elongatus* fixed CO_2 into sucrose, supporting *Pseudomonas putida* in converting 5-hydroxymethylfurfural into FDCA. Coupling the two species with modular binding domains increased yields to nearly 100%, offering a carbon-neutral route to renewable plastic precursors. Finally, *Chlamydomonas reinhardtii* was engineered for the secretion and surface display of PETase, enabling environmentally friendly degradation of polyethylene terephthalate (PET). Under low-cost, photosynthetic cultivation, PET powder was converted into terephthalic acid and intermediates, showcasing algae as sustainable biocatalyst platforms. Together, these strategies demonstrate the versatility of synthetic microbial consortia in valorizing lignocellulosic biomass and plastic waste. Compared to single-strain systems, consortia distribute metabolic burdens, expand modular design, and unlock emergent ecological functions. With continued advances in microbial community engineering, synthetic consortia represent a powerful platform for scalable bioprocesses and the transition to a circular bioeconomy.

POLYHYDROXYALKANOATES PRODUCTION BY RECOMBINANT *Ralstonia eutropha* FROM CO_2 AS SOLE CARBON SOURCE

Takeharu Tsuge[1],*
[1]Department of Materials Science and Engineering, Institute of Science Tokyo, 4259 Nagatsuta, Midori-ku, Yokohama 226-8502, Japan
*e-mail: tsuge@mac.isct.ac.jp

Abstract:
Ralstonia eutropha strain H16 is a chemoautotrophic bacterium that oxidizes hydrogen and accumulates poly[(*R*)-3-hydroxybutyrate] [P(3HB)], a prominent polyhydroxyalkanoate (PHA), within its cell. *R. eutropha* utilizes fructose or CO_2 as its sole carbon source for cell growth and P(3HB) accumulation. A PHA-negative mutant of strain H16, known as *R. eutropha* strain PHB−4, cannot produce PHA. Strain 1F2, derived from strain PHB−4, is a leucine analog-resistant mutant. Remarkably, the recombinant 1F2 strain exhibits the capacity to synthesize 3HB-based PHA copolymers containing 3-hydroxyvalerate (3HV) and 3-hydroxy-4-methyvalerate (3H4MV) comonomer units from fructose or CO2. This ability is conferred by the expression of a broad substrate-specific PHA synthase and tolerance to feedback inhibition of branched amino acids. However, the total amount of comonomer units incorporated into PHA was up to around 5 mol%. In this study, strain 1F2 underwent genetic engineering to augment the comonomer supply incorporated into PHA. This enhancement involved several modifications, including the additional expression of the broad substrate-specific 3-ketothiolase gene (*bktB*), the heterologous expression of the 2-ketoacid decarboxylase gene (*kivd*), and the phenylacetaldehyde dehydrogenase gene *(padA*). Furthermore, the genome of strain 1F2 was altered through the deletion of the 3-hydroxyacyl-CoA dehydrogenase gene (*hbdH*). The introduction of *bktB-kivd-padA* resulted in increased 3HV incorporation, reaching 13.9 mol% from fructose and 6.4 mol% from CO_2. Additionally, the hbdH deletion resulted in the production of PHA copolymers containing (S)-3-hydroxy-2-methylpropionate (3H2MP).

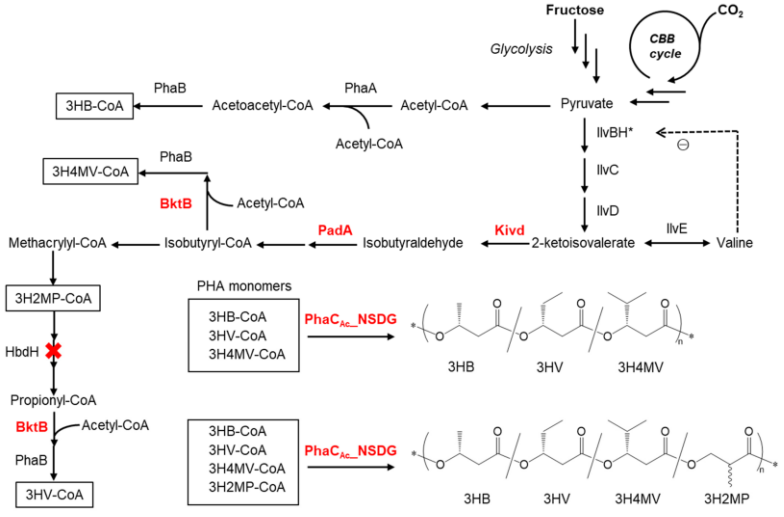


Figure 1.
Metabolic pathway for PHA copolymer biosynthesis from CO_2.

IMPACT OF *HOG1* DELETION ON GLUCOSE FERMENTATION AND REDOX STRESS RESPONSE IN *Saccharomyces cerevisiae*

Nunthaphan Vikromvarasiri,[1] Ryosuke Mitsui[1], Takashi Hirasawa[2], Akihiko Kondo[1,3], Tomokazu Shirai[1,*]
[1]RIKEN Center for Sustainable Resource Science, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[2]School of Life Science and Technology, Institute of Science Tokyo, 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan
[3]Department of Chemical Science and Engineering, Graduate School of Engineering, Kobe University, 1-1 Rokkodai, Nada, Kobe, 657-8501, Japan
*e-mail: tomokazu.shirai@riken.jp

Abstract:
The mitogen-activated protein kinase *HOG1* functions as a core regulator of the high-osmolarity glycerol pathway in *Saccharomyces cerevisiae*, enabling adaptation to osmotic stress. While its role in stress signaling has been extensively studied, its contribution to glucose fermentation has remained unclear. In this study, we examined the impact of *HOG1* deletion during glucose fermentation. The Δ*hog1* mutant exhibited faster glucose utilization and achieved a 14.3% increase in ethanol production relative to the wild type, along with reduced production of glycerol, acetate, and 2,3-butanediol. However, the absence of *HOG1* impaired tolerance to osmotic stress when cultures were initiated with high glucose concentrations, a drawback that was successfully mitigated through intermittent feeding. To further investigate metabolic adjustments, central metabolic genes such as *PDC1* and *ADH1* were deleted, leading to NADH accumulation and redox imbalance, accompanied by altered expression of genes associated with ethanol, glycerol, and acetate production. These findings identify *HOG1* as a critical determinant of both stress adaptation and fermentation efficiency, offering insights for industrial yeast engineering.

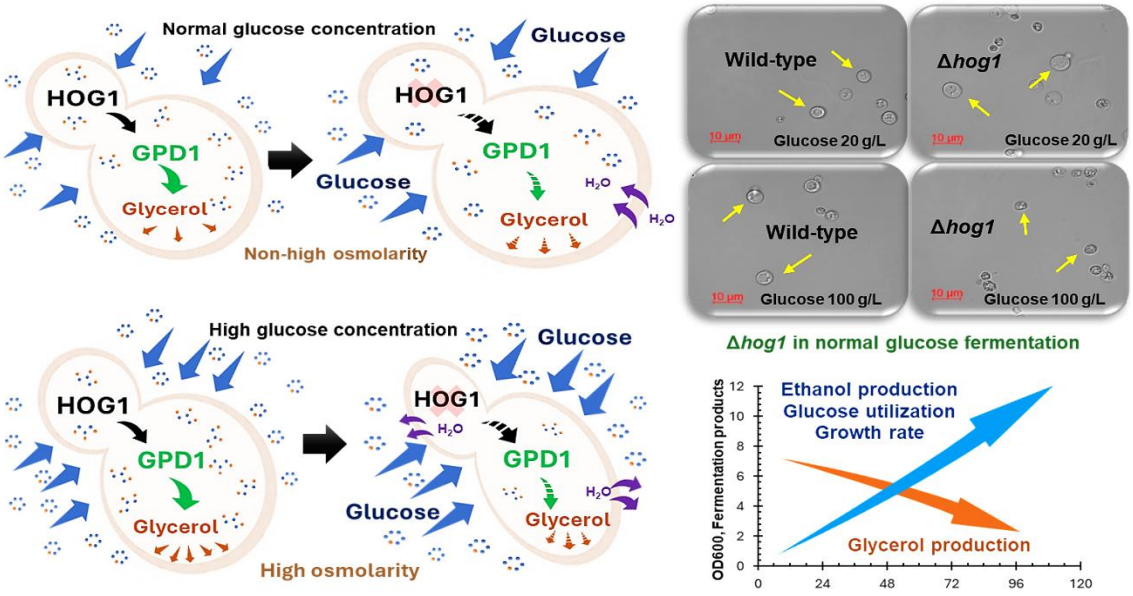


Figure 1.
Effects of *HOG1* deletion in *Saccharomyces cerevisiae* under normal and high glucose conditions.

TRANSCRIPTOMICS ANALYSIS OF *Starmerella riodocensis* GT-SL1R UNDER HIGH CARBON TO NITROGEN RATIO CONDITION FOR ENHANCED SOPHOROLIPID PRODUCTION

Sirawich Sapsirisuk[1], Nitnipa Soontorngun[1]*
[1]Excellent Research Laboratory for Yeast Innovation, Biochemical Technology Division, School of Bioresources & Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok 10150, Thailand
*Correspondence to: Excellent Research Laboratory for Yeast Innovation, Biochemical Technology Division, School of Bioresources & Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok 10150, Thailand.
*e-mail: nitnipa.soo@kmutt.ac.th

Abstract:
Sophorolipid (SL) is a one of biosurfactant produced by the yeast strain *Starmerella bombicola*, a well-known SL producing yeast. SLs have potential applications in various fields, including food preservation, cosmetics, antimicrobial agents, and bioremediation. In this study, we identified a new SL-producing yeast species, *Starmerella riodocensis* GT-SL1R, which was isolated from honey. This yeast strain demonstrates the potential to produce SLs, and its production performance was further evaluated under different cultivation conditions. Specifically, *S. riodocensis* GT-SL1R was cultivated under varying carbon-to-nitrogen (C/N) ratios to investigate its metabolic response and SL production capacity. At a high C/N ratio of 100, the yeast produced nearly 30 g/L of SL after 7 days, compared to 18 g/L at a low C/N ratio of 25, while biomass accumulation was significantly reduced. Transcriptomic profiling revealed a global metabolic shift under nitrogen-limited conditions, with approximately 500 genes upregulated and more than 500 downregulated. Genes involved in cell cycle regulation, DNA replication, ribosome biogenesis, and ergosterol synthesis were strongly repressed, suggesting growth arrest. In contrast, key SL biosynthetic genes (*CYP52M1*, *UgtA1*, *UgtB1*, *At*, and *Sble*) and the transporter *MDR* were highly induced, along with genes related to nitrogen uptake and recycling. These findings demonstrated that *S. riodocensis* reprogrammed its metabolism under nitrogen limitation, suppressing growth and redirecting resources toward SL biosynthesis. Thus, this transcriptomic data provided insights for optimizing glycolipid production at an industrial scale.

Keywords: Biosurfactant, C/N ratio, Sophorolipid production, *Starmerella riodocensis*, Transcriptomics

RECOMBINANT ARSENITE OXIDASE (*aioA* & *aioB*) FROM *Thiomonas cuprina*: COMPARATIVE INSIGHTS INTO NATIVE AND SYNTHETIC GENE CONSTRUCTS

Mahesh Mannacharaju,[1] Soichiro Tanaka[1] and Naoko Okibe[1,*]
[1]Department of Earth Resources Engineering, Faculty of Engineering, Kyushu University, Fukuoka, Japan.
*e-mail: okibe@mine.kyushu-u.ac.jp

Abstract:
Arsenic contamination is a major global concern linked to cardiovascular, neurological, and carcinogenic risks. Microbial arsenite oxidation, a key biogeochemical process, transforms the toxic arsenite [As(III)] into the less toxic arsenate [As(V)]. *Thiomonas* species are important arsenite oxidizers frequently detected in arseniccontaminated environments. In this study, we performed comparative sequence alignment and phylogenetic analysis of the *aioA* and *aioB* genes from *Thiomonas delicata* DSM 16361, followed by construction of a synthetic plasmid (pRSFDuet-1::*aioA*–*aioB*) and heterologous expression in *Escherichia coli* BL21. In parallel, the native *aioA* (~2600 bp) and *aioB* (~600 bp) genes were PCR-amplified from *Thiomonas cuprina* DSM 5495, cloned into pRSFDuet1, and expressed in *E. coli* and purified using Ni-NTA column. SDS-PAGE confirmed ~90 kDa (AioA) and ~18-35 kDa (AioB). Kinetic analysis of the synthetic system, AioA exhibited a V_{max} of 36 ± 2 µmol/min/mg and a K_m of 280 ± 25 µM, while AioB showed a V_{max} of 1.1 ± 0.1 µmol/min/mg and a K_m of 102 ± 30 µM. In the native *T. cuprina* derived expression system, AioA exhibited a V_{max} of 41 ± 5 µmol/min/mg and a K_m of 330 ± 85 µM, while AioB exhibited a V_{max} of 1.1 ± 0.1 µmol/min/mg and a K_m of 102 ± 30 µM.

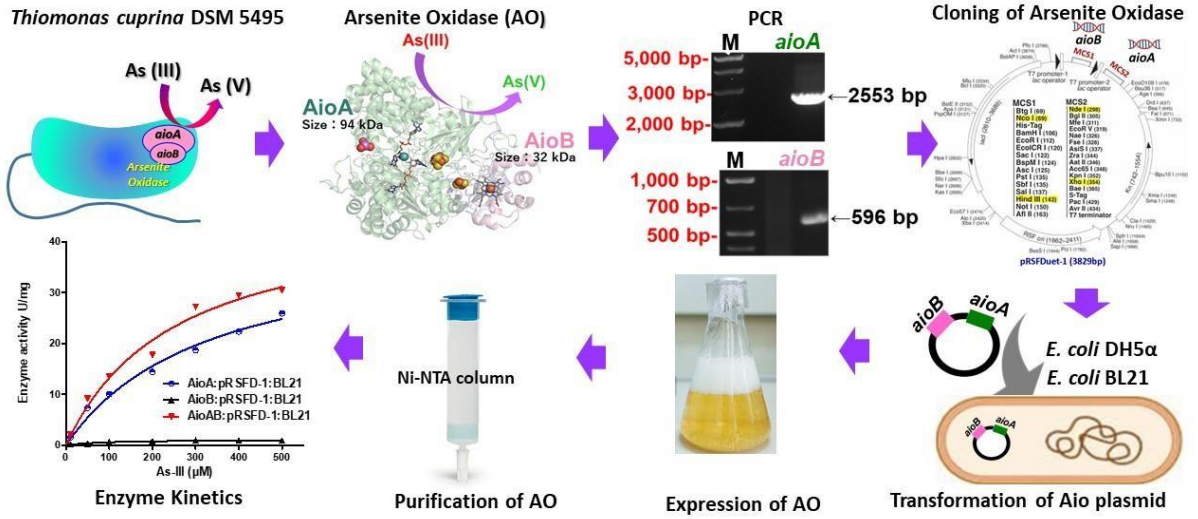


Figure.1.
Workflow of Cloning, Expression, and Characterization of Arsenite Oxidase (*aioA & aioB*) from *Thiomonas cuprina.*

UPCYCLING OF CHICKEN MANURE FERTILIZER INTO PROLINE BY ENGINEERED HALOPHILIC *Halomonas elongata* CELL FACTORY

Hideki Nakayama[1,2,*], Huynh Cong Khanh[2,3], Pulla Kaothien-Nakayama[1]

[1] Graduate School of Integrated Science and Technology, Nagasaki University, 1-14 Bunkyo-machi, Nagasaki City, Nagasaki 852-8521, Japan

[2] Graduate School of Fisheries and Environmental Sciences, Nagasaki University, 1-14 Bunkyo-machi, Nagasaki City, Nagasaki 852-8521, Japan

[3] College of Environment and Natural Resources, Can Tho University, Campus II, 3/2 street, Ninh Kieu Ward, Can Tho City 94000, Viet Nam

*e-mail: nakayamah@nagasaki-u.ac.jp

Abstract:

Previously, we successfully developed an engineered halophilic *Halomonas elongata* HN6 (Δ*ectABC*::*mCherry-proB*$_{m1}$*AC* Δ*putA* with *H. elongata* OUT30018 background), which overproduces and accumulates L-proline (Pro) instead of ectoine as an osmolyte. Because glutamate is a precursor for Pro biosynthesis, the mutant *H. elongata* Glutamic acid Over-Producing (GOP) strain was used as a host to generate an improved *H. elongata* Pro-producing cell factory. We found that the resulting *H. elongata* HN10 (Δ*ectABC*::*mCherry-proB*$_{m1}$*AC* Δ*putA* with *H. elongata* GOP genetic background) could tolerate higher levels of salt stress than the previously developed *H. elongata* HN6. With faster and better growth, *H. elongata* HN10 cultures produced more Pro than *H. elongata* HN6 in a shorter cultivation time, making them a better candidate as a Pro-producing cell factory. Furthermore, to address a significant environmental problem caused by the poultry industry, we developed a simple alkaline hydrolysis method to convert nitrogen-rich chicken manure (CM) fertilizer into media suitable for culturing *H. elongata* HN10. Since Pro is used as a feeding stimulant in the aquaculture industry, *H. elongata* HN10 could be further developed into a Pro-rich single-cell ecofeed, thereby enhancing the sustainability of the poultry, feed, and aquaculture industries.

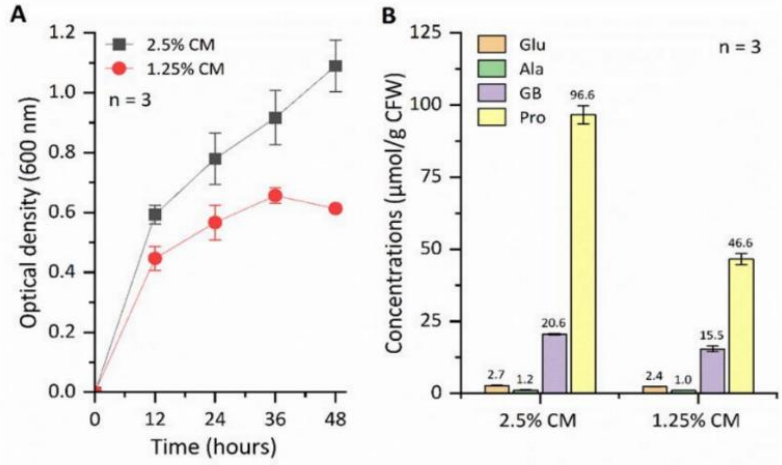


Figure 1.

Effect of chicken manure (CM) hydrolysate concentrations in CM-derived media on the growth and intracellular osmolytes accumulation of *H. elongata* HN10 strain.

A. Growth curve of *H. elongata* HN10 grown in media made from 1.25% or 2.5% w/v CM hydrolysates. Both media also include 6% w/v NaCl.
B. Profiles of major osmolytes in *H. elongata* HN10 cultures shown in A.

Glu, glutamate; Ala, alanine; GB, glycine betaine; Pro, proline.

TAILORING PHOSPHITE DEHYDROGENASE FOR A HIGHLY EFFICIENT AND ROBUST NAD(P)H COFACTOR REGENERATION SYSTEM

Gamal Nasser Abdel-Hady[1,2], Akio Kuroda[1], Ryuichi Hirota[1]*
[1]Unit of Biotechnology, Division of Biological and Life Sciences, Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan
[2]Department of Genetics, Faculty of Agriculture, Minia University, Minia, Egypt
*e-mail: hirota@hiroshima-u.ac.jp

Abstract:
Biocatalysis has the potential to transform the chemical, pharmaceutical, and energy industries. Dehydrogenases are particularly valuable biocatalysts due to their high enantioselectivity and substrate specificity. However, their dependency on costly NAD(P)H cofactors has limited their large-scale application. Cofactor regeneration systems provide an effective solution by producing a catalytic pool of NAD(P)H for bioconversions.

Phosphite dehydrogenase (PtxD) is a promising enzyme for NAD(P)H regeneration due to the substantial change in the free energy of the reaction. However, its strict NAD specificity and susceptibility to salt and organic solvents limit its practical applications. To overcome these limitations, we engineered a thermotolerant PtxD from *Ralstonia* sp. 4506 (RsPtxD) by substituting five residues (Cys174-Pro178) in the C-terminus of β7-strand of the Rossmann-fold domain via site-directed mutagenesis. The resulting RsPtxD^{HARRA} mutant exhibited significantly enhanced catalytic efficiency with NADP, high thermostability, and strong tolerance to organic solvents when bound to NADP. To obtain a salt-resistant variant, we cloned a PtxD from the marine cyanobacterium *Cyanothece* sp. ATCC 51142 (Ct-PtxD). Compared with previously reported PtxDs, Ct-PtxD showed high resistance to salts such as Na^+, K^+, and NH_4^+ up to 1.5 M, as well as high tolerance to organic solvents when bound to NAD^+. Overall, these findings highlight engineered and naturally obtained PtxD variants as robust tools for NAD(P)H regeneration and broaden the potential of PtxD in biotechnological applications.

HIGH-TEMPERATURE UPCYCLING OF POLY(3-HYDROXYBUTYRATE-CO-3-HYDROXYVALERATE) BY A NOVEL *Actinomadura* sp. SCN-SB

Natthaphat Phothong[1], Siritouch Bhamarasuta[1] Shiho Morikane[2], Hiroya Tomita[2], Kohsuke Honda[2], and Suchada Chanprateep Napathorn[1,2]*
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Phayathai Road, Patumwan, Bangkok, Thailand
[2]International Center for Biotechnology, The University of Osaka, Suita, Osaka, Japan
*e-mail: suchada.cha@chula.ac.th

Abstract:
Poly(3-hydroxybutyrate-co-3-hydroxyvalerate) (PHBV) is a biodegradable plastic with applications in food packaging and biomedicine, but its slow degradation under landfill and conventional composting limits environmental implementation. High-temperature composting using thermophilic microorganisms offers a solution. In this study, strain 93 was isolated from soil samples as a potential PHBV-degrading bacterium. Based on 16S rRNA gene sequencing, the isolate exhibited 98.19% similarity to *Actinomadura adrarensis* ACD12. Whole-genome analysis revealed that strain 93 represents a novel species, designated *Actinomadura* sp. SCN-SB, as supported by low digital DNA–DNA hybridization (dDDH = 25.40%) and average nucleotide identity (ANIb = 80.07%) values. Genome annotation further confirmed the presence of extracellular short-chain-length (scl-PHA) depolymerase genes, which are associated with PHBV biodegradation. Functional assays conducted at 50 °C demonstrated a maximum clear zone of 28.0 ± 2.9 mm on PHBV agar plates. Similarly, PHBV films in submerged culture exhibited a weight loss of 50.4 ± 4.7%. Comparison of degradation efficiency among different media revealed that the degradation rate was higher in YP medium than in MSM medium, regardless of the C/N ratio. Moreover, the crude scl-PHA depolymerase exhibited optimal enzymatic activity (0.27 ± 0.01 U/mL) at pH 9.0 and 50 °C. Overall, these findings establish *Actinomadura* sp. SCN-SB as a novel thermophilic bacterium with strong enzymatic potential for efficient PHBV degradation. This strain offers significant promise for biological recycling and upcycling of PHBV under high-temperature composting and landfill conditions, contributing to sustainable management of biodegradable plastics.

Keywords: *Actinomadura* sp., Thermophilic enzyme, Closed-loop supply chain, Thermophilic actinomyces

CAPTURING VIRAL DIVERSITY AND ADAPTATION THROUGH METAGENOMICS

Worakorn Phumiphanjarphak,[1,2,*]
[1]Department of Microbiology, Faculty of Science, Mahidol University, Bangkok, Thailand
[2]Pornchai Matangkasombut Center for Microbial Genomics, Department of Microbiology, Faculty of Science, Mahidol University, Bangkok, Thailand
*e-mail: worakorn.phu@mahidol.ac.th

Abstract:
Viruses exist as complex, genetically diverse populations. Understanding this vast genetic diversity is a fundamental challenge in virology. Unbiased metagenomics emerged as an important method that can capture this spectrum of the viral diversity. This presentation showcases two applications of metagenomics, demonstrating its versatility across different levels of virus populations. First, at the population level, we mined human whole-genome sequencing data from Thai individuals to discover and characterise the diversity of anelloviruses. This work revealed a unique and previously unreported population of anelloviruses, significantly expanding the known human anelloviruses in Thailand. Second, we used deep sequencing to track the adaptation of SARS-CoV-2 during propagation in different cell lines. We showed that the virus is highly and readily adaptable and can generate cell line-specific mutations. These two works collectively demonstrate the power of metagenomics for studying microbial diversity at multiple levels.

KNOWLEDGE GRAPHS TO PREDICT BIOACTIVITY OF NATURAL PRODUCTS

Pitchapong Chouchanakij,[1] Natapol Pornputtapong[2,*]
[1]Pharmaceutical Sciences and Technology Program, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Thailand
[2]Department of Biochemistry and Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Thailand
*e-mail: Natapol.p@chula.ac.th

Abstract:
Accelerating natural product research requires overcoming the challenge of fragmented and heterogeneous data scattered across chemical, biological, and taxonomic domains. This study tackles that barrier by constructing a comprehensive knowledge graph that unifies diverse datasets—including chemical structures, bioactivity profiles, taxonomic hierarchies of source organisms, protein targets, and chemical classifications—into a single, interconnected framework. By organizing these complex relationships, the graph enables more efficient exploration, pattern recognition, and hypothesis generation, ultimately streamlining the discovery of bioactive compounds and their potential therapeutic targets. The graph captures hierarchical and relational dependencies to support the prediction of natural product bioactivity against human single-protein targets. Knowledge graph embeddings were generated for its capacity to represent complex relational patterns. Model evaluation focused on predicting bioactivity for previously unseen chemical structures, achieving an accuracy of 65.70%, which increased to 73.68% with the incorporation of contextual embeddings. These findings demonstrate the potential of integrating fragmented data into a unified graph-based framework, emphasizing the value of hierarchical and relational information in enhancing predictive performance. This research lays the groundwork for future developments in computational bioactivity discovery of natural products.

Session II.
Medical Biotechnology
& One Health

DYNAMIC REGULATION OF CELLS AND ECMS FOR TISSUE ENGINEERING

Michiya Matsusaki*
[1]Department of Applied Chemistry, Graduate School of Engineering, The University of Osaka
*e-mail: m-matsus@chem.eng.osaka-u.ac.jp

Abstract:
Since the concept of Tissue Engineering using cells and scaffold materials was proposed by Robert Langer in 1993, various cell integration techniques have been reported. However, the technologies to date have focused on "construction of tissue structures" and have not been able to "reproduction of functional tissues" the most important aspect. This is mainly due to the fact that cells are particles with a diameter of only 15 μm, so the scaffold material is necessary for tissue structure construction. However, if the scaffold material increases, cell-cell interactions are inhibited, and cells cannot interact with each other. Conversely, when scaffold material is reduced, tissue structures cannot be formed and cell aggregates are formed, and it is difficult to construct tissues with diameters of 200~300 μm or more due to internal cell necrosis. To solve this dilemma and realize the "creation of functional tissue constructs," it was necessary to innovate with cell integration technology based on a completely new principle.

To solve this dilemma, we discovered new concept “cooperative tissue engineering” that means cells and materials interacted each other to fabricate tissue constructs cooperatively. Nano-sized scaffolds formed on the cell surfaces induced cell-cell adhesion and integration of multiple cell types, and then the scaffolds grown to microscopic sizes, and the adhered cells on the scaffolds proliferated to cover the scaffold surfaces. The micrometer-sized grown scaffolds induced the elasticity and molecular orientation to control the cell orientation and differentiation to fabricate “functional tissue constructs”. This new concept will be powerful technology to fabricate functional tissue constructs for implantation in biomedical applications, construction of cultivated meat in food-tech applications and drug assessment in pharmaceutical applications.

ALLELIC VARIATIONS AND GENE CLUSTER MODULARITY ACT AS NON-LINEAR BOTTLENECKS FOR CHOLERA EMERGENCE

Deepak Balasubramanian[a#], Mario López-Pérez[b#], Alicia Campos-Lopez[a,b], Cole Crist[a], and Salvador Almagro-Moreno[a*]

[a]Department of Host-Microbe Interactions, St. Jude Children's Research Hospital, Memphis, Tennessee, USA. [b]Microbial Genomics and Evolution Group, División de Microbiología, Universidad Miguel Hernández, Alicante, Spain.

# Contributed equally

*Address correspondence to: Salvador Almagro-Moreno, samoreno@stjude.org

Running title: Evolutionary bottlenecks of pathogen emergence

Abstract:

The underlying factors that lead to specific strains within a species to emerge as human pathogens remain mostly enigmatic. The diarrheal disease cholera is caused by strains from a phylogenetically confined group within the Vibrio cholerae species, the pandemic cholera group (PCG), making it an ideal model system to tackle this puzzling phenomenon. Comprehensive analyses of over 1,840 V. cholerae genomes, including novel environmental isolates from this study, reveal that the species consists of eleven groups, with the PCG belonging to the largest and located within a lineage shared with environmental strains. This hierarchical classification provided us with a framework to unravel the eco-evolutionary dynamics of the genetic determinants associated with the emergence of toxigenic V. cholerae. Our analyses indicate that this phenomenon is largely dependent on the acquisition of unique modular gene clusters and allelic variations that confer a competitive advantage during intestinal colonization. We determined that certain PCG-associated alleles are essential for successful colonization whereas others provide a non-linear competitive advantage, acting as a critical bottleneck that clarifies the isolated emergence of PCG. For instance, toxigenic strains encoding non-PCG alleles of a) tcpF or b) a sextuple allelic exchange mutant for genes tcpA, toxT, VC0176, VC1791, rfbT and ompU, lose their ability to colonize the intestine. Interestingly, these alleles do not play a role in the colonization of newly stablished model environmental reservoirs. Our study uncovers the evolutionary roots of toxigenic V. cholerae offering a tractable approach for investigating the emergence of pathogenic clones within an environmental population.

Keywords: Pathogen emergence / *Vibrio cholerae* / modularity / population genomics / allelic variation / environmental reservoirs

AMELIORATIVE EFFECTS OF *Lactobacillus paracasei* ISOLATED FROM MALAYSIAN WATER KEFIR GRAINS ON SPATIAL LEARNING AND MEMORY OF D-GALACTOSE-INDUCED AGING MICE

Nurulain Syahirah Razali[1], Muhammad Asyraaf Haja Maideen[1], Nurul Elyani Mohamad[3], Che Norma Mat Taib[2], Janna Ong Abdullah[1], Suraini Abd-Aziz, and Noorjahan Banu Alitheen[1]*

[1] Department of Cell and Molecular Biology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia.

[2] Department of Human Anatomy, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia.

[3] Biotechnology Research Institute, Universiti Malaysia Sabah, Kota Kinabalu 88400, Sabah, Malaysia.

*Corresponding author email address: noorjahan@upm.edu.my

Abstract:

Neurodegeneration is characterized by a progressive decline in brain function, often associated with aging, and manifests as cognitive impairments. Without timely intervention, the loss of neurons contributes to disorders such as Alzheimer's disease. Probiotics are emerging as neuroprotective agents that modulate gut-brain communication and systemic health through the gut-brain axis. This study aimed to evaluate the neuroprotective effects of *Lactobacillus paracasei* , a probiotic strain isolated from Malaysian water kefir grains, on neurodegeneration in D-galactose-induced aging mice. Aging was induced in mice using D-galactose, followed by long-term administration of *L. paracasei* HBUAS52231 at 10^7 (low-dose) and 10^9 (high-dose) CFU. Behavioral analysis was performed using the Morris Water Maze test, while biochemical assays assessed antioxidant activities, oxidative stress markers, and pro-inflammatory cytokines. High-dose *L. paracasei* HBUAS52231 (10^9 CFU) administration significantly improved memory and learning abilities in D-galactose-induced aging mice compared to the D-galactose and low-dose (10^7 CFU) group. Biochemical assays showed restoration of antioxidant activities, including glutathione (GSH) and superoxide dismutase (SOD), while oxidative stress markers 4-hydroxynonenal (4-HNE) and nitric oxide (NO) were reduced in the hippocampus, frontal cortex, and colon of aging mice treated with 10^9 CFU of *L. paracasei* HBUAS52231. Systemic pro-inflammatory cytokines TNF-α and IL-1β were significantly decreased in the high-dose group compared to the D-galactose group. The therapeutic effects of *L. paracasei* HBUAS52231 were dose-dependent, with higher doses yielding greater benefits. These findings highlight the potential of *L. paracasei* HBUAS52231 as a probiotic therapy for aging-related neurodegenerative conditions by modulating oxidative stress and inflammation.

Keyword: Aging, neuroinflammation, neurodegeneration, D-galactose, probiotic

AUTOMATED CENTRIFUGAL MICROFLUIDIC PLATFORM FOR DRUG SCREENING

Yi-Chen Ethan Li
Department of Chemical Engineering, Feng Chia University, Taichung 407102, Taiwan
e-mail: yicli@fcu.edu.tw

Abstract:
Drug screening is a critical step in drug development and pharmaceutical research. In cell-based assays, cells are exposed to compounds at varying concentrations to evaluate cellular responses and determine the effects of the compounds. A concentration gradient allows cultured cells to grow under different compound levels, expediting the analysis of dose-dependent effects. However, conventional gradient generation is typically performed manually, making the process labor-intensive and time-consuming. Microfluidic technology addresses these challenges by enabling drug screening in miniaturized systems that enhance efficiency, sensitivity, and reduce reagent usage and operational time. Centrifugal microfluidics, in particular, harnesses disk rotation to drive fluidic operations such as pumping, metering, and mixing, achieving automation with a simple, low-cost motor without the need for complex pumping systems. In this study, we present a centrifugal microfluidic platform designed for automated drug screening. The device features a two-zone architecture, including an inner disk with branching channels to generate concentration gradients and an outer disk for cell culturing, which facilitates periodic medium exchange through rotational control. In summary, the proposed platform enables rapid formation of concentration gradients and automated cell culture maintenance, offering a cost-effective and efficient solution for high-throughput drug screening.

ADAPTIVE QUORUM SENSING REWIRING IN *Vibrio campbellii* SUPPRESSOR MUTANTS: IMPLICATIONS FOR AQUACULTURE AND ONE HEALTH

Jiranan Pattano, [1] William Robins,[2] John Mekalanos,[2] Maria Ericsson,[3] Korakot Wichitsa-nguan Jetwanna,[4] Pimonsri Mittraparp-arthorn[1,*]
[1]Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla 90110, Thailand
[2]Department of Microbiology, Harvard Medical School, Boston, MA 02115, USA
[3]Department of Cell Biology, Harvard Medical School, Boston, MA 02115, USA
[4]Division of Computational Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla 90110, Thailand
*e-mail: pimonsri.m@psu.ac.th

Abstract:
Vibrio campbellii is a luminous marine bacterium responsible for larval mortality in shrimp hatcheries, causing serious aquaculture losses. This study investigated motility regulation and the emergence of spontaneous suppressor mutations in flagellar regulator mutants. Deletion of *flrA*, *flrC*, and *flrAflrC* abolished swimming motility and reduced biofilm formation. Remarkably, spontaneous suppressor mutants from Δ*flrC* and Δ*flrA*Δ*flrC* backgrounds regained motility despite retaining the original deletions. Genomic and transcriptomic analyses revealed secondary mutations in quorum sensing (QS)-associated genes (*luxO*, *luxR*, *luxP*, *ihfA*, *motY*), which rewired regulatory networks governing motility, biofilm, and secretion systems. Some suppressor strains exhibited multiple flagella, altered morphology, and misregulation of *flhF*, suggesting disrupted flagellar placement. These mutants also showed increased susceptibility to lytic phages and variable bioluminescence. Collectively, the findings demonstrate adaptive QS rewiring as a compensatory strategy for flagellar regulator loss, underscoring the evolutionary flexibility of *V. campbellii*. Beyond aquaculture relevance, this study provides broader insights into the adaptive potential of *Vibrio* species, including human pathogens, and contributes to a One Health understanding of microbial persistence and virulence evolution in marine environments.

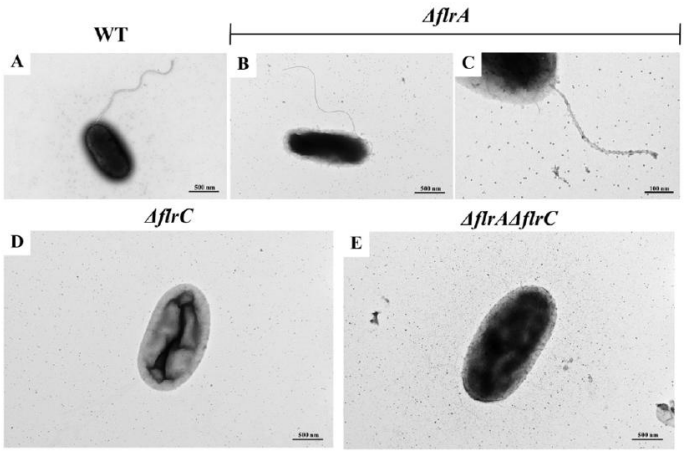


Figure 1.
Comparison of flagellar structures in wild-type (WT) and mutants (Δ*flrA*, Δ*flrC*, Δ*flrA*Δ*flrC*) of *V. campbellii* HY01. WT exhibits a sheathed polar flagellum (A), while mutants show altered or absent flagella (B–E).

PHYCOCYANIN-LOADED HIERARCHICAL MICRO/NANOFIBROUS MEMBRANE FOR GUIDED BONE REGENERATION

Se-Chang Kim,[1,2] Da-Bin Kim,[3] Won-Kyo Jung[1,2,3,*]
[1]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Major of Biomedical Engineering, Division of Smart Healthcare, Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
Bone tissue possesses an inherent regenerative capacity; nevertheless, the repair of defects associated with osteoporosis, osteosarcoma, and congenital deformities remains challenging. Biomaterials such as hydrogels, 3D scaffolds, and nanofibrous scaffolds have been developed to deliver bioactive compounds and promote bone healing. Here, we evaluated the cytotoxicity, alkaline phosphatase activity, and mineral deposition of MC3T3-E1 cells treated with phycocyanin (PC) derived from *Spirulina maxima*, and further assessed its effects on the expression of osteogenic protein markers including osteocalcin and osteopontin. Next, PC was incorporated into poly lactic acid and sodium alginate micro/nanofibrous membrane using emulsion electrospinning, and hierarchically structured membranes were constructed with atelocollagen isolated from *Paralichthys olivaceus*. The microstructural architecture and physicochemical properties of the fabricated fibrous membranes were characterized using scanning electron microscopy (SEM), Fourier transform infrared spectroscopy (FT-IR), X-ray diffraction (XRD), and water contact angle analysis. *In vitro*, the hierarchical micro/nanofibrous membranes demonstrated favorable cytocompatibility, maintained cytoskeletal integrity, and induced mineral deposition. *In vivo*, implantation into calvarial bone defects followed by micro-CT and histological analysis at 12 weeks confirmed significantly enhanced bone regeneration. These results indicate that PC loaded hierarchical micro/nanofibrous membranes are promising candidates for bone regeneration applications.

THERAPEUTIC EFFICACY OF FUCOIDAN-LOADED GELATIN/OXIDIZED CARBOXYMETHYL CELLULOSE HYDROGELS IN ACCELERATING WOUND HEALING

Ji-Won Jeong,[1] Se-Chang Kim,[1,2] Dong-Joo Park,[2,3] Yu-Jin Ahn,[2,3] Won-Kyo Jung[1,2,3,*]
[1]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Major of Biomedical Engineering, Division of Smart Healthcare Major of Biomedical Engineering and New-senior Healthcare Innovation Center (BK21 Plus), Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
Hydrogels are advanced wound dressings that sustain a moist microenvironment and enable localized delivery of bioactive agents. We engineered a fucoidan-loaded gelatin/oxidized carboxymethyl cellulose hydrogel (GOC/F) and evaluated its cytocompatibility, bioactivity, and *in vivo* efficacy. The prepared GOC/F hydrogels exhibited favorable water retention and biodegradability, and demonstrated cytoprotective activity against oxidative stress by reducing intracellular reactive oxygen species (ROS). Furthermore, hydrogels reduced LPS-induced nitric oxide (NO) production in RAW 264.7 macrophages and significantly increased HDF cell migration. *In vivo* evaluation in a full-thickness ICR mouse model demonstrated that GOC/F5 promoted faster re-epithelialization and greater collagen deposition, resulting in superior wound healing. Collectively, these results support GOC/F5 as a promising candidate for hydrogel dressings in the repair of skin defects.

SUPPRESSION OF *Pseudomonas aeruginosa* VIRULENCE AND BIOFILM FORMATION BY CIPROFLOXACIN-LOADED ZNO@LIGNIN@CHITOSAN NANOPARTICLES

Nadia Fattahi,[1,2] Fazlurrahman Khan,[2] Won-Kyo Jung[1,2,3,*]
[1]Major of Biomedical Engineering, Division of Smart Healthcare Major of Biomedical Engineering and New-senior Healthcare Innovation Center (BK21 Plus), Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
The rapid development of antimicrobial resistance (AMR) in bacterial infections leads to increased mortality and reduced treatment efficacy, emphasizing the need for alternative antimicrobial strategies. Chitosan, a biocompatible and biodegradable biopolymer, has antimicrobial activity and serves as an effective antibacterial coating by damaging bacterial membranes. On the other hand, lignin, the most abundant renewable aromatic biopolymer, has great potential for novel material applications due to its chemical versatility and biodegradability. In this study, ZnO@lignin nanoparticles (NPs) were synthesized, coated with chitosan, and used to efficiently load and deliver ciprofloxacin (CIP). *In vitro* CIP release was highly pH-dependent, reaching 90% at pH 2.0 and decreasing to 45% at pH 5.6, 40% at pH 7.4, and 30% at pH 10 over 150 hours. The antibacterial, antivirulence, and antibiofilm effects of ZnO@lignin, ZnO@lignin@chitosan, ZnO@lignin@chitosan@CIP, and lignin were tested against *Pseudomonas aeruginosa*. Among the tested samples, ZnO@lignin@chitosan@CIP NPs showed the strongest antibacterial and antibiofilm activity and significantly reduced virulence factors, including protease, pyocyanin, and pyoverdine. Scanning electron microscopy further revealed a marked decrease in biofilm formation with ZnO@lignin@chitosan@CIP compared to the other formulations. In conclusion, this study highlights ZnO@lignin@chitosan@CIP NPs as a promising multifunctional antibacterial agent with significant potential for addressing bacterial infections.

FUNCTIONAL ANALYSIS OF AROMATIC AMINO ACID TRANSPORTER GENE *aaaT* ON ANTIMICROBIAL RESISTANCE IN *Pseudomonas aeruginosa*

Pacharapon Phoopanish,[1] Jintana Duang-nkern,[2] Saharit Wijitpittayanon,[3] Adisak Romsang,[1,3,*]

[1]Department of Biotechnology, Faculty of Science, Mahidol University, Bangkok 10400, Thailand

[2]Laboratory of Biotechnology, Chulabhorn Research Institute, Bangkok 10210, Thailand

[3]Center for Emerging Bacterial Infections, Faculty of Science, Mahidol University, Bangkok 10400, Thailand

*e-mail: adisak.rom@mahidol.ac.th

Abstract:

Pseudomonas aeruginosa is a multidrug-resistant opportunistic pathogen capable of surviving diverse environmental stresses through efflux pumps, detoxification systems, and chemical transporters. Amino acid transporters have recently been recognized for roles beyond nutrient uptake, particularly in stress adaptation. In this study, the physiological function of the aromatic amino acid transporter gene (*aaaT*) was examined using knockout and complementation approaches, verified by sequencing. Plate sensitivity assays revealed that the *aaaT*-knockout strain exhibited pronounced sensitivity to paraquat (PQ), a superoxide generator, while complementation restored resistance, underscoring the role of *aaaT* in PQ tolerance. Strains with ectopic *aaaT* expression from a pBBR vector displayed growth defects compared with both wild-type and knockout strains, though no significant differences were observed under exposure to other oxidative agents, including hydrogen peroxide, cumene hydroperoxide, sodium hypochlorite, and N-ethylmaleimide. Antibiotic susceptibility testing by disk diffusion showed that the *aaaT*-knockout strain was more susceptible to ciprofloxacin and norfloxacin, but exhibited modestly increased resistance to cefepime, with no substantial changes to most other antibiotics. Collectively, these findings demonstrate that *aaaT* contributes to *P. aeruginosa* tolerance against oxidative stress and modulates its susceptibility to specific antibiotics, especially fluoroquinolones. Targeting *aaaT* may therefore represent a promising strategy to sensitize *P. aeruginosa* to existing antibiotics and enhance therapeutic efficacy.

DISTRIBUTION OF *Vibrio* spp. IN RELATION TO WATER QUALITY IN THE SONGKHLA LAKE BASIN, THAILAND

Jutamas Manit,[1] Kurrotulayunee Kareeya,[2] Rattanaruji Pomwised[1,*]
[1]Division of Biological Science, Faculty of Science, Prince of Songkla University, Songkhla, Thailand
[2]Department of Biomedical Sciences and Biomedical Engineering, Faculty of Medicine, Prince of Songkla University, Songkhla, Thailand
*e-mail: Rattanaruji Pomwised

Abstract:
Songkhla lake basin is an important brackish water ecosystem in Thailand, supporting both biodiversity and aquaculture. Environmental changes and human activities affect water quality and the spread of *Vibrio* spp. which are associated with vibriosis in aquatic animals and severe infections in humans. This study investigated the occurrence of *Vibrio* spp. using the most probable number (MPN) method and examined correlations with water quality parameters. Isolates were identified using selective media, multiplex PCR for *Vibrio vulnificus*, and MALDI-TOF MS for other species. While *V. vulnificus* was not detected, *V. albensis* and other *Vibrio* species were present. Bacterial abundance correlated with elevated ammonia, nitrite, and organic matter, along with variations in pH, salinity, and temperature. These findings provide baseline data on *Vibrio* ecology in the Songkhla lake basin and underscore the importance of water quality monitoring to reduce risks for public health and aquaculture.

TOWARDS RAPID BIOSENSING OF INVASIVE FUNGAL DISEASES: A PCR-ENHANCED LATERAL FLOW ASSAY FOR CLINICAL APPLICATION

Ariff Khalid,[1] Jacinta Santhanam[1,*] Tzar Mohd-Nizam,[2] Ang-Lim Chua,[3] Sharifah Fadilah Abdul-Wahid,[4] Wan Rahiza Wan-Mat,[5] Raha Abd-Rahman,[5] Petrick Periyasamy,[4] Jasper Elvin James,[6]

[1]Biomedical Science Programme, Faculty of Health Sciences, Universiti Kebangsaan Malaysia, Jalan Raja Muda Abdul Aziz, 50300 Kuala Lumpur, Malaysia
[2]Department of Medical Microbiology and Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Jalan Yaacob Latif, Cheras, 56000 Kuala Lumpur, Malaysia
[3]Department of Medical Microbiology & Parasitology, Faculty of Medicine, Universiti Teknologi MARA, 47000 Sungai Buloh, Selangor, Malaysia
[4]Department of Medicine, Faculty of Medicine, Universiti Kebangsaan Malaysia, Jalan Yaacob Latif, Cheras, 56000 Kuala Lumpur, Malaysia
[5]Department of Anaesthesiology & Intensive Care, Faculty of Medicine, Universiti Kebangsaan Malaysia, Jalan Yaacob Latif, Cheras, 56000 Kuala Lumpur, Malaysia
[6]Department of Biological Sciences and Biotechnology, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, 43600 Bangi, Selangor, Malaysia
*e-mail: jacinta@ukm.edu.my

Abstract:
Invasive fungal infections (IFIs) caused by *Candida* and *Aspergillus* species remain a major cause of morbidity and mortality worldwide. Conventional diagnostics are often slow or insufficiently sensitive, underscoring the need for rapid and accurate tools. We developed a hybrid platform that combines multiplex PCR with a lateral flow assay (LFA) dipstick to detect fungal DNA from clinical specimens. The assay targeted the internal transcribed spacer region at genus and species levels, with *Candida glabrata*, *Candida krusei*, and *Aspergillus terreus* as proof-of-concept species. Amplicons labelled with biotin, digoxigenin, or TAMRA were captured on antibody-coated LFA strips and visualised using gold nanoparticles. A total of 203 clinical samples from suspected IFI cases were evaluated against EORTC/MSGERC criteria. Analytical testing with spiked blood demonstrated detection limits of 5–100 CFU/mL. Clinical evaluation showed high specificity (99.4%) and predictive values (>90%), though sensitivity was moderate (47.8%) due to challenges in fungal DNA extraction from blood. Interestingly, fungal DNA was detected in several culture-negative fluids, but the clinical significance of these results remains to be established. This PCR-enhanced LFA shows strong potential as a rapid diagnostic platform for IFIs. Improved extraction protocols may further enhance sensitivity and facilitate clinical translation for early fungal diagnosis.

Staphylococcus aureus-DERIVED EXTRACELLULAR VESICLES PROMOTE PATHOGENICITY OF *Pseudomonas aeruginosa*

Phawinee Subsomwong,[1,2] Krisana Asano,[2,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
[2]Department of Microbiology and Immunology, Hirosaki University Graduate School of Medicine, Hirosaki University, Aomori, Japan
*e-mail: krisana@hirosaki-u.ac.jp

Abstract:

Staphylococcus aureus and *Pseudomonas aeruginosa* are the most common pathogens isolated from chronic wounds; however, the synergistic interaction between these two pathogens mediated by extracellular vesicles (EVs) is unknown. Here, we investigated the effect of EVs derived from *S. aureus* (SaEVs) on the pathogenicity of *P. aeruginosa*. The fusion of SaEVs with *P. aeruginosa* membranes was observed using lipophilic fluorescent dye. Protein composition in SaEVs and in *P. aeruginosa* with or without SaEVs was analyzed using LC-MS/MS. Human keratinocytes and murine macrophage cell lines were used for cell infection. Biofilm formation and gene expression of *P. aeruginosa* treated with and without SaEVs were evaluated by crystal violet assay and real-time PCR. Fusion between SaEVs and *P. aeruginosa* was confirmed. The lipopolysaccharide (LPS) biosynthesis protein in *P. aeruginosa* was increased after the SaEV treatment. SaEVs promote LPS production, biofilm formation, and the expression of polysaccharide polymerization-related genes. SaEVs-treated *P. aeruginosa* promoted epithelial cell invasion and reduced phagocytosis by macrophages. Proteins related to host cell colonization, immune evasion, anti-phagocytosis, protein translocation, and iron uptake were identified in SaEVs. In conclusion, SaEVs promote the pathogenicity of *P. aeruginosa* by enhancing LPS biosynthesis, biofilm formation, epithelial cell invasion, and impairment of macrophage uptake.

Session III.
Industrial & Environmental Biotechnology, & Alternative Energy

MICROBIAL ECOTOXICOLOGY: MICROBIAL ECOLOGY OF CONTAMINATED ENVIRONMENTS

Robert Duran
Universite de Pau et des Pays de l'Adour, UPPA, CNRS, IPREM, Institut des Sciences Analytiques et de Physico-chimie pour l'Environnement et les matériaux, Pau, France
*e-mail: Robert.duran@univ-pau.fr

Abstract:
Human activities threaten the environment by realizing multiple and various compounds such as metal(loid)s, hydrocarbons, and pesticides. The aquatic environment, particularly coastal marine areas are among the main exposed ecosystems because they receive contaminants inputs from both the land and the sea.

Microbial communities exhibit exceptional functional capabilities to thrive in the presence of contaminants, being able to transform metal(loid)s, and degrade organic compounds under aerobic and anaerobic conditions using a variety of electron acceptors. However, despite the accumulated knowledge on the microbial mechanisms involved in contaminants resistance, transformation and degradation it is still a challenge to predict the effect of contaminants on microbial communities and ecosystems as well as to implement effective microbial based bioremediation strategies.

Microbial ecology approaches, based on high throughput sequencing, provide the opportunity to gain useful information at multiple biological scales (from the community to the population, including the cell and the gene), and at several levels (local, regional, and global). Our investigations at global scale have demonstrated the difficulties in obtaining a global pattern specific to a contamination while microbial taxa were identified as specialist at regional and local scale. Such observation paves the way for the development of microbial indicators that can be used for reporting the ecological status of an ecosystem, ushering in a new era in the field of microbial ecology: microbial ecotoxicology. The presentation also discuss the significant understanding gained on the mechanisms underlying microbial assembly process and dispersion in metal(loid)s contaminated areas, the coalescence mechanisms in land-sea continuum, and the identification of ecotypes in oxic/anoxic oscillating according to tidal cycles. As much useful information gained to help for establishing microbial tools for managing and monitoring microbial resources with the aim of preserving ecosystem services.

PRODUCTION OF NICOTINAMIDE MONONUCLEOTIDE BY HIGH CELL DENSITY CULTURE OF METABOLICALLY ENGINEERED *Escherichia coli*

Beom Soo Kim[1,*]
[1]Department of Chemical Engineering, Chungbuk National University, Cheongju, Chungbuk 28644, Republic of Korea
*e-mail: bskim@chungbuk.ac.kr

Abstract:
Nicotinamide mononucleotide (NMN) presents significant therapeutic potential against aging-related conditions, such as Alzheimer's disease, due to its consistent and strong pharmacological effects. NMN, a precursor of NAD^+, is synthesized through the salvage pathway by converting nicotinamide with the help of nicotinamide phosphoribosyl transferase (NAMPT). In this study, we engineered a recombinant strain of *Escherichia coli* by introducing the *Homo sapiens* genes *NAMPT*, phosphoribosyl pyrophosphate synthetase 1 (*PRPS1*), and *PRPS2*. Using these metabolically engineered *E. coli* strains, NMN was produced intracellularly in a high-cell-density bioreactor via fed-batch cultures employing different feeding strategies (exponential feeding and pH-stat feeding). The highest NMN concentration, 19.3 g/L, was achieved within 28 h, with a dry cell weight of 117 g/L. NMN production was confirmed through liquid chromatography-mass spectrometry analysis. Furthermore, continuous cultivation of recombinant *E. coli* at various dilution rates in a bioreactor enhanced NMN productivity beyond that of fed-batch cultures. This approach offers a cost-effective strategy for large-scale NMN production while maintaining high quality and yield.

CRADLE-TO-GATE CARBON FOOTPRINT OF INDUSTRIAL-SCALE FERMENTATIVE PRODUCTION OF POLY(3-HYDROXYBUTYRATE-CO-3-HYDROXYHEXANOATE) (PHBH)

Hsien-Tse Chen[1,#], Yu-Hsiang He[1,#], Pei-Yi Lin[1,#], Wei-Shu Huang[1,#], Kaarmukhilnilavan R Srinivasan[1], Jun-You You[1], Pei-Yu Sun[1], Allen H. Hu[2], Penjit Srinophakun[3], Maythee Saisriyoot[3,*], and Si-Yu Li[1,*]

[1]Department of Chemical Engineering, National Chung Hsing University, Taichung 402, Taiwan, [2]Institute of Environmental Engineering and Management, National Taipei University of Technology, Taiwan,

[3] Department of Chemical Engineering, Kasetsart University, Bangkok 10900, Thailand

*e-mail: syli@dragon.nchu.edu.tw (S.-Y. Li); fengmts@ku.ac.th (M. Saisriyoot)

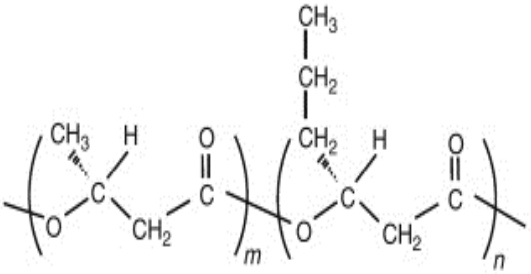
Abstract:

Poly(3-hydroxybutyrate-co-3-hydroxyhexanoate) (PHBH) is a marine-biodegradable polyhydroxyalkanoate (PHA) with increasing relevance as a sustainable alternative to conventional plastics. This study presents a cradle-to-gate life cycle assessment (LCA) of PHBH production in Taiwan, using crude palm oil (CPO) sourced from Thailand and Malaysia. The system boundary includes CPO production, CPO transport, fermentation in a 400-m^3 fermentor (0.63 kg-PHBH/kg-CPO), and extraction (80% recovery). The LCA incorporates both experimental data, i.e., fermentation conditions and extraction recipes, and practical assumptions for operational details that are typically not reported in the literature but are based on established industrial practices, including air compression, liquid transfer, centrifuge efficiency, and other critical process parameters. Additionally, a model incorporating theoretical oxygen transfer and utilization in fermentation is developed and considered in the LCA to quantify emission sensitivity to oxygen demand. Results show that PHBH extraction is the largest carbon hotspot, contributing 37% of the total global warming potential (GWP) in the Base case (12.04 kg-CO_2eq/kg-PHBH), due to high electricity demand for aeration and agitation. The Base/OUR-OTR provides the GWP of 11.31 kg-CO_2eq/kg-PHBH, a 6 % reduction. Substituting Malaysian CPO significantly reduces emissions to 9.05 kg-CO_2eq/kg-PHBH, owing to a trade-off between biogenic carbon flows (CC-B) and land-use change emissions (CC-LUC). Renewable energy integration, including solar electricity and biomass steam, further reduces GWP to 7.57 kg-CO_2eq/kg-PHBH, achieving a 16.4 % reduction from the fossil-based baseline. Notably, PHBH extraction is dominated by material-related CC-F emissions, particularly from surfactants and NaOCl, highlighting the importance of chemical selection in downstream processing.

EFFICIENT PRODUCTION AND CHARACTERISTICS OF BIOBASED AND BIODEGRADABLE POLYHYDROXYALKANOATES FROM OIL PALM WASTES

Kumar Sudesh
School of Biological Sciences, Universiti Sains Malaysia, 11800 Penang
e-mail: ksudesh@usm.my

Abstract:
Plastic waste has become a serious global problem. A recent study indicated that large quantities of microplastics are accumulated in oceans, and these then enters our food chain. Various measures have been implemented to reduce plastic pollution, but the problem keeps growing. Polyhydroxyalkanoates (PHA) is one of the promising alternatives that has been identified to substitute non-biodegradable petroleum-based plastics. PHA can be efficiently biosynthesized by certain bacteria from sugars and vegetable oils. Malaysia is the second largest producer and exporter of palm oil. The palm oil industry generates oily by-products that can be used as low-cost feedstock for the large-scale production of PHA. In addition, huge amounts of underutilized palm biomass such as the fronds and old oil palm trunks are potential feedstock for PHA production. Currently, efficient microorganisms that have been genetically modified are used to produce various types of PHA from both sugars and oils derived from the palm biomass. The characteristics of these PHA can be controlled by adjusting the molar fractions of the monomer units in the copolymer. Rigid, soft, flexible and/or PHA with different opacity can be produced for various applications. Finally, to further reduce the cost of producing PHA, a unique biological recovery process has been developed which employs insects such as mealworm to extract and purify the PHA granules from the bacterial cells. These processes are being scaled up and the feasibility studies are ongoing in collaboration with industry.



Poly(3-hydroxybutyrate-*co*-3-hydroxyhexanoate)

(PHBHx)

Figure 1.
Chemical structure of PHA copolymer and an example of its application.

SORGHUM STEM JUICE VALORIZATION TO PRODUCE BIOETHANOL: PROCESS SIMULATION AND LIFE CYCLE ASSESSMENT

Jutima Tantrakool,[1] Aye Myat Theint Kyaw,[2] Penjit Srinophakun,[2] Anusith Thanapimmetha,[2] Maythee Saisriyoot,[2] Khemmathin Lueangwattanapong,[2] and Nutchapon Chiarasumran[2,*]
[1]Master of Engineering Program in Sustainable Energy and Resources Engineering, Faculty of Engineering, Kasetsart University, Bangkok, Thailand
[2]Department of Chemical Engineering, Faculty of Engineering, Kasetsart University, Bangkok, Thailand
*e-mail: fengnpc@ku.ac.th

Abstract:
The increasing global demand for renewable raw materials has intensified interest in bioethanol as a versatile chemical feedstock. This study adopts an industrial ecology perspective to valorize sorghum stem juice, a low-value agricultural byproduct associated with Thailand's furniture industry. Although limited utilized, it contains fermentable sugars that render it a promising substrate for bioethanol production. Two process scenarios were evaluated, the first utilized a mixture of sorghum stem juice and sugarcane molasses, while the second relied solely on molasses, a conventional feedstock. Process simulation was conducted using Aspen Plus V14 to optimize the bioethanol production pathway, achieving an ethanol purity of 95%. In parallel, a life cycle assessment (LCA) was performed to evaluate the environmental impacts of both scenarios within the context of Thailand's expanding bio-based sector. The LCA was conducted using a cradle-to-gate approach and a functional unit of 1 kg of bioethanol. The results indicated that the co-utilization of sorghum stem juice and sugarcane molasses had more environmental benefits, with a global warming potential (GWP) of 5.71 $kgCO_2eq$, compared to 8.42 $kgCO_2eq$ for the molasses-only pathway. The major environmental impacts were primarily attributed to the reliance on nonrenewable energy sources in Thailand and the sugarcane cultivation stage.

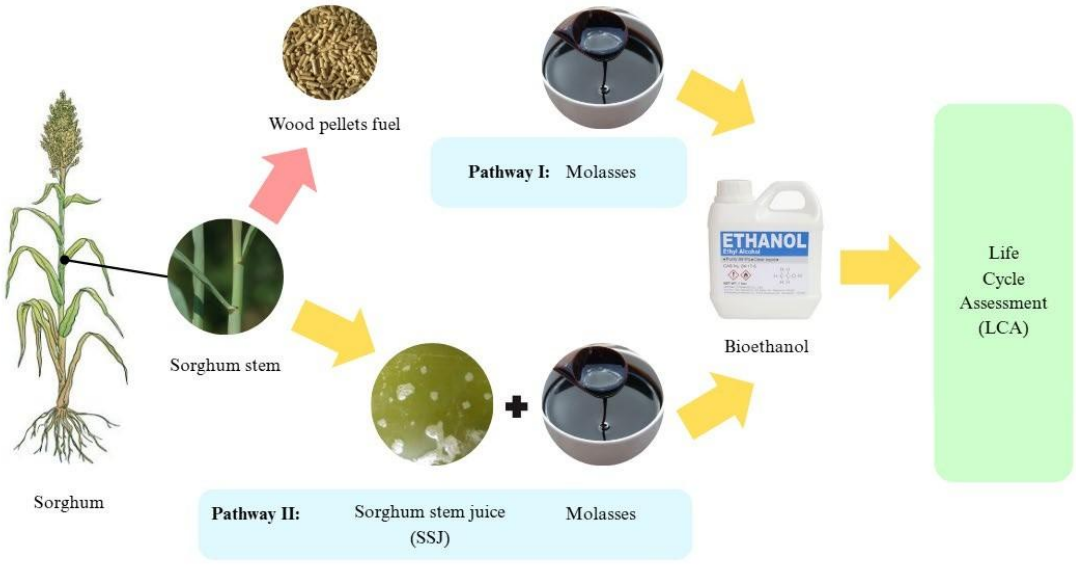


Figure 1.
Bioethanol production pathways from sorghum and molasses for LCA

A NOVEL DESIGN OF INTERMITTENT WATERWHEEL CARBON FIXATION BIOREACTOR

Mei-Chen Ko,[1] Le-Vi Yang,[1] Yan-Yu Chen [1,*]
[1]Department of Chemical Engineering, National Chung Hsing University, No. 145, Xingda Rd., South Dist., Taichung, 40227, Taiwan (R.O.C.)
*e-mail: annayyc0707@dragon.nchu.edu.tw

Abstract:
This study introduced a waterwheel-type bioreactor for low-energy carbon fixation. A wheel with biofilm-loaded blades swept intermittently through a shallow nutrient pool, promoting efficient gas-liquid contact. This design converted gravitational potential energy into kinetic energy, reducing dependence on external pumps and lowering capital costs. Computational fluid dynamics simulations were used to assess the following operating variables: blade number (8, 16, or 32 blades), rotational speed (0.1, 1, or 10 rpm), and gas feed rate (1 cm^3/s, 1 cm^3/min, or 1 cm^3/h). Gas-trajectory plots for the 8-, 16-, and 32-blade wheels (Fig. 1a-c) revealed that under identical speeds and flows, the 16-blade wheel produced richer collision paths than the others. A gas distribution analysis of the 16-blade wheel (Fig. 1d) further indicated that the internal contact area decreased when the speed exceeded 10 rpm, suggesting enhanced mixing and residence time near bioactive surfaces at modest speeds. Operating at 1-10 rpm with a gas feed of 1 cm^3/min concentrated more than 50% of the airflow in and around the wheel. This condition ensured frequent gas-biofilm encounters on blade surfaces. The operating window that balanced mixing efficiency and energy use with minimal energy demand was adopted for subsequent biological validation experiments.

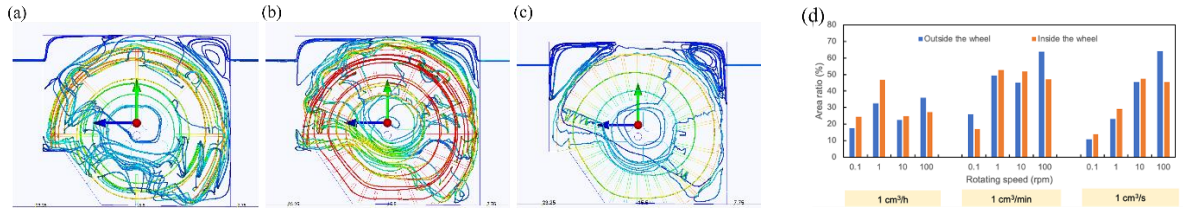


Figure 1.
CFD simulation results diagram of fluid behavior: (a) 8 blades, (b) 16 blades, and (c) 32 blades. (d) The fluid area contact with the 16-blade in the statistical charts of the results of water wheels.

BACTERIAL CELLULOSE: GENOME ANALYSIS OF STRAINS PRODUCING CELLULOSE FROM SUCROSE

Toshiharu Yakushi,[1] Morio Ishikawa,[2] Naoto Tonouchi[3,]*
[1]Yamaguchi University, Japan
[2]Tokyo University of Agriculture, Japan
[3] Bio-Polymer Research, Japan.
*e-mail: naoto.tonouchi@outlook.jp

Abstract:
Some kinds of acetic acid bacteria produce large amounts of cellulose, called bacterial cellulose (BC). This cellulose is known as nata de coco (Figure (a)). This cellulose has the ultrafine network structure (Figure (b)) and the unique properties such as high purity, high strength, high water retention and biocompatibility. At present, it is used practically as a speaker diagram and artificial skin, however, it is expected to be used widely in industry.

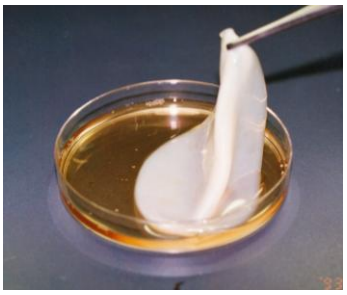
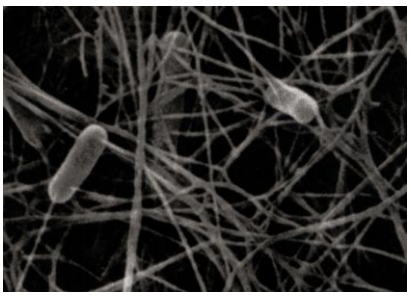
(a)  (b) 

Figure 1.
(a)Bacterial cellulose produced in the static culture (nata de coco). (b) Ultrafine network structure of bacterial cellulose.

Bio-Polymer Research (BPR) was a project to construct an industrial production system of bacterial cellulose. In this project, we have many isolated and mutant strains for efficient production of cellulose from sucrose as the carbon source. In this study, the new information from the genome analysis of these strains will be presented, including the topics below.

The first topic is characterization of the isolated strains. We have isolated four efficient cellulose-producing strains from sucrose. These strains have a common phenotype; no oxidation ability of acetate or lactate, previously identified as *Acetobacter xylinum* subsp. *nonacetoxidans*. However, through the several changes of the taxonomic system, re-identification of these strains was essential. Genome analysis revealed that these isolated strains were close to *Komagataeibacter xyli*nus, but they should be classified as a new species of *Komagataeibacter*.

The second topic is about the levansucrase gene. Levansucrase (LS) is the extracellular enzyme and the key enzyme for sucrose utilization, but some of the mechanism is still unknown. Two types of LS (Type I and II) were reported in acetic acid bacteria, but the distribution pattern is not clear. Actually, both types were reported in *K. xylinus*. Genome analysis revealed that all the isolated strains have Type I LS, and no Type II gene was observed. Further, we have an LS-deficient mutant strain (BPR3003D). A mutation was found in the LS gene of the mutant (G101D). The effect of the mutation on the enzyme activity will be discussed.

ENHANCING BIOTRANSFORMATION OF CASSAVA PULP TO BIOMETHANE WITH LIQUID HOT WATER AND MICROBIAL PRETREATMENTS

Saengmany Phommakod,[1] Suppanut Varongchayakul,[1] Warinthorn Songkasiri,[2] Pawinee Chaiprasert[1,*]
[1]Biotechnology Program, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
[2]National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Pathum Thani, Thailand
*e-mail: pawinee.cha@kmutt.ac.th

Abstract:
Cassava pulp (CP), a major agro-industrial byproduct of cassava starch processing in Thailand, contains high residual organic matter, making it a potential feedstock for anaerobic digestion. However, much of its starch is trapped within the lignocellulosic cell wall, which limits biodegradability. This study investigated two pretreatment strategies to improve CP conversion: (a) liquid hot water (LHW) under optimized conditions, and (b) microbial hydrolysis and fermentation of starchy lignocellulose using *Clostridium manihotivorum* CT4^T (CT4^T), both aimed to disrupt the cell wall structure of CP and solubilized hemicellulose and starch into saccharides as well as enhancing volatile fatty acids (VFAs) production for biomethane generation. Under the selected optimum LHW condition (186.67 ºC and 6.97 min), glucose was released at 444 mg/gTS-CP, along with detectable amount of galactose, xylose, L-arabinose and mannose. Inhibitory compounds, including furfural and hydroxymethylfurfural, were presented only at low concentrations (0.031 and 0.032 g/L, respectively). Biochemical methane potential tests of LHW-pretreated CP showed a biomethane yield of 328±2.59 mL/g VS and substrate degradation efficiency of 75.0±2.28%, representing a 35% improvement over untreated CP and reducing the anaerobic digestion time from 22 d to 10 d. These results demonstrated that LHW was an efficient, chemical-free pretreatment for enhancing CP biodegradability. In the biological pretreatment, CP hydrolysis and fermentation by CT4^T found only low sugar accumulation (0.21–0.24 mg/mL) but generated substantial yields of acetic acid (0.24–0.28 g/g VS) and butyric acid (0.29–0.32 g/g VS). Subsequent methanogenesis, initiated with a syntrophic-methanogenic consortium and fed with the VFAs-rich leachate, biomethane yielded of 325±3.94 mL/g VS, with a substrate degradation efficiency of 66.8±1.79%; a 30% improvement compared to untreated CP. Both LHW and CT4^T effectively disrupted the CP cell wall, releasing starch that was readily utilized and completely degraded. These pretreatment strategies significantly enhanced CP conversion to biomethane in a shorter time than non-pretreated CP. Overall, LHW and CT4^T provide environmentally friendly and promising approaches for accelerating and improving biomethane production in the cassava starch industry.

EFFECTS OF THAI HERBAL EXTRACTS ON MITIGATING ALACHLOR-INDUCED ER STRESS IN *Saccharomyces cerevisiae*

Pham Ngoc Nhi Huynh[1,2] and Choowong Auesukaree[1,2]*
[1]Department of Biotechnology, Mahidol University, Bangkok, Thailand
[2]Mahidol University- The University of Osaka Collaboration Research Center for Bioscience and Biotechnology, Bangkok, Thailand
*e-mail: choowong.aue@mahidol.ac.th

Abstract:
Alachlor is a chloroacetanilide herbicide used to control broad leaf weeds and annual grasses in agricultural crops such as corn, soybean, and sorghum. Due to its intensive application, alachlor has been detected in soil and water resources worldwide at concentrations exceeding safety limits. In *Saccharomyces cerevisiae*, prolonged exposure to alachlor has been reported to result in increased reactive oxygen species (ROS) accumulation and the activation of antioxidant defenses. This study aimed to investigate the protective potential of three Thai medicinal extracts, namely *Cissus quadrangularis* L. (CQ), *Moringa oleifera* Lam (MO) and *Mucuna pruriens* (L.) DC. (MP), in alleviating alachlor-induced oxidative stress. Yeast cells exposed to alachlor and supplemented with ethanolic CQ, MO, or MP exhibited significantly enhanced growth compared with untreated controls. Moreover, all three extracts markedly decreased intracellular ROS levels compared with untreated controls, reflecting strong antioxidant capacity. These findings indicate that ethanolic extracts of CQ, MO, and MP play a protective role against alachlor-induced oxidative stress, likely through their antioxidant and cytoprotective properties. Overall, our results highlight the potential of these Thai herbal extracts, particularly in ethanolic form, as natural candidates for mitigating herbicide-induced oxidative damage.

BIOFILM STRUCTURAL DIFFERENCES IN *Mycolicibacterium parafortuitum* IMPACT ON CELL COLONIZATION AND PYRENE DEGRADATION

Kallayanee Naloka,[1] Satoko Suzuki,[2] Felipe Vejarano,[2] Prinpida Sonthiphand,[3] Nuttapon Pombubpa,[4] Kenshi Suzuki,[2] Chiho Suzuki-Minakuchi,[2,5] Masaki Shintani,[6] Hideaki Nojiri,[2,5] and Onruthai Pinyakong[1,4,*]
[1]Center of Excellence in Microbial Technology for Marine Pollution Treatment (MiTMaPT), Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
[2]Agro-Biotechnology Research Center, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan
[3]Department of Biology, Faculty of Science, Mahidol University, Bangkok, Thailand
[4]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
[5]Collaborative Research Institute for Innovative Microbiology, The University of Tokyo, Tokyo, Japan
[6]Department of Engineering, Graduate School of Integrated Science and Technology, Shizuoka University, Shizuoka, Japan
*e-mail: onruthai.p@chula.ac.th

Abstract:
Polycyclic aromatic hydrocarbon contamination poses a significant environmental challenge. This study investigates the roles of biofilm architecture in pyrene degradation by *Mycolicibacterium parafortuitum* strains D3 and PO1. The rough colony D3 was isolated from soil using fluorescence-activated cell sorting, while the smooth colony PO1 was obtained from a pyrene-degrading consortium. Although D3 and PO1 share 99.9% genome identity and identical pyrene degradation genes, their degradation efficiencies differ significantly. Under static and stress conditions (37°C, pH 6, 5% NaCl) over 9 days, D3 achieved only 25% pyrene degradation compared to 72% by PO1. Genomic analysis revealed variations in genes related to biofilm formation, including the NlpC/P60 family protein and a putative FdhF/YdeP oxidoreductase. These genetic variations may impact protein function and biofilm characteristics. High biofilm production in the rough D3 strain appears to inhibit cell displacement, leading to lower pyrene degradation. Fluorescent 3D imaging and scanning electron microscopy revealed that D3 formed upward-growing, tree-like biofilms, three times taller than the flat, widespread biofilms formed by PO1. This hindered direct contact with surface-coated pyrene crystals and restricted cell movement. This research underscores the critical influence of biofilm different architecture impact on cell displacement and the efficiency of pyrene degradation by *Mycolicibacterium parafortuitum*.

GLUTAMATE-INDEPENDENT PRODUCTION OF POLY-γ-GLUTAMIC ACID BY *Bacillus subtilis* FSO3: MEDIUM OPTIMIZATION AND BIOMASS VALORIZATION POTENTIAL

Thanaporn Wichai[1], Emmanuel O. Opadokun[2], Nindi Syahputri Lubis[2], Nunthida Limsettho[2], Panaya Kotchaplai[1,3,4]*

[1]Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, Thailand

[2]Program in Biotechnology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand

[3]Center of Excellence in Bioconversion and Bioseparation for Platform Chemical Production, Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, Thailand

[4]Water Science and Technology for Sustainable Environment Research Unit, Chulalongkorn University, Bangkok, Thailand

*Corresponding author: E-mail: panaya.k@chula.ac.th

Abstract:

Bacillus subtilis FSO3, a strain previously isolated from a traditional Thai fermented soybean product, forms a distinctive slimy colony. Analysis of its extracellular polymeric substances (EPS) confirmed that poly-γ-glutamic acid (γ-PGA) is the major component. As a water-retentive biopolymer, the γ-PGA-rich fermentation medium from this strain has previously been shown to retain soil moisture and improve the germination of waxy corn (Sweet Violet F1). To better understand and optimize the production of γ-PGA, in addition to genomic characterization, we used a Plackett-Burman experimental design to evaluate key factors influencing both cell growth and γ-PGA synthesis. Our results showed that cell turbidity, a measure of growth, was significantly affected by glucose, yeast extract, and glutamic acid. However, γ-PGA production was influenced by only two factors: glucose and yeast extract. This finding is crucial as it confirms that *B. subtilis* FSO3 is a glutamate-independent γ-PGA producer, making its cultivation more cost-effective. Furthermore, the strain's ability to utilize both glucose and xylose for γ-PGA synthesis suggests its potential for valorizing lignocellulosic biomass. These findings highlight the biotechnological significance of *B. subtilis* FSO3 and provide a basis for optimizing its cultivation toward sustainable γ-PGA production.

Session IV.
Biodiversity, Natural Products and Applications

LIFESPAN EXTENSION MEDIATED BY METHIONINE METABOLITE

Masaki Mizunuma
Hiroshima University, Japan
e-mail: mmizu49120@hiroshima-u.ac.jp

Abstract:
Aging research is an extremely important issue not only for clarifying the mechanisms of biological aging, but also for understanding human aging and extending “healthy lifespan”. In aging research, eukaryotic model organisms such as yeast, nematodes, Drosophila, and mice have been extensively studied. In fact, studies using these model organisms have led to the identification of many lifespan regulators that the basic principles of aging. In particular, insulin-like signals, oxidative stress, and calorie restriction have been found to be factors in the regulation of lifespan.

Recently, it has become clear that metabolites have other important roles in addition to metabolism. For example, NAD^+, which is important for redox reactions, has been shown to regulate aging through post-translational modifications of proteins such as deacetylation. Thus, elucidation of new functions of metabolites is an important issue in terms of both basic and applied research.

We found that stimulating the synthesis of methyl group donor *S*-adenosylmethionine (SAM) extends lifespan in budding yeast. Specifically, since SAM is biosynthesized from Met and ATP, the consumption of Met and ATP by high SAM production induces Met limitation and activates AMP-dependent kinase Snf1 (energy sensor and longevity gene), respectively. Interestingly, *S*-adenosylhomocysteine (SAH), a competitive inhibitor of SAM methylation reactions, extends lifespan in yeast and *C. elegans*. This is because SAH induces Met restriction and AMPK activation by enhancing SAM synthesis. Furthermore, inhibition of TOR complex 1 (target of rapamycin) and induction of autophagy were observed, which are lifespan extending effects reported for Met restriction. As described above, we found a novel activity of the metabolite, in which SAH behaves as a signaling molecule.

Hence, we are currently analyzing the health benefits of SAH in detail using yeast and nematodes.

STRATEGY FOR HETEROLOGOUS PRODUCTION OF NEW PEPTIDES BASED ON GENOME MINING

Shinya Kodani
College of Agriculture, Academic Institute, Shizuoka University, Japan
e-mail: kodani.shinya@shizuoka.ac.jp

Abstract:
In recent years, genome mining has demonstrated that gene clusters for the biosynthesis of lanthipeptides are widely distributed in bacteria. To utilize these gene clusters, establishing a method for producing these peptides is necessary. Our group has been performing heterologous biosynthesis of ribosomally synthesized and post-translationally modified peptides (RiPPs) such as lasso peptides and graspetides using hosts such as *Escherichia coli*. In this presentation, I will present successful examples of heterologous biosynthesis of new peptides in my laboratory. Particularly, we have achieved heterologous production of lanthipeptides from biosynthetic gene clusters of bacteria that have not been screened so much previously, such as ktedonobacteria and myxobacteria.[1-3] Notably, the myxobacterial lanthipeptides, melittapeptins, demonstrated strong and specific antibacterial activity against the Gram-positive bacterium *Micrococcus luteus*. I will present strategy for the heterologous biosynthesis of new peptides being undertaken in my laboratory.

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HARNESSING BIOTECHNOLOGY FOR ANTIMICROBIAL RESISTANCE SURVEILLANCE AND DETECTION: PATIENT TO ENVIRONMENT; GENOTYPING TO GENOME SEQUENCING

Hui-min Neoh
The National University of Malaysia, Malaysia

Abstract:
Antimicrobial resistance (AMR) is a global health challenge in the 21st century. Morbidity and mortality due to infections caused by AMR pathogens such as methicillin-resistant *Staphylococcus aureus* and extended-spectrum beta-lactamase (ESBL)-producing Enterobacterales contribute significantly to the burden of disease, especially in low- and middle-income countries. Development of antimicrobials is important for treatment; nonetheless, timely diagnostics and surveillance of both nosocomial and community sources of transmission will be crucial to stop transmission and might even prevent initiation of infection. We started employing biotechnological strategies for AMR pathogen surveillance and tracking in Hospital Canselor Tuanku Muhriz (HCTM), teaching hospital of the National University of Malaysia from 2009. Our efforts successfully identified circulating and changes of MRSA clones, outbreaks of ESBL-producing Klebsiella pneumoniae, and the HCTM hospital environment microbiome. This initiative is now expanded to the community, with investigations into silent carriage of AMR pathogens in marginalized migrant communities of Klang Valley, Malaysia.

GC-MS PROFILING OF *Piper Sarmentosum*: IMPACT OF SOLVENT SELECTION ON PHYTOCHEMICAL EXTRACTION

Narmatha Gurumoorthy[1], Yong Sze Min[1], Ong Pei Feng, Nurriza Ab Latif[1] and Nurzila Ab Latif[1]*
Department of Biosciences, Faculty of Science, Universiti Teknologi Malaysia, 81310 UTM Skudai, Johor, Malaysia
*Corresponding author: nurzila@utm.my

Abstract:
Piper sarmentosum, commonly known as daun kaduk and a member of the Piperaceae family, has been extensively studied for its diverse phytochemical properties using various solvent extraction methods. This research highlights the findings from GC-MS analyses of chloroform, methanol, and ethanol extracts of *P. sarmentosum*, emphasizing the role of solvent type in profiling bioactive compounds. Chloroform extracts revealed key phytochemical constituents such as myristicin, asarone, caryophyllene, and fatty acids, with significant cytotoxic activity against chronic myelogenous leukemia (CML) K562 cells. Methanolic extracts demonstrated the presence of phenolic and flavonoid compounds, contributing to antimicrobial effects against *Streptococcus mutans* and *Streptococcus sobrinus*, along with biofilm inhibition. Ethanolic extracts, particularly from shade-dried leaves, identified six vital essential oils, including asarone, and showed higher yields of phenolic (186 mg GAE/g) and flavonoid content (242 mg QE/g) compared to aqueous or oven-dried extracts. These findings emphasize the influence of solvent polarity and extraction conditions on the qualitative and quantitative outcomes of GC-MS profiling. This comparative analysis of GC-MS data demonstrates the potential of *P. sarmentosum* as a source of diverse bioactive compounds. By optimizing solvent systems, future studies can refine the extraction process to maximize the therapeutic applications of these phytochemicals.

Keywords: *Piper sarmentosum*, GC-MS, K562, phytochemical, antioxidant, anticancer, cytotoxicity, dental plaque-causing bacteria.

BIOLOGICAL ACTIVITIES AND MECHANISMS OF DMC DERIVATIVES IN HUMAN COLON CANCER CELL LINES

Atchara Janthong,[1] Kraikrit Utama,[2] Nopawit Khamto,[3] Hien Van Doand,[4] Puttinan Meepowpan,[1,5] Padchanee Sangthong[5,6]*
[1]Department of Chemistry, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand
[2]Office of Research Administration, Chiang Mai University, Chiang Mai, Thailand
[3]Department of Biochemistry, Faculty of Medical Science, Naresuan University, Phitsanulok, Thailand
[4]Department of Animal and Aquatic Sciences, Faculty of Agriculture, Chiang Mai University, Chiang Mai, Thailand
[5]Center of Excellence in Materials Science and Technology, Chiang Mai University, Thailand
[6]Division of Biochemistry and Biochemical Innovation, Department of Chemistry, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand
*e-mail: padchanee.sangthong@cmu.ac.th

Abstract:
Natural compounds have attracted growing interest as potential anti-cancer agents due to their generally lower toxicity when compared with conventional chemotherapy. Among these, 2',4'-dihydroxy-6'-methoxy-3',5'-dimethyl-chalcone (DMC), a chalcone derivative extracted from the seeds of *Syzygium nervosum* A. Cunn. ex DC., has shown promising anti-cancer activities. In this study, DMC was structurally modified by introducing an acryloyl functional group to enhance its anti-cancer potential. The most notable compound is DMC modified with a single acryloyl group, designated as 4´-*o*-acryloyloxy DMC, or **1a**, which demonstrated potent cytotoxicity (IC_{50} = 2.49 ± 0.39 µM) and significant activity against HCT116 human colon cancer cells (IC_{50} = 1.14 ± 0.09 µM). The anticancer drug osimertinib which also contains a functional group similar to that of **1a**, **1a** exhibited approximately 1.83fold lower cytotoxicity but 1.35-fold greater activity against HCT116 colon cancer cells (osimertinib IC_{50} = 1.36 ± 0.08 and 1.54 ± 0.09 µM, respectively). Mechanistic investigations revealed that treatment with **1a** effectively activated the extrinsic apoptosis and autophagy signaling pathways before cell cycle progression. These findings suggest that **1a** possesses enhanced anti-cancer efficacy and provide insights into the underlying signaling mechanisms, supporting the development of more effective therapeutic agents for colon cancer.

Ecklonia cava EXTRACT-INCORPORATED SILVER NANOPARTICLES: DUAL THERAUPETIC POTENTIAL AS BIOFUNCTIONAL AGENTS WITH IN VIVO INSIGHTS IN ZEBRAFISH MODEL

Ningrum Tri Purwa,[1,2] Nam-Gyun Kim,[1,3] Tae-Hee Kim,[2,4] Won-Kyo Jung[1,2,4,*]
[1]Major of Biomedical Engineering, Division of Smart Healthcare Major of Biomedical Engineering and New-senior Healthcare Innovation Center (BK21 Plus), Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Jeju Bio Research Center, Korea Institute of Ocean Science and Technology (KIOST), Jeju 63349, Republic of Korea
[4]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
Green synthesis of nanomaterials has gained increasing attention as an alternative to conventional chemical synthesis. In this study, silver nanoparticles (AgNPs) were synthesized using green approach with phlorotannin-rich *Ecklonia cava* extract, which is known for excellent biological activities, such as anti-bacterial and anti-oxidant activities. As the therapeutic efficacy of $AgNP_S$ is highly dependent on particle size, controlling synthesis condition is crucial for biomedical applications. To optimize particle size, response surface methodology (RSM) with Box-Behnken design was applied, analyzing the role of pH, silver precursor concentration, and phlorotannin concentration. A total of 15 experimental combinations were generated through Box-Behnken model. The optimal conditions of 5.15 mM silver nitrate, 5.56 mM phlorotannin, and pH 11.69 yielded particles with a predicted size of 37.19 nm. Antibacterial activity was evaluated through minimum inhibitory concentration assays, showing variable effects across microbial strains, with values ranging from 64 to 1,024 µg/mL. Biofilm inhibition tests revealed the strongest activity at 1,024 µg/mL, whereas lower concentrations often reduced or negated the inhibitory effect, indicating a strong concentration-dependent response. ECP-AgNPs did not exhibit toxicity in zebrafish at concentration below 25 µg/mL. Furthermore, ECP-AgNPs demonstrated significant antioxidative activity at 15-25 µg/mL and protective effects against H2O2-indcued cell death and lipid peroxidation at 5-25 µg/mL. In conclusion, ECP-AgNPs exhibit dual anti-bacterial and anti-oxidative activities. Their potential for biomedical application is promising, although careful attention to concentration is essential due to dose-dependent cytotoxicity.

INVESTIGATION OF THE ANTIOXIDANT ACTIVITY OF A SELECTED COMPOUND DERIVED FROM *Curcuma comosa* ROXB. IN *Saccharomyces cerevisiae*

Trin Tangnararatchakit[1], Anyaporn Sangkaew[1], Apichart Suksamrarn[2], Chulee Yompakdee[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand
[2]Department of Chemistry and Center of Excellence for Innovation in Chemistry, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand
*e-mail: chulee.y@chula.ac.th

Abstract:
Excess reactive oxygen species (ROS) can cause oxidative stress, damaging macromolecules and organelles like mitochondria, and contributing to chronic diseases such as cancer, cardiovascular, and neurodegenerative disorders. Exogenous antioxidant supplementation helps neutralize ROS, preventing cellular damage. *Saccharomyces cerevisiae* is an excellent eukaryotic model for studying oxidative stress due to its highly conserved redox-regulatory pathways with higher eukaryotes. *Curcuma comosa* Roxb. is an abundant source of many bioactive compounds. This study aimed to screen and evaluate the antioxidant activity of pure compounds derived from *C. comosa*. Using DPPH and ABTS assays to screen compounds with *in vitro* antioxidant activity, ASCY181 showed the highest antioxidant activity among thirteen compounds tested with 70.13% and 81.9% in the DPPH and ABTS assays, respectively. To further investigate the *in vivo* antioxidant capability, intracellular ROS levels and cell viability in wild-type and Δ*sod2* mutant yeast were measured. ASCY181 significantly protected the wild-type strain from H_2O_2-induced oxidative stress by markedly reducing intracellular ROS levels. However, its efficacy was diminished in the Δ*sod2* mutant strain, where only a slight reduction in ROS levels was observed. Taken together, our findings indicate that *SOD2* is crucial for the protective role of ASCY181 against oxidative stress. Nonetheless, whether ASCY181 engages additional mechanisms contributing to its antioxidant activity remains to be investigated.

BACTERIAL COMMUNITY STRUCTURE AND DIVERSITY IN AGRICULTURAL SOILS ACROSS NORTHEAST THAILAND

Pakkawan Kamolklang[1,*], Ratmanee Chanabun[2,3], Rungdawan Wongsamart[1], Naraporn Soomboonna[1,4]

[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

[2]Program in Animal Science, Faculty of Agricultural Technology, Sakon Nakhon Rajabhat University, Sakon Nakhon 47000, Thailand

[3]Biodiversity and Utilization Research Unit, Center of Excellence in Modern Agriculture, Sakon Nakhon Rajabhat University, Sakon Nakhon

[4]Multi-Omics for Functional Products in Food, Cosmetics and Animals Research Unit, Chulalongkorn University, Bangkok 10330, Thailand

*e-mail: Pakkawan7716@gmail.com (Pakkawan Kamolklang)

Abstract:

Northeastern Thailand depends heavily on agriculture as a key economic activity, with major crops including rice, sugarcane, cassava, rubber, and maize. However, the region faces multiple challenges, including limited water resources due to geographic conditions, unpredictable annual rainfall, and saline sandy soils. These factors have led to the widespread and intensive use of agrochemicals to maintain crop productivity. Each crop species can shape soil bacterial communities through unique root exudates and rhizosphere interactions, while variations in soil type, salinity, and water availability further modulate bacterial diversity. This study used 16S rRNA gene qPCR and sequencing to profile soil bacterial communities from 52 agricultural sites across eight geographic zones, and to investigate crop–soil–bacterial community interactions. NMDS analysis revealed four distinct geographic groups: *Proteobacteria*-Dominated (n=16), *Acidobacteria*-Rich (n=15), Mixed-Balanced (n=17), and Extreme-Unique (n=4), with core phyla including *Proteobacteria*, *Acidobacteria*, *Actinobacteria*, *Firmicutes*, and *Bacteroidetes*. Genus-level analysis showed functional signatures: *Proteobacteria*-Dominated zones harbored *Candidatus Koribacter* and *Rhodoplanes* (nitrogen-cycling specialists), *Acidobacteria*-Rich areas included *Massilia* and *Sphingomonadales* (phosphate-solubilizers and biocontrol agents), Mixed-Balanced systems contained versatile *Acidobacteriales*, while Extreme-Unique sites featured salt-tolerant *Gammaproteobacteria* and plant-beneficial *Rhizobiales*. Soil physicochemical properties varied widely, with 67% of samples showing suboptimal pH (<6.0) and most with low water content (<15%). Environmental vector analysis identified total nitrogen as the primary driver of bacterial community structure (p = 0.022). These distinct functional groups suggest that the characterized bacterial communities may serve as a foundation for developing bacterial community-based management strategies. Future research investigating bacterial inoculants and cultivation practices that promote these beneficial taxa could potentially contribute to improved soil health and agricultural productivity in Northeast Thailand.

TARGETED GENOME EDITING IN *Pleurotus ostreatus* USING PRE-ASSEMBLED CAS9 RIBONUCLEOPROTEIN AND SPLIT-MARKER DONOR DNA TEMPLATE

Tatpong Boontawon[1, 2, *], Takehito Nakazawa[2], Yoichi Honda[2]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand
[2]Graduate School of Agriculture, Kyoto University, Japan
*e-mail: tatpong.b@chula.ac.th

Abstract:
Until recently, the improvement of commercial mushroom strains has relied primarily on traditional breeding methods, which are both time-consuming and labor-intensive. In this study, we employed a plasmid-free genome editing approach using Cas9 ribonucleoprotein (Cas9 RNP) to induce targeted gene mutations in *Pleurotus ostreatus*, one of the most commercially valuable edible mushrooms. Specifically, a pre-assembled Cas9/sgRNA complex designed to target the *pyrG* gene was introduced into fungal protoplasts derived from the wild-type monokaryotic strain PC9. This treatment produced mutant strains resistant to 5-fluoroorotic acid (5-FOA). Sequence analysis of genomic PCR products confirmed the presence of small insertions and deletions at the targeted locus. These findings demonstrate that Cas9 RNP-mediated mutagenesis could be used for molecular breeding in *P. ostreatus* and potentially in the other species of edible mushroom. Moreover, successful gene disruption through split-marker donor DNA template using the Cas9 RNP technique was achieved in the wild-type PC9 strain. This approach effectively addresses the limitations associated with NHEJ-deficient strains in traditional gene-targeting studies and may expand the applicability of precise genome editing in diverse non-model agaricomycetes.

SCALABLE AND GREEN BIOPROCESSES FOR ZWITTERIONIC BIOSURFACTANT PRODUCTION USING MIXED LIGNOCELLULOSIC RESIDUES UNDER ALKALINE FERMENTATION

Nichakorn Khondee[1,*], Khantharot Ditchat[1], Natcha Ruamyat[1], Tuangtip Jaramai[1], Anawin Junsawang[1], and Ekawan Luepromchai[2]
[1]Department of Natural Resources and Environment, Faculty of Agriculture, Natural Resources and Environment, Naresuan University, Phisanulok, Thailand
[2]Center of Excellence in Microbial Technology for Marine Pollution Treatment (MiTMaPT), Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
*e-mail: nichakornk@nu.ac.th

Abstract:
To advance scalable and sustainable biosurfactant production, this study developed an integrated green bioprocess combining efficient zwitterionic biosurfactant production with environmentally friendly downstream operations. An alkaliphilic bacterium was cultivated in a stirred-tank fermenter using mixed lignocellulosic residues as substrates. The production medium comprised two agro-industrial lignocellulosic wastes serving as both carbon and nitrogen sources, together with Na_2CO_3 as an alkaline agent, thereby eliminating the need for conventional medium components. The modified substrate composition resulted in a threefold increase in biosurfactant yield and an eightfold reduction in medium cost compared with the Horikoshi medium using a single residue. Green downstream processes were implemented for biosurfactant recovery, purification, and concentration, including (i) acid precipitation, (ii) freeze-drying, (iii) spray-drying, (iv) hybrid salting-out and de-micellization, and (v) evaporation. These bioprocesses were successfully scaled up from laboratory to pilot scale, utilizing a 1,500 L stirred-tank fermenter with an 800 L working volume. The productivity of zwitterionic biosurfactants exceeded 6 g/L, and recovery efficiencies across all downstream processes remained above 80%. Lignin, identified as the major residual impurity, was consistently recovered at concentrations above 5 g/L. The combined biosurfactant–lignin fractions were formulated into eco-friendly agents for agro-environmental applications. A biosurfactant–lignin–citric acid formulation achieved 96% and 82% removal of Cu and Cr from industrial wastewater sludge, respectively. Meanwhile, a biosurfactant–lignin–vegetable oil formulation acted as an effective bioherbicide, causing biomass reductions of 91% and 92% in *Tridax procumbens* L. and *Dactyloctenium aegyptium* (L.) Willd., respectively. This integrated bioprocess demonstrates a scalable and sustainable strategy for waste valorization and the production of bio-based products for agricultural and environmental applications.

Session V.
Agriculture Biotechnology

BIOSYNTHETIC REGULATION AND BIOLOGICAL ACTIVITIES OF UV-ABSORBING COMPOUNDS IN CYANOBACTERIA

Hakuto Kageyama
Meijo University, Japan
e-mail: kageyama@meijo-u.ac.jp

Abstract:
Cyanobacteria are found all over the Earth, including extreme environments such as salt lakes and deserts, and they have unique molecular mechanisms to adapt to various environmental stresses. UV-absorbing compounds, which are biosynthesized in response to UV radiation stress, are one of the important compounds in the survival strategy of cyanobacteria. Well-known UV-absorbing compounds in cyanobacteria are mycosporine-like amino acids (MAAs) and scytonemin. In addition, we recently discovered novel UV-absorbing oxylipin compounds, saclipins, from a cyanobacterial strain endemic to Japan. It has been found that the biosynthesis of UV-absorbing compounds in cyanobacteria is affected not only by UV radiation stress but also by various environmental stresses. The physiological effects that these UV-absorbing compounds can exert in cyanobacteria are an interesting research topic. In this presentation, we would like to report on our research on the regulatory mechanism of the biosynthesis of MAAs and saclipins, as well as the useful effects of these compounds from an applied perspective.

THE APPLICATION OF RNA TECHNOLOGIES TO DRIVE INNOVATIONS IN ANIMAL HEALTH

Timothy Mahony,[1,*] Jodie Robinson,[1] Tatiana Briody,[1] Sandy Jarrett[2], Elizabeth Fowler[2]
[1]Centre for Animal Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia QLD 4072, Australia
[2]Animal Science, AgriScience, Department of Primary Industries, Dutton Park QLD 4102, Australia
*e-mail: t.mahony@uq.edu.au

Abstract:
The human population continues to grow and is predicted to approach 10 billion by 2050, consequently there is a parallel imperative that agricultural productivity must also increase to adequately feed this number of people. In the past agricultural productivity gains have largely been achieved by expanding production footprints. However, there is increasing focus of how agriculture impacts on global sustainability in the context of climate change, with methane produced by ruminants in particularly sharp focus. Notwithstanding their cultural importance in many societies, the capacity of ruminants to convert low quality forage in areas otherwise unsuitable for food production suggests they will have an enduring role in global food security. A pathway forward while addressing these multiple juxtapositions would be to address the losses in current production systems. Pests and diseases are major limiters of livestock productivity and addressing their impacts would provide a pathway to increased availability of edible protein in a sustainable manner.

Where available, vaccines have clearly improved animal productivity. However, there are many endemic and transboundary diseases for which effective and fit for purpose vaccines are not available. The existing vaccines have mostly been developed using a standard pipeline where the development of a vaccine is dependent on the capacity to isolate and propagate the pathogen of interest. The accelerated maturing of mRNA vaccines through unprecedented investment due to the COVID-19 pandemic has provided an opportunity to addressing the deficits in veterinary medicine and enable the development of more effective vaccines for many livestock diseases. This presentation will examine the capacity of RNA based vaccination to improve the control of the transboundary disease, lumpy skin disease virus (LSDV). It will describe how RNA platforms could be the pathway to the development of an LSDV vaccine that enables has the capacity for differentiating infected from vaccination animals (DIVA). DIVA capacity is an essential element for the eradication of endemic diseases and control of exotic diseases. The LSDV example serves as a blueprint for how RNA technologies could provide the flexibility to develop effective vaccines for pests and diseases that have proved recalcitrant to conventional vaccine development pipelines. These productivity gains are essential to ensure that the world's population of the future have equitable access to sustainably produced high quality protein.

RECENT PROGRESS AND PROSPECTS IN MOLECULAR GENETICS AND APPLICATION OF MUSHROOM-FORMING FUNGUS, *Pleurotus ostreatus*

Yoichi Honda[1*]
[1] Graduate School of Agriculture, Kyoto University, Japan
* Email: honda.yoichi.5n@kyoto-u.ac.jp

Abstract:
Mushroom forming fungi have been studied for edible and medicinal uses and some of them are cultivated all over the world. Most of the mushroom forming fungi belong to basidiomycetes and have various life styles belonging to saprophytic, parasitic and symbiosis forms; some of saprophytic fungi can degrade plant cell wall components including recalcitrant aromatic polymer, lignin. These lignin-degrading white-rot fungi have been a focus of research aiming for pretreatment of lignocellulosic resources for biorefinery and degradation of environmental pollutants. More recently, there is a new trend away from the traditional biotechnology that applies mushroom mycelium as eco-friendly bioresources to produce mycelial materials and meat alternatives. In this talk, recent progress of molecular genetics in an edible, medicinal, cultivated and white-rot fungus, *Pleurotus ostreatus* (oyster mushroom) will be reviewed with an example of molecular breeding of sporeless cultivars by combining post-genomics and genome editing. Moreover, a new approach to develop 'cell wall engineering' for sustainable mycelial products are introduced.

Keywords: *genetic transformation, genome editing, CRISPR/Cas9, cell wall engineering.*

POTENTIAL APPLICATIONS OF *Z*-ISOMER-ENRICHED CAROTENOIDS IN THE FOOD, COSMETIC, AND FEED INDUSTRIES

Masaki Honda[1,2,*]
[1]Department of Chemistry, Faculty of Science & Technology, Meijo University, 1-501 Shiogamaguchi, Tempaku-ku, Nagoya, Aichi 468-8502, Japan
[2]Graduate School of Environmental and Human Sciences, Meijo University, 1-501 Shiogamaguchi, Tempaku-ku, Nagoya, Aichi 468-8502, Japan
*e-mail: honda@meijo-u.ac.jp

Abstract:
Carotenoids are a class of naturally occurring pigments whose dietary presence has been demonstrated to confer health benefits in humans. Moreover, carotenoids have diverse applications across the food, cosmetic, and animal feed industries. As carotenoids contain multiple conjugated double bonds in the molecule, a large number of geometric (*E/Z*, *trans/cis*) isomers are theoretically possible. In general, (all-*E*)-carotenoids are the most prevalent geometric isomers in nature, exhibiting high crystallinity and low solubility in various media, which leads to their low processing efficiency and bioavailability. In recent years, technological developments to improve the processing efficiency and bioavailability of carotenoids by means of *Z*-isomerization have been gaining in importance (Figure 1). *Z*-Isomerization of carotenoids induces significant alterations in their physicochemical properties (e.g., solubility and crystallinity), resulting in enhanced processing efficiency and bioavailability. Furthermore, several studies have shown that the *Z*-isomerization improves biological activities of carotenoids, e.g., anti-inflammatory and anti-cancer activities as well as skin-quality improving action. This presentation outlines the recent advancements in isomerization technology of carotenoids as well as the potential applications of materials rich in carotenoid *Z*-isomers.

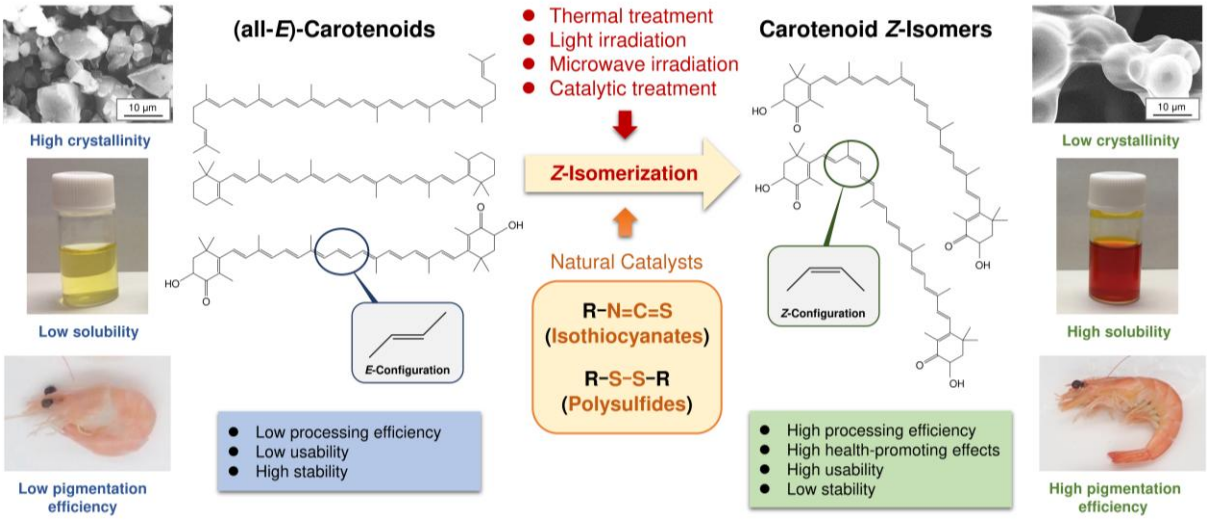

Figure 1.
Overview of carotenoid isomerization studies.

MICROBIAL-BASED BIOINSECTICIDES, BIOHERBICIDES AND BIOFUNGICIDES: A SUSTAINABLE APPROACH TO PEST, WEED AND DISEASE CONTROL

Alongkorn Amnuaykanjanasin[1*], Rudsamee Wasuwan[1], Wachiraporn Toopaang[1], Chettida Srisuksam[1], Somruetai Jaiyen[1], Nuchnudda Wichienchote[1], Wararom Jampanya[1], Varangkana Junda[1], Siwarin Sriket[1], Maenam Nuangchaiyot[1] and Morakot Tanticharoen[2]
[1]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 113 Thailand Science Park, Paholyothin Rd., Tambon Khlong Nueng, Amphoe Khlong Luang,
Pathum Thani 12120, Thailand
[2]Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Bangkok 10150, Thailand
*e-mail: alongkorn@biotec.or.th

Abstract

Thailand's rich microbial biodiversity offers great potential for sustainable agriculture by reducing reliance on imported chemical pesticides. Our work focuses on the development of microbial-based bioproducts for managing insect pests, weeds, and plant diseases.

Beauveria bassiana BCC 2660 and *Metarhizium anisopliae* BCC 4849, two entomopathogenic fungi, exhibited high efficacy against insect pests. A formulation combining *B. bassiana* with neem oil reduced whitefly (*Bemisia tabaci*) populations by up to 86% over six months. As for culture degeneration observed in entomopathogenic fungi, target of rapamycin (TOR) signaling was linked to attenuated conidiation and virulence against insects in *B. bassiana*. Microbial secondary metabolites are important for insect pathogenesis. The gene *pks15*, for polyketide biosynthesis, is necessary for conidiation, cell wall formation, anti-phagocytosis and virulence. Comparative transcriptomes and metabolomes verified that the gene was associated with production of various secondary metabolites, including bassianolide, siderophores, tenellin, oosporein, and several unidentified secondary metabolites and cell wall remodeling. *M. anisopliae* BCC 4849 also showed high pathogenicity (80-99%) against six pests under laboratory conditions., for example, spider mite (*Tetranychus truncatus*), sweet potato weevil (*Cylas formicarius*) and oriental fruit fly (*Bactrocera dorsalis*). In development of bioherbicides, cell-based *Colletotrichum siamense* TBRC 12768 and *Phoma multirostrata* TBRC 12769 caused 60–98% disease incidence in a broad-leaf weed at 15–20 days after inoculation. By contrast, secondary metabolites from *Lasiodiplodia theobromae* TBRC 15112 induced wilting and collapse of treated weed plants within three days. Biofungicides including *Trichoderma*, *Bacillus subtilis*, and *Streptomyces* effectively inhibited pathogens responsible for root and stem rot in durian, anthracnose, and sooty mold in crops such as coffee and yard-long bean. Our data support the potential of microbial bioproducts to enhance sustainable agricultural practices in Thailand.

Keywords: Bioinsecticide; Bioherbicide; Biofungicide; Biological control; Entomopathogen; Metabolome; Transcriptome

VARIATON OF GROWTH AND YIELD PLASITICITY TO DROUGHT IN HIGH-YIELDING THAI CASSAVA VARIETIES

Monica Ode Adu-Gyamfi[1], Treenut Saithong[2,3], Jittrawan Thaiprasit[3], Tobias Wojciechowki[4], Johannes Postma[4], Saowalak Kalapanulak[2,3*]

[1]Biotechnology Program, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

[2]Bioinformatics and Systems Biology Program, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

[3]Center for Agricultural Systems Biology (CASB), Systems Biology and Bioinformatics Research Group, Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

[4]Institute of Bio- and Geosciences, IBG-2: Plant Sciences, Forschungszentrum Jülich GmbH, Germany

*Corresponding Author email: saowalak.kal@kmutt.ac.th

Abstract

Cassava shows ample genotype variability in morphological traits under varying soil moisture. Understanding these responses is key to improving drought tolerance. We investigated the responses of seven high-yielding Thai cassava varieties by aiming to study their plasticity and acclimation to drought. These genotypes include Rayong 11 (R11), Kasetsart 50 (KU50), Huay Bong 60 (HB60), Kasetsart 72 (KU72), Rayong 72 (R72), Rayong 7 (R7), and Rayong 9 (R9). Herein, cassava plants were planted under various levels of drought stress, from well-watered (80% field capacity [FC], estimated at 72% w/w) to severely stressed levels (70%–20% FC, corresponding to 63% - 18% w/w, respectively) for 22 days, released to re-watering condition (72% w/w) for 15 days. At 30 days after planting under well-watered conditions, R11 had a larger canopy, while KU50 and HB60 had fewer leaves. To account for early differences, relative growth rates across moisture levels were used to build dose-response curves. The results showed distinct genotype responses in leaf number, plant height, stem length, and leaf abscission. KU72 and R72 displayed complex trends, with steady leaf production and stem elongation until growth plateaued. HB60 and KU50 maintained leaf numbers even under drought. R11 was less responsive to moisture changes, while R9 showed steep declines at low %FC, confirming susceptibility. KU72 and R72 slowed growth only at supra-optimal levels (70–80% FC), indicating saturation limits. Upon rewatering, all genotypes except R11 recovered, reinforcing its drought sensitivity. Key plastic traits were root dry mass, stem dry mass, and root–leaf ratio. Overall, KU50, R72, HB60, and KU72 were drought-tolerant, while R9, R11, and R7 were less tolerant. These findings identify critical moisture thresholds and the limited benefit of excess water, guiding cassava breeding for drought resilience.

BIOMASS PRODUCTION OF *in vitro Microchirita involucrata* ROOTS AND EVALUATION OF BIOLOGICAL ACTIVITY OF ROOT CULTURE EXTRACTS ELICITED WITH ELICITORS

Adsadayu Thonnondang[1], Onrut Inmano[2], Anupan Kongbangkerd[2], Apinun Limmongkon[1]*
[1]Department of Biochemistry, Faculty of Medical Science, Naresuan University, Phitsanulok, 65000, Thailand
[2]Department of Biology, Faculty of Science, Naresuan University, Phitsanulok 65000, Thailand
*e-mail: apinunl@nu.ac.th

Abstract:
Microchirita involucrata is a plant from the Gesneriaceae family that produce secondary metabolites with antioxidant and antimicrobial properties. This study aimed to optimize auxin hormone treatments for enhancing root biomass and evaluate the biological activity of culture medium extract under elicitor conditions. Roots were cultured with Indole-3-acetic acid (IAA), 1-Naphthaleneacetic acid (NAA) and Indole-3-butyric acid (IBA) at varying concentrations of 0.5, 1.0, 2.0 and 4.0 mg/L, while methyl jasmonate (MeJA) and cyclodextrin (CD) served as the elicitor. TLC and HPLC were used for metabolite profiling, and antioxidant activity was measured via ABTS assay. Roots treated with 4 mg/L IBA produced the highest biomass (6.11 ± 0.75 g). Elicitation led to medium color changes and intensified TLC bands. HPLC revealed major peaks at 15–25 min retention time, indicating enhanced metabolite accumulation. ABTS assay showed significantly increased antioxidant activity in IBA-treated roots under elicitor treatment. This study demonstrates that optimized hormone application can effectively promote root biomass and bioactive compound production in *M. involucrata*, supporting potential industrial applications.

EXTREMOPHILIC CYANOBACTERIA AND THEIR PHOTOPROTECTIVE COMPOUNDS

Sasiprapa Samsri,[1] Stephen Brian Pointing,[2] Hakuto Kageyama,[3,4] Rungaroon Waditee-Sirisattha[1,*]

[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Phayathai Road, Pathumwan, Bangkok 10330, Thailand

[2] Department of Biological Sciences, National University of Singapore, Singapore 117557, Singapore

[3]Department of Chemistry, Faculty of Science and Technology, Meijo University, 1-501 Shiogamaguchi, Tenpaku-ku, Nagoya, Aichi 468-8502, Japan

[4]Graduate School of Environmental and Human Sciences, Meijo University, 1-501 Shiogamaguchi, Tenpaku-ku, Nagoya, Aichi 468-8502, Japan

*e-mail: Rungaroon.W@chula.ac.th

Abstract:

Ozone depletion has increased the amount of solar UV radiation reaching the Earth's surface, leading to a growing interest in naturally occurring photoprotective compounds found within ecosystems. One promising group of UV-screening compounds is mycosporine-like amino acids (MAAs), known for protecting cells by converting harmful UV energy into heat, without generating reactive oxygen species. Most known MAAs are currently produced by cyanobacteria, particularly extremophilic types that thrive in harsh environments. This study aims to provide insights into the production of MAAs by exploring the evolutionary relationships and diverse gene cluster arrangements involved in MAA biosynthesis among extremophilic cyanobacteria. We observed the accumulation of MAAs from unique xerophilic, halophilic, and thermophilic cyanobacteria by modulating environmental conditions such as desiccation, salinity, and thermal stress. By understanding the genetic and environmental factors that influence MAA biosynthesis, this research supports the use of cyanobacteria in sustainable strategies to produce natural UV-screening compounds for many biotechnological applications.

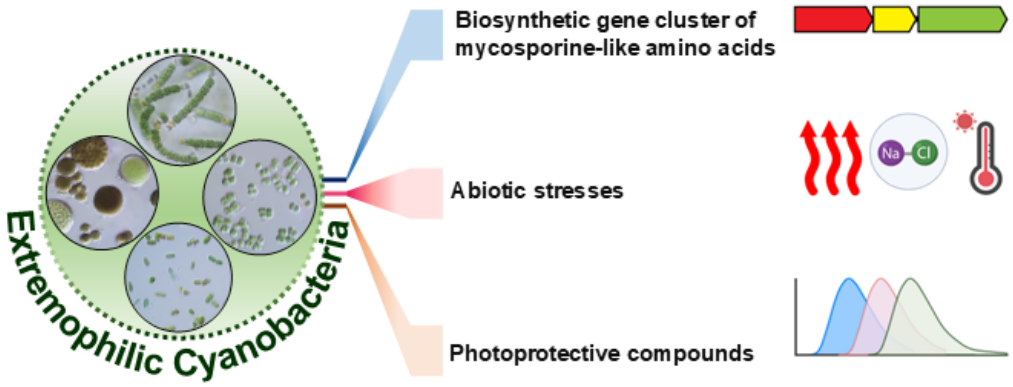

Figure 1.

GELLING AGENT-FREE TEMPORARY IMMERSION MICROPROPAGATION OF *LABISIA PUMILA*: A COST-EFFECTIVE APPROACH

Nurnadiah Roslan,[1]*
[1]Forestry Biotechnology Division, Forest Research Institute Malaysia (FRIM), Malaysia
*e-mail: nurnadiah@frim.gov.my

Abstract:
The sustainable commercial production of medicinal plants requires propagation systems that are both cost-efficient and scalable. This study presents a micropropagation protocol for the valuable Southeast Asian medicinal herb *Labisia pumila* (*L. pumila*) using a temporary immersion system (TIS) in combination with gelling agent–free nutrient media to improve production efficiency. The method involves the cultivation of explants in liquid nutrient media without solidifying agents, which are periodically immersed briefly in an automated temporary immersion system to ensure maximum uptake of nutrients and aeration, with limited incidence of hyperhydricity. *L. pumila* has traditionally been multiplied by seeds or vegetative cuttings, which are time- and labour-intensive, limiting their suitability for large-scale production. Compared to conventional gelled-nutrient media micropropagation, this gelling agent-free TIS protocol lowers material costs by eliminating agar and reduces handling time, hence decreasing labor costs. In order to overcome these further, a comprehensive cost analysis of plant micropropagation through tissue culture was conducted, taking into account reagent components, water and electricity usage and labor wages relative to *in vitro* activities excluding fixed costs such as laboratory infrastructure and equipment. The primary expenses were to trained labor for plantlet transfer and electricity consumption, particularly during sterilization and growth stages. Uniformity and quality check between the immersion cycles was maintained by standard immersion time, regular inspection of the explant condition which together minimized contamination and physiological abnormalities even in the absence of a gelling agent. Of most importance is that gelling agent–free nutrient media was cost-effective and scalable, offering a feasible and practical system for the sustainable production and conservation of *L. pumila*.

ANTIFUNGAL ACTIVITY OF *Priestia aryabhattai* PTKU-123 CRUDE EXTRACT AGAINST *Fusarium* spp. ASSOCIATED WITH DURIAN DIE-BACK DISEASE

James Konkov, Nisit Watthanasakphuban, Paiboon Tunsagool*
Special Research Incubator Unit of Fermentomics, Department of Biotechnology, Faculty of Agro-Industry, Kasetsart University, Bangkok, Thailand
*email: paiboon.tu@ku.ac.th

Abstract:
Durian (*Durio zibethinus*) production is increasingly threatened by fungal pathogens, including *Fusarium* spp., that was recently discovered to be implicated in die-back disease. Sustainable alternatives to synthetic fungicides are urgently required. This study investigated the antifungal potential of crude metabolites produced by *Priestia aryabhattai* strain PTKU-123. The bacterial isolate, maintained on nutrient agar, was fermented in Luria-Bertani broth, and metabolites were recovered through acid precipitation and ethanol extraction. Crude extracts were profiled using thin-layer chromatography (TLC), which revealed bands with Rf values consistent with lipopeptide fractions, as confirmed by ninhydrin and iodine staining. Antimicrobial efficacy was assessed using the poison food technique against *Fusarium* spp., a pathogen isolated from diseased durian tissue and validated by morphological and ITS-based identification. The crude extract significantly inhibited fungal growth in a concentration-dependent manner, with complete inhibition achieved at 5 mg/mL. These findings highlight *P. aryabhattai* PTKU-123 as a promising biocontrol candidate for durian disease management and provide a foundation for further purification and characterization of its antifungal metabolites.

BIOLOGICAL PROPERTIES OF ALKALINE LIGNIN EXTRACT FROM LONGAN PEEL FOR COSMETIC APPLICATION

Kittiya Phiguntong[1], Jidapha Tinoi[2,3,*]
[1]Interdisciplinary Program of Biotechnology, Multidisciplinary and Interdisciplinary School, Chiang Mai University, Chiang Mai, Thailand
[2]Department of Chemistry, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand
[3]Center of Excellence in Materials Science and Technology, Chiang Mai University, Chiang Mai 50200, Thailand
*e-mail: jidapha.tinoi@cmu.ac.th

Abstract:
Longan peel is a significant by-product generated in large quantities during the processing of longans. It has been found to contain lignin, an essential component with biological properties. The purpose of this study was to extract and apply lignin as a cosmetic ingredient. Lignin was extracted from the longan peel using an alkaline extraction method under autoclave conditions. A dark brown alkaline lignin powder was obtained, with a yield of approximately 2.7% and a purity of 82.21%. The lignin particle size distribution ranged from 340 to 460 nm and had a granular shape. FTIR analysis confirmed the typical polyphenolic structure of lignin with guaiacyl enrichment and the presence of carbonyl groups. The antioxidant properties of alkaline lignin were investigated using DPPH and ABTS assays. The results showed that the lignin extract exhibited good antioxidant activity, with IC50 values of 14.84 ± 0.15 and 7.31 ± 0.23 µg/mL, respectively. Moreover, alkaline lignin exhibited tyrosinase inhibitory activity of approximately 50% at a concentration of 1.52 µg/mL, corresponding to 2.46 ± 0.56 mg KAE/g extract in kojic acid equivalents. The cell cytotoxicity of lignin was investigated using the MTT method using the L929 fibroblast cell. The results demonstrated that cell viability significantly decreased, with an IC50 of 19.41 µg/ml. This research indicated that alkaline lignin extract from longan peel possesses potent antioxidant activity and remarkable tyrosinase inhibition, suggesting its potential as a cosmetic ingredient in skincare formulations. However, it remains necessary to assess cytotoxicity at higher concentrations further.

FUNCTIONAL STUDY OF *Litopenaeus vannamei* ALPHA-2-MACROGLOBULIN AND WHITE SPOT SYNDROME VIRAL PROTEIN TARGETS IN RESPONSE TO WHITE SPOT SYNDROME

Kittisak Chawichan[1], Saengchan Senapin[2,3], Tipachai Vatanavicharn[1], Bunyarit Meksiriporn[1], Sirikwan Ponprateep[4,5*]

[1]Department of Biology, School of Science, King Mongkut's Institute of Technology, Ladkrabang, Bangkok, Thailand

[2]Fish Health Platform, Center of Excellence for Shrimp Molecular Biology and Biotechnology (Centex Shrimp), Faculty of Science, Mahidol University, Bangkok, Thailand

[3]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Pathum Thani, Thailand

[4]Research Unit in Stem Cell Innovation and Tissue Engineering, Srinakharinwirot University, Bangkok, 10110, Thailand

[5]Department of Chemistry, Faculty of Science, University of Srinakharinwirot, Thailand

* Corresponding author: sirikwanp@g.swu.ac.th

Abstract:

Alpha-2-macroglobulin (A2M) is involved in several immune pathways, such as the blood clotting system, phagocytosis, and melanization. In White Spot Syndrome Virus infected shrimp, the mRNA expression level of *Litopaneaus vannamei*-A2M (*Lv*-A2M) was up-regulated in the shrimp hemocyte. In addition, the recombinant *Lv*A2M protein (r*Lv*A2M) can stimulate the shrimp immune-related genes and can reduce viral infectivity. To explore the anti-viral mechanism, yeast two-hybrid screening showed the interaction between *LV*A2M and several viral proteins (WSSV076, WSSV144, and WSSV454). The recombinant WSSV076, WSSV144, and WSSV454 were produced using the *E. coli* expression host and purified to confirm the viral-host interaction using indirect ELISA. The protein-protein interaction of *Lv*A2M and its cognate partners, WSSV076 and WSSV144, demonstrated binding activity against *Lv*A2M. Additionally, molecular docking analysis was performed to determine the binding epitope of each protein partner. WSSV076 and WSSV144 bind to *Lv*A2M at non-overlapping epitopes. However, the function of WSSV076 and WSSV144 remains to be characterized; the identification of specific viral-host proteins provides a foundation for understanding the molecular mechanisms underlying shrimp antiviral immunity.

Session VI.
Food Biotechnology & Food Security

mycoSMART: A PORTABLE DEVICE FOR MULTIPLEX DETECTION OF MYCOTOXINS

Nitsara Karoonuthaisiri
The National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand
e-mail: nitsara.kar@biotec.or.th

Abstract:
Mycotoxins are one of the key threats to food safety due to their harmful effects on human and animal health. Climate change has exacerbated the frequency and severity of mycotoxin co-occurrence, underscoring the urgent need for rapid, accurate, and cost-effective detection systems to monitor and control their entry into the food chain. We therefore developed and validated a multiplex microarray-based lateral flow immunoassay integrated with a portable reader for on-site, simultaneous detection of five regulated mycotoxins: aflatoxin B1 (AFB1), T-2 toxin (T2), zearalenone (ZEA), deoxynivalenol (DON), and fumonisin B1 (FB1). The assay operates on a competitive binding principle, with microarray spot signals generated using an in-house designed and synthesized novel luminescent organic dye. These signals are captured and analyzed by a portable reader equipped with a user-friendly interface. The sample preparation method was developed to be environmentally friendly and features a simple, ultrafast extraction protocol. The assay demonstrated reliable performance across a wide range of concentrations, achieving recovery rates of 75–127%, comparable to those obtained by LC-MS/MS. Limits of detection for AFB1, T2, ZEA, DON, and FB1 were 1.80, 1.21, 1.39, 1.17, and 0.56 μg/kg, respectively. This validated system offers a practical, point-of-care solution for the simultaneous detection and quantification of multiple mycotoxins in rice and rice-based products.

FLAVOR FORMATION DURING FOOD FERMENTATION

Inthawoot Suppavorasatit [1,*]
[1]Department of Food Technology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand
*e-mail: inthawoot.s@chula.ac.th

Abstract:
Flavor development in fermented foods is driven by complex biochemical and thermochemical reactions initiated by microorganisms and shaped by processing conditions. This presentation highlights the mechanisms of aroma formation during food fermentation using two representative models: thua nao (Northern Thai fermented soybean) and cocoa. In thua nao, controlled fermentation with Bacillus subtilis enhanced desirable aroma-active compounds—particularly organic acids, alcohols, and pyrazines—while reducing lipid oxidation–derived volatiles responsible for off-notes, as demonstrated through GC–MS/O, SAFE, AEDA, OAV, and omission studies. These analyses identified key contributors to nutty, smoky/woody, and fermented notes that govern sensory perception in both black and yellow soybean products. Similarly, in cocoa, controlled postharvest fermentation and drying promoted the formation of precursor molecules that, upon roasting, yielded a wider range of aroma-active compounds associated with chocolate, roasted, floral, and fruity attributes, while minimizing undesirable aldehydes from uncontrolled oxidation. Sensory results in both models confirmed that process control is critical for achieving superior aroma quality and product consistency. Together, these findings demonstrate that microbial selection, precursor management, and controlled fermentation environments are essential strategies for directing flavor pathways and enhancing consumer acceptance in fermented foods.

AMR IN THE AGRICULTURAL ENVIRONMENT

Nobuyuki Kijima
Institute of Food Research, National Agriculture and Food Research Organization
*E-mail:kijima.nobuyuki995@naro.go.jp

The discovery of penicillin heralded a new era in the treatment of infectious diseases, but the emergence of antimicrobial resistance, AMR has become serious problem in our lives. Antimicrobial agents are now being used not only for medical purposes but also for food production., accounting for almost 60 % of total consumption in Japan. Of these, six antimicrobial agents, including human-applicable streptomycin and oxytetracycline can be applied as agricultural chemicals.

We focus on the agricultural environment, particularly prevalence of antibiotic-resistant bacteria in the edible parts of fresh produces as One Health approach.

Microbial analysis of the edible parts of organic lettuce by culture dependent methods showed that bacterial population was 5 Log CFU/g on non-selective agar medium, R2A and 3 Log CFU/g on selective agar medium, R2A with streptomycin, SM (40mg/L). And thirty percent of SM resistant isolates survived in higher levels of SM, 120-1200 mg/L. Genetic analysis of these isolates revealed that well-known genes for SM resistance in clinical isolates, only conferred low-level resistance, 40-80 mg/L and were not involved in resisting higher levels of SM.

These results suggest that major genetic factors for SM resistance in agricultural environment may be different from clinical scenes.

Keywords: AMR; agricultural environment; agricultural chemicals; streptomycin

DIVERSITY OF MDR *Enterobacteriaceae* IN THAI MEAT PRODUCTS

Soraya Chaturongakul
Institute of Molecular Biosciences, Mahidol University
e-mail: soraya.cha@mahidol.ac.th

Abstract:
Enterobacteriaceae represents a large family of Gram-negative bacteria, with numerous members recognized as ESKAPE pathogens. This group of antimicrobial resistant (AMR) bacteria causes nosocomial infections and serves as an indicator of food safety and water quality. Contamination of food or the environment with these bacteria can lead to serious illnesses. Moreover, AMR is often synonymous with multidrug resistance (MDR), meaning the bacteria are resistant to multiple drugs and standard antibiotic treatments become ineffective. Therefore, both monitoring of the prevalence of MDR *Enterobacteriaceae* and in-depth understanding of their genomic diversity are necessary. In this research, we investigated MDR *Enterobacteriaceae* from meat products in Thailand. Our results showed high prevalence of *Escherichia coli*, *Klebsiella* spp., and *Salmonella enterica* in local meat products at 72%, 72%, and 54%, respectively. Co-contamination percentages were also high e.g., 73% for *E. coli Klebsiella* spp. and 47% for *Klebsiella* spp.-*S. enterica*. Antibiotic susceptibility tests, both microbroth dilution and disk diffusion methods, were applied to assess the MDR properties. Ampicillin resistance was the most common AMR property in *E. coli* and *Klebsiella*, while streptomycin resistance was the most common in *S. enterica*. Extended-spectrum beta lactamase (ESBL) strains were also identified. Colistin resistance was found in six *E. coli* isolates and four *Klebsiella* isolates. Genomic studies of these isolates further indicated that corresponding resistance genes are located on the plasmids, raising the alarm that MDR *Enterobacteriaceae* incidence, particularly ESBL and colistin-resistant strains, in Thailand is transmissible and continues to pose a serious problem. A conjugation study also confirmed that plasmid-mediated transfer contributes to the diversity of MDR isolates. Overall, this study demonstrated that the prevalence of MDR *Enterobacteriaceae* in the Thai local market is at a critical level. Systemic strategies are essential to mitigate the contamination levels and to lower the chances of MDR foodborne infections in consumers.

PROCESS OPTIMIZATION OF LIQUEFACTION IN ENZYMATIC HYDROLYSIS OF WASTE BREAD USING RESPONSE SURFACE METHDOLOGY

Hsu Yadanar Htun[1], Natta Laohakunjit[1]*, Nattapon Kaisangsri[2], Apiradee Uthairatanakij[3], Punchira Vongsawasdi[4], Ratchadaporn Kaprasob[2], Orrapun Selamassakul[2]
[1]Division of Biochemical Technology, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
[2]Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
[3]Division of Postharvest Technology, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
[4]Department of Microbiology, Faculty of Science, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
*e-mail: nutta.lao@kmutt.ac.th

Abstract:
Enzymatic hydrolysis is an eco-friendly and efficient approach for converting starchy waste into fermentable sugars. Expired bread is a rich source of carbohydrates, that can be valorized as a renewable raw material in creating functional products, rather than being discarded as waste. In the enzymatic hydrolysis of starch-rich substrates such as waste bread, liquefaction is a crucial first step that directly influences the efficiency of the subsequent saccharification process. In this study, the liquefaction step was optimized using a response surface technique with Box-Behnken Design to determine the best conditions for fungal α-amylase activity prior to saccharification by examining the combined effects of enzyme concentrations (X_1), temperature (X_2), and pH (X_3). There were three center points out of a total of 15 experimental runs. The highest concentrations of total sugar (459.29 g. L^{-1}) and reducing sugar (331.57 g. L^{-1}) were obtained at 3% enzyme concentration, temperature 45─50°C and pH 5─6. The highest dextrose equivalent (44.21%) was also observed at 3% enzyme concentration, 50°C and pH 5. Thus, the optimal liquefaction conditions were 3% enzyme concentration, temperature 50°C and pH 5─6. This study revealed that effective liquefaction optimization is essential for efficient hydrolysis and sustainable utilization of waste bread.

DEVELOPMENT AND CHARACTERIZATION OF CELLULOSE ACETATE/CHITOSAN FILMS INCORPORATED WITH *Piper betel* EXTRACT FOR ANTIMICROBIAL FOOD PACKAGING

Prapot Kumhang[1], Piyarat Khanthawaro[2], Nichapat Takiaw[1]
Thanaporn Srichomphu[1], Thanaporn Srichomphu[1], Songsirin Ruengvisesh[1] *
[1]Department of Microbiology, Faculty of Science, King Mongkut's University of Technology Thonburi, Bangkok, 10140, Thailand
[2]Food Safety Center, Institute for Scientific and Technological Research and Services, King Mongkut's University of Technology Thonburi, Bangkok, 10140, Thailand
*email: songsirin.rue@kmutt.ac.th

Abstract:
This study investigated the development of chitosan/cellulose acetate (CS/CA) composite films incorporated with Piper betel leaf extract (PBE) for potential food packaging applications. The films were prepared by optimizing the cellulose acetate (CA) concentration to achieve a balance between mechanical strength, transparency, and flexibility. The optimal formulation, 1% chitosan and 0.12% cellulose acetate, was selected for incorporating varying concentrations of PBE (0%, 1%, 1.5%, and 2%). The films were characterized for thickness, light transmittance, tensile strength, extensibility, color, and antimicrobial activity. Results indicated that increasing the concentration of PBE enhanced the antimicrobial properties, with films containing 1% PBE exhibiting significant inhibition against *Salmonella* Newport (16.09 ± 0.30 mm), *Salmonella* Typhimurium (17.21 ± 0.51 mm), and *Listeria innocua* (18.14 ± 0.49 mm). The 1% PBE formulation achieved the best balance of mechanical strength (34.43 ± 1.99 MPa), extensibility (1.66 ± 0.28 mm), and moderate transparency (27.70±2.0% transmittance), making it a promising candidate for food packaging applications. Although higher PBE concentrations (1.5% and 2%) further improved antimicrobial activity, they reduced film transparency and whiteness. Overall, the developed CS/CA-PBE films may provide a sustainable and active packaging solution, offering enhanced food safety and extended shelf life, which contributes to the growing demand for eco-friendly alternatives in the food industry.

DISCREPANCIES OF ANTIMICROBIAL RESISTANT GENOTYPES AND PHENOTYPES IN FOODBORNE BACTERIA *Vibrio parahaemolyticus* FROM AQUATIC BIRD FECES IN THAILAND

Wijitra Khaosoong[1], Yuki Matsumoto[2], Shota Nakamura[2], Tetsuya Iida[3,4], Carla N. Mavian[5], Chonchanok Muangnapoh[1]*
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
[2]Department of Infection Metagenomics, Bioinformatics Center, Research Institute for Microbial Diseases (RIMD), The University of Osaka, Suita, Osaka 565-0871, Japan
[3]Department of Bacterial Infections, Research Institute for Microbial Diseases (RIMD), The University of Osaka, Suita, Osaka 565-0871, Japan
[4]Center for Infectious Disease Education and Research, The University of Osaka, Suita, Osaka 565-0871, Japan
[5]Emerging Pathogens Institute, Department of Pathology, College of Medicine, University of Florida, Gainesville, Florida, USA
*e-mail: chonchanok.m@chula.ac.th

Abstract:
Vibrio parahaemolyticus is a foodborne pathogen associated with seafood and marine environments, but it has also been detected in wildlife and environmental reservoirs. In this study, we isolated and characterized antimicrobial resistance (AMR) of *V. parahaemolyticus* from aquatic bird feces in Thailand. Antimicrobial susceptibility testing of confirmed *V. parahaemolyticus* isolates were performed by the Kirby–Bauer disc diffusion method, and whole-genome sequencing (WGS) was used to characterize AMR determinants. A total of 12 *V. parahaemolyticus* were isolated from 33.3% (5/15) of the collected samples. All isolates were resistant to streptomycin, while resistance to ampicillin (8/12; 66.7%) and gentamicin (2/12; 16.7%) was also observed. In contrast, WGS revealed no known streptomycin- or gentamicin-resistance genes, suggesting possible involvement of chromosomal mutations or uncharacterized mechanisms. On the other hand, β-lactamase genes (*bla*$_{\text{CARB}}$) were identified in all isolates, and the quinolone resistance gene of the *qnrVC* family (*qnrVC6*) was detected in one isolate (8.3%). Notably, *qnrVC6* was located on the chromosome and associated with mobile genetic elements. Our findings suggest that aquatic birds may act as carriers of AMR *V. parahaemolyticus*. The phenotype–genotype discrepancies warrant further investigation and highlight the importance of One Health-based surveillance integrating wildlife, environment, and foodborne pathogens.

IMPACT OF BACTERIOPHAGE CONTAMINATION FROM SILAGE ON YOGURT FERMENTATION

Noppakorn Thadasawate[1], Jeeranan Kamchai[1], Suratsa Nuansakun[1], Punyawee Dulyayangkul[2], Thanyaporn Srimahaeak[1,*]
1 Department of Biotechnology, Faculty of Engineering and Industrial Technology, Silpakorn University, Nakhon Pathom 73000, Thailand
2 Laboratory of Biotechnology, Chulabhorn Research Institute, Bangkok 10210, Thailand
*e-mail: srimahaeak_t@su.ac.th

Abstract:
Silage is a common fermented feed used in dairy cattle diets and is considered a possible source of bacteriophages that can contaminate raw milk and disrupt yogurt fermentation. This study investigated phage contamination in silage samples collected from small-scale dairy farms in Ratchaburi, Thailand, across three seasons (2024–2025). No phages were detected in summer, while silage samples from the rainy and dry seasons showed concentrations of 4.8×10^3 and 2.5×10^5 PFU/g, respectively, from which 36 and 31 phage isolates were picked and purified. Host range analysis revealed that the commercial starter culture *Lactobacillus delbrueckii* spp. *bulgaricus* YB01 was susceptible to all rainy-season phages, whereas none of the dry-season phages infected this strain. Bacteriophages were grouped into five infectivity levels based on Efficiency of Plating (EOP) values ranging from 0.01 to 4.39. Representative phages from each group were selected for yogurt fermentation tests. Phage contamination delayed fermentation, increasing the final pH from 4.29 to 4.52 and loosening the yogurt's texture. These findings highlight the seasonal impact of silage-derived phages on yogurt quality and emphasize the need for monitoring phage contamination in dairy production.

LATERAL FLOW DIPSTICK ASSAY FOR DNA-BASED DETECTION OF *Ochratoxin* A PRODUCING FUNGI IN COFFEE

Nachapon Mathupo[1,3], Lin Yunyi[1,2], Sunita Chamyuang[1,2] and Amorn Owatworakit [1,2,3]*
[1]School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand
[2]Microbial Product and Innovation Research Center, Mae Fah Luang University, Chiang Rai 57100, Thailand
[3]Coffee Quality Research Center, Mae Fah Luang University, Chiang Rai 57100, Thailand
*e-mail: Amorn@mfu.ac.th

Abstract:
Ochratoxin A (OTA) is a polyketide mycotoxin produced by *Aspergillus* and *Penicillium* species, posing significant food safety concerns in coffee. Their occurrence is primarily associated with post-harvesting processing and storage conditions. In this study, we present a rapid and sensitive polymerase chain reaction–lateral flow dipstick (PCR-LFD) assay for the detection of OTA-producing fungi in coffee samples. This procedure requires three main steps:(1) PCR amplification of DNA fragments specific to the polyketide synthesis gene (*pks*), OTA synthesis gene was used as a species-specific marker; (2) an allele-specific extension reaction using thermocycle PCR with specific primers with a 141 bp fragment of the *pks* gene. This procedure was evaluated for specificity with the OTA-producing fungal strain (*A. carbonarius*) and the non-OTA-producing strain (*A. flavus*) and (3) rapid visual detection of the extension products using a dipstick assay. The PCR-LFD test exhibited for detecting OTA-producing strains, with a detection limit of 50 fg of fungal genomic DNA. Thus, this method provides a rapid and sensitive method to monitor the toxigenic strain of fungal contamination in coffee.

CHARACTERIZATION AND SCREENING OF FLAVOR-PRODUCING non-*Saccharomyces* YEASTS FOR FERMENTATION APPLICATIONS

Manutsanun Boonyanuwat[1] Thamonwan Tassanaset[1] Jirasin Koonthongkaew[1,*]
[1] Department of Microbiology, Faculty of Sciences, Chulalongkorn University, Thailand
*e-mail: Jirasin.K@chula.ac.th

Abstract:
The fermentation of alcoholic beverages, such as beer, wine, and distilled spirits, has undergone continuous evolution, both in terms of production processes and the improvement of product aroma and flavor. A key factor influencing beverage quality is yeast, particularly non-*Saccharomyces* yeasts, which contribute to expanding the diversity and uniqueness of flavors and aromas. Non-*Saccharomyces* yeasts were isolated from natural sources, including pineapple fruit, mango leaves, and kale leaves, as well as two sugar factories in Thailand: The Thai Multi-Sugar Industry and the Ratchaburi Sugar Factory. Researchers have suggested that non-*Saccharomyces* yeasts can produce aroma compounds distinct from those generated by *Saccharomyces*, which play a crucial role in contributing to the flavor and aroma of beverages within the same category. The results of the study indicated that *Candida sake* JK315 and JK316 exhibited good fermentation efficiency, as demonstrated by accumulated net CO_2 loss of 1.093±0.387 and 1.243±0.583 g, respectively, which were greater than *S. cerevisiae*, 0.713±0.235 g. Their results revealed the trend in production of primary aroma compounds, tolerance to ethanol concentrations up to 16% v/v, and the ability to grow within a pH range of 2–10. These non-*Saccharomyces* yeasts show promising potential for enhancing alcoholic beverage fermentation and can be used in combination with *S. cerevisiae* to increase aroma diversity. Furthermore, they are amenable to scale-up for assessing fermentation yields and exploring their applications in commercial production.

Special Symposiums

ANTIBACTERIAL ACTIVITY AND FATTY ACID CONTENT OF MANGROVE-DERIVED THRAUSTOCHYTRIDS

Kustiariyah Tarman[1,2*], Qonita Khoirunissa[1], Anto Budiharjo[3], Safrina Dyah Hardiningtyas[1], Souvia Rahimah[4]

[1)] Department of Aquatic Product Technology, Faculty of Fisheries and Marine Sciences, IPB University, Indonesia

[2)] Center for Coastal and Marine Resources Studies, International Research Institute for Maritime, Ocean and Fisheries, IPB University

[3)] Department of Biology, Faculty of Science and Mathematics, Diponegoro University, Indonesia

[4)] Department of Food Industrial Technology, Faculty of Agro-Industrial Technology, Universitas Padjadjaran, Indonesia

*e-mail: kustiaz@apps.ipb.ac.id

Abstract:

Mangrove are coastal ecosystems that not only play essential ecological roles but also harbor unexplored microorganisms, including thraustochytrids. These oleaginous protists are known to produce polyunsaturated fatty acids (PUFA) and bioactive compounds with various biological activities. This study aimed to explore the potential of thraustochytrids isolated from mangroves as a source of antibiotics and fatty acids. Six isolates were screened through antagonistic tests, bioautography, and 2,3,5-triphenyl tetrazolium chloride (TTC) reduction assays. Potential isolates were further cultured and analyzed using well diffusion method for antibacterial activity and fatty acid profiling. Four isolates were verified as thraustochytrids. Antibacterial screening showed that two isolates were active against *Staphylococcus aureus* strongly, while C4(1) also strongly inhibited *Escherichia coli*. Isolate C4(1) produced the highest biomass yield of 3.10 ± 0.19 g/L dry weight. Fatty acid profiles were dominated by palmitic, oleic, and linoleic acids, with linolenic acid (ω-3) detected only in isolate G and trans-fatty acids in C4(1). In conclusion, isolate C4(1) shows potential as an antibacterial agent, and isolate G as a PUFA producer, highlighting the applicative prospects of local thraustochytrids as bioactive and fatty acid sources.

Keywords: antibiotic, omega 3, profiling, protist, PUFA

INSIGHTS INTO UTILIZATION OF CHITIN-CHITOSAN FROM MARINE BY PRODUCTS FOR AGRICULTURAL, PHARMACEUTICAL AND MEDICAL APPLICATIONS

Rath Pichyangkura,[1,*]
Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok. Thailand
*e-mail: Rath.p@chula.ac.th

Abstract:
Chitin-chitosan is one the most abundant biopolymer in nature. It is one of the major components of marine byproducts such as shrimp, crab and mollusk. Chitin can be easily produced from chitinous material such as shrimp shells, crab shells and squid pen, by acid and base treatment. Chitin can then be converted into chitosan by heterogenous deacetylation process by strong base. The biological, chemical and physical properties of chitosan is dependent on degree of polymerization and size distribution of chitin-chitosan. Chitin-chitosan can be applied and utilize in agriculture, as plant grow stimulator, plant yield enhancer, food and feed additive. In pharmaceutical and medical applications chitin-chitosan is used for glucosamine production, drug carrier and anti-inflammation in skincare and cosmetic products. Despite the large amount of research found in the literature, very little application and utilization is present in the real market. This was due to the lack of in-depth knowledge in the mechanism of action and the characteristics and the production standard of chitin-chitosan for different applications.

PRODUCTIVITY AND BIOACTIVITY OF *Spirulina platensis* CULTIVATED IN INCLINED PLASTIC COLUMN PHOTOBIOREACTOR

Iriani Setyaningsih[1,*], Desniar[1], Nanda Rizky Harnowo[1], Tjandra Chrismadha[2], Kustiariyah Tarman[1]

[1]Department of Aquatic Product Technology, Faculty of Fisheries and Marine Sciences, IPB University. Jl. Agatis Kampus IPB, Darmaga, Bogor, Indonesia

[2]Research Center for Limnology, National Research and Innovation Agency (BRIN), Bogor, Indonesia (16911)

*e-mail: isetyaningsih@apps.ipb.ac.id

Abstract:

Spirulina platensis (*S. platensis*) is a single-celled cyanobacterium characterized by its spiral shape and blue-green pigments. The cultivation of *S. platensis* has been developed to meet the demands of various industries. This study focuses on the productivity and bioactivity of *S. platensis* cultivated using an inclined plastic column photobioreactor (I-PBR). The research aimed to evaluate the productivity and bioactivity of *S. platensis* cultivated in an outdoor inclined plastic column photobioreactor (I-PBR). The cultivation was carried out using an I-PBR containing 300 L of freshwater, 10 L of *S. platensis* inoculum, and a Zarrouk medium. The cultivation period lasted for 28 days to achieve the desired biomass density. During cultivation, several parameters were monitored, including cell density (measured based on turbidity), temperature, pH, and dry biomass weight. The active compounds identified in *S. platensis* extracts included polyphenols, steroids, and saponins. Biomass productivity reached 126.8 mg/L/day. The total phenolic content of the extracts was 19.11 ± 0.13 mg GAE/g, with an antioxidant activity of 359.25 ± 5.76 ppm. The phycocyanin concentration was 1.01 ± 0.04 mg/mL, and its antioxidant activity was 48.14 ± 0.79 ppm.

Keywords: antioxidant, biomass, microalgae, phycocyanin, Zarrouk

CULTIVATION AND APPLICATION OF CYCLOPOID COPEPOD IN FISH AND SHRIMP HATCHERIES

Paveena Tapaneeyaworawong,[1,2] Maliwan Kutako[3,*] , Sorawit Powtongsook[1,2*]
[1]Integrative Aquaculture Biotechnology Research Group, National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand
[2]Center of Excellence for Marine Biotechnology, Department of Marine Science, Faculty of Science, Chulalongkorn University, Thailand
[3]Faculty of Marine Technology, Burapha University Chanthaburi Campus, Thailand
*e-mail: sorawit@biotec.or.th

Abstract:
Copepods are zooplankton present in both freshwater and seawater environments. They serve as a food source for animals at higher trophic levels within ecosystems. Calanoid copepods can synthesize long-chain polyunsaturated fatty acids, which is relatively uncommon among animals. As a result, copepods are utilized as live feed in aquaculture, particularly in fish larva culture that requires very small zooplankton. Despite their known benefits, the use of copepods remains limited due to factors such as the availability of specific copepod strains, complexity of cultivation, and feeding methodologies. To increase copepod use in aquaculture, technology for mass cultivation has been developed using the local cyclopoid copepod *Apocyclops royi* strain AMBT201601. Owing to its small nauplius size, this strain has been used as live feed for Asian seabass and Pacific white shrimp larviculture. The combination of mixed microalgae feedings and refined cultivation techniques has contributed to improved production yields. Developing a cost-effective and simplified copepod production system is important for supporting hatchery operations.

SUPPLY CHAIN OF SEAWEED AND ITS IMPACT ON BIOPROSPECTING

Heti Mulyati[1], Muhammad Arief Budiman[2], Kustiariyah Tarman[2,3]
[1)] Department of Management, Faculty of Economics and Management, IPB University, Indonesia
[2)] Department of Aquatic Product Technology, Faculty of Fisheries, IPB University, Indonesia
[3)] Center for Coastal and Marine Resources Studies, International Research Institute for Maritime, Ocean and Fisheries, IPB University

Abstract:
The increasing interest in seaweed as a source of functional food, pharmaceutical ingredients, cosmeceuticals, and other biotechnological applications underscores the importance of an efficient supply chain. The seaweed supply chain covers post-harvest handling, transportation, storage, and delivery to processing facilities or end consumers under maintained conditions. Proper supply chain practices are essential to preserve seaweed quality, including its physical condition, chemical composition, biochemical stability, and microbiological safety. Inefficiencies in handling and distribution can lead to structural degradation, quality deterioration, and the loss of high-value bioactive compounds, thereby limiting its potential for bioprospecting. This study highlights the direct relationship between supply chain conditions and the quality, as well the yield of bioactive compounds such as polysaccharides, pigments, and other metabolites that are sensitive to temperature, light, and other physical stress. A comprehensive understanding of these factors is critical for maximizing the value of seaweed in bioprospecting efforts, while also supporting economic sustainability and the preservation of its biological functionality. By identifying key challenges and proposing best practices in seaweed logistics, this paper provides strategic insights for stakeholders across the seaweed industry, from upstream harvesters to downstream processor, regarding the crucial role of supply chain management in maintaining seaweed quality and enhancing its bioprospecting potential.

Keywords: bioactive compounds, distribution, handling, transportation

EFFECT OF NPK FERTILIZATION ON WATER PHYSICOCHEMICAL PROPERTIES AND THE NUTRITIONAL COMPOSITION OF *Ulva lactuca*

Amalia Putri Firdausi[1], Dimas Andrianto[2*], Muhammad Arif Mulya[1], Sri Nuryati[3], Rahman[3], Asma' Fakhriyatul Jannah[2], Nabila Nurul Izzatiddieni[2]

[1]Aquaculture Production Technology and Management Program, Vocational School, IPB University, Bogor, West Java 16680, Indonesia

[2]Department of Biochemistry, Faculty of Mathematics and Natural Science, IPB University, Bogor, West Java 16680, Indonesia

[3]Department of Aquaculture Technology and Management, Faculty of Fisheries and Marine Science, IPB University, Bogor, West Java 16680, Indonesia

*e-mail: dimasandrianto@apps.ipb.ac.id

Abstract:

Seaweed cultivation remains highly dependent on environmental conditions, often resulting in inconsistent yields. To enhance productivity, fertilization strategies such as the optimization of nutrient dosage are increasingly explored. This study investigates the impact of varying NPK fertilizer concentrations on the physicochemical properties of seawater, as well as the protein and fat content of *Ulva lactuca* cultivated using a rope seeding method over 60 days. Five treatments were applied in triplicate: a control (seawater without seaweed), and four fertilized groups with NPK concentrations of 0 ppm, 10 ppm, 20 ppm, and 30 ppm, respectively. Fertilizer was administered every seven days. Proximate analysis was used to determine the biochemical composition of *U. lactuca*. Results indicated that the 30 ppm treatment yielded the highest biomass (29.28 g) and optimal nutritional profile, with protein and fat contents of 17.37% and 6.49%, respectively. These findings suggest that 30 ppm NPK supplementation can significantly improve the growth and nutritional quality of *U. lactuca*, offering a promising approach for more stable and productive seaweed aquaculture.

Keywords: NPK fertilizer, physicochemical, proximate, rope seeding method, *Ulva lactuca*

FIBER DIGESTIBILITY IN THE IN VITRO RUMEN FERMENTATION WITH THE PRESENCE OF MARINE ENDOPHYTIC FUNGI

Sri Suharti[1*], Ade Dimas Kurnia[1], Sheren Nabila[1], Kustiyariah[2], Ali Bain[3], Rahman[3], Komang Gede Wiryawan[1]

[1)] Department of Nutrition and Feed Technology, Faculty of Animal Science, Bogor Agricultural University, Indonesia

[2)] Department of Aquatic Product Technology, Faculty of Fisheries, Bogor Agricultural University, Indonesia

[3)] Faculty of Animal Science, Halu Oleo University, Kendari, Southeast Sulawesi, Indonesia

*e-mail: sri_suharrti@apps.ipb.ac.id

Abstract:

The potential of endophytic marine fungi as fiber degraders in the rumen system has not yet been fully investigated; therefore, further research is needed on the use of marine fungi to promote fiber digestibility in the rumen. This study aimed to evaluate the effect of inoculating endophytic marine fungi isolates on fiber digestibility in an in vitro rumen incubation. The research used a completely randomized design with four treatments and five replications. The treatments included control/C (Napier grass, palm leaves, and concentrate mix with a ratio of 30:30:40, consecutively); C + 1.5% (0.75 ml x 10^6/ml) marine fungi isolate; C + 3% (1.5 ml x 10^6/ml) marine fungi isolate; C + 4,5% (2.25 ml x 10^6/ml) marine fungi isolates. Variables observed were digestibility of crude fiber, neutral detergent fiber (NDF), acid detergent fiber (ADF), cellulose, hemicellulose, lignin, dry matter, and organic matter digestibility (DMD, OMD) at 48 h incubation. The result showed that the addition of marine fungi isolates up to a level 4.5% did not change crude fiber digestibility. In contrast, the content of NDF, hemicellulose, ADF, and lignin significantly decreased ($p \leq 0.05$), and cellulose content increased ($p \leq 0.05$) in the presence of the marine fungi isolate at levels 1.5-2.5 %. The addition of marine fungi at level 4.5% decreased ($p < 0.05$) DMD and OMD. In conclusion, inoculation of marine fungi at a level of 1.5% (0.75 ml x 10^6/ml) has cellulolytic activity and gives a beneficial effect on lignin and fiber digestibility in vitro.

Keywords: fungi; natural-resources; digestibility; fermentation; rumen microbe

RECOMBINANT PROTEINS FOR AQUATIC SCIENCE IN THAILAND: CHALLENGES AND OPPORTUNITIES

Wanchai Assavalapsakul
Department of Microbiology, Faculty of Science, Chulalongkorn University
e-mail: wanchai.a@chula.ac.th

Abstract:
Recombinant proteins, produced from genetically engineered constructs, are evaluated to confirm that they reflect the biochemical and immunological properties of native proteins in aquatic organisms. This validation supports their application in aquaculture for prevention, diagnosis, and control of infectious diseases. In fish health, recombinant proteins can function as immunogens for vaccines or subunit vaccines targeting priority pathogens such as nervous necrosis virus (NNV) and infectious spleen and kidney necrosis virus (ISKNV). They also enable production of specific antibodies in laboratory animals, which can be used to develop serological diagnostics for farmed species, including ELISA and lateral flow tests for Asian seabass, groupers, tilapia, and ornamental fish. Establishing standardized, safe, and effective vaccine evaluation systems for aquatic species, including controlled challenge models, clear potency and efficacy endpoints, and field-relevant trial designs, would strengthen Thailand's capacity to develop fit-for-purpose aquatic vaccines and create opportunities for regional export.

AMORPHOUS CELLULOSE MICROFIBER FROM GREEN SEAWEED *Ulva lactuca* PREPARED WITH HYDROPHOBIC DEEP EUTECTIC SOLVENT AND IN SILICO CHARACTERIZATION

Rizfi Fariz Pari[1,3], Uju[3,4], Wahyu Ramadhan[3,5], Safrina Dyah Hardiningtyas[3],
Rie Wakabayashi[1], Noriho Kamiya[1,2], Masahiro Goto[1]
[1]Department of Applied Chemistry, Graduate School of Engineering, Kyushu University, 744 Motooka, Fukuoka, Japan
[2]Division of Biotechnology, Center for Future Chemistry, Kyushu University, Japan
[3]Department of Aquatic Product Technology, Faculty of Fisheries and Marine Sciences, IPB University, Bogor, Indonesia
[4]Surfactant and Bioenergy Research Center (SBRC), IPB University, Bogor, Indonesia
[5]Center for Coastal and Marine Resources Studies, IPB University, Bogor, Indonesia
e-mail: rizfi-fp@apps.ipb.ac.id

Abstract:
Seaweed cellulose derived from the green seaweed *Ulva lactuca* offers significant industrial potential as a sustainable source for cellulose microfiber (CMF) production. Compared to terrestrial plants, *U. lactuca* is abundant, fast-growing, and largely underutilized. Conventional CMF production typically relies on strong acids such as HCl, which are environmentally harmful and can damage cellulose structure. To address this issue, the present study investigates the use of a hydrophobic deep eutectic solvent (HDES) as a green alternative for cellulose pretreatment. Based on density functional theory (DFT) calculations, a combination of thymol as the hydrogen bond acceptor and decanoic acid as the hydrogen bond donor was selected as the optimal HDES system. Pretreatment was performed at 80 °C for 2 hours, followed by homogenization and sonication. The HDES-pretreated cellulose yielded CMF with an average diameter of 154 nm, comparable to that obtained using HCl pretreatment. Notably, the yield of CMF from HDES treatment (84%) was significantly higher than that from HCl treatment (59%). X-ray diffraction (XRD) analysis revealed that the HDES pretreatment preserved the amorphous nature of cellulose while enhancing its crystallinity index from 6.0% to 31.4%. The resulting CMF exhibited excellent dispersibility in water. Molecular dynamics simulation further elucidated the interaction mechanism between HDES components and cellulose. The hydroxyl group of thymol and the carboxyl group of decanoic acid were found to interfere with the hydrogen bonding network among cellulose hydroxyl groups, facilitating fiber separation and fibrillation. Overall, this study demonstrates that hydrophobic DES can serve as an environmentally friendly and efficient alternative to acid-based pretreatment methods for producing cellulose microfibers from *Ulva lactuca*. This approach highlights the potential of HDES-assisted green processing in advancing sustainable cellulose valorization.

Keywords: amorphous, cellulose microfiber, deep eutectic solvent, green seaweed, hydrophobic

PHAGE THERAPY FOR A SUSTAINABLE STRIPED CATFISH INDUSTRY IN VIETNAM

Hoang A. Hoang[*,1, 2], Trong-Tuong Ho[1, 2], Le P. Nga[1, 2], Tu Q. Vinh[1,2], Dang T.H. Oanh[3], BA Diep[4], Andrew Millard[5], Nguyen T. Trung[6]

[1]Faculty of Chemical Engineering, Ho Chi Minh City University of Technology, HCMC, Vietnam

[2]Vietnam National University Ho Chi Minh City, Thu Duc District, HCMC, Vietnam

[3]College of Aquaculture and Fisheries, Can Tho University, Can Tho, Vietnam

[4]Department of Medicine, University of California, San Francisco, CA, USA

[5]Department of Genetics and Genome Biology, University of Leicester, Uni. Road, Leicester, UK

[6]Institut Européen de Chimie et Biologie, U1212 Inserm, Université de Bordeaux, France

[*]e-mail: hoang.a.hoang@hcmut.edu.vn

Abstract:

Antibiotics are commonly used as the main prevention and treatment of disease-causing bacteria in both human and animals. In agriculture, antibiotic occupies significant niche in food producing animals and plants. In contrast, the antimicrobial resistance (AMR) is a naturally occurring phenomena of microorganisms through which they become resistant to antimicrobial compounds. In Vietnam, a high antibiotic-resistant rate of pathogenic bacteria has been reported in fish farms. Phages are virus infecting bacteria. The use of lytic phages as a prevention and treatment for bacterial diseases in fishery industry has gained serious attention in the last 40 years, especially due to the widespread evolution of antibiotic-resistant bacteria. We will present major achievements of our research group about phage therapy in striped catfish. The research works are in the terms of bacterial isolation, pathogenicity and genome analysis; phage isolation, infection activity, phage genome analysis; and *in vivo* phage trial at wet lab.

Keywords: phage therapy, AMR, genome, striped catfish, bacterial pathogens.

THE NEXT GENERATION OF INTEGRATED ECO-FRIENDLY ANTI-BIOFOULING AND ANTI-BIOCORROSION MARINE NATURAL PRODUCTS

Novriyandi Hanif
Department of Chemistry, Faculty of Mathematics and Natural Sciences, IPB University, Bogor, Indonesia
e-mail: nhanif@apps.ipb.ac.id

Abstract:
Marine organisms are known to biosynthesize complex anti-biofouling secondary metabolites offering a direct source of inspiration for scalable eco-friendly anti-biofouling and anti-biocorrosion agents for maritime industry-related applications. Biofouling and biocorrosion are interconnected issues that cannot be effectively addressed using traditional single-function antifouling or anticorrosion materials. To address these issues, a new approach is needed to search for dual eco-friendly anti-biofouling and anti-biocorrosion marine natural products. Such approach focuses on identifying molecules that aim to meet three key criteria: (1) environmentally friendly and biodegradable molecules with minimal toxicity, (2) biosurfactant properties to prevent microbial adhesion, and (3) disruption of bacterial biofilm formation by interfering with bacterial quorum-sensing (QS) systems, thereby reducing the risk of resistance development. The present study identifies the novel class of marine natural products that function on such requirements.

PHYCOCYANIN FROM *Spirulina platensis*: A GREEN-DERIVED BIOACTIVE FOR SKIN PROTECTION AND NANOCOSMETIC INNOVATION

Safrina Dyah Hardiningtyas[1]*, Iriani Setyaningsih[1], Zahrotul Firdaus[1], Amelia Gustiningtyas[1], Eirene Tentua[1], Noriho Kamiya[2,3]

[1] Department of Aquatic Product Technology, Faculty of Fisheries and Marine Sciences, IPB University (Bogor Agricultural University), Jalan Agathis, Bogor 16680, Indonesia

[2] Department of Applied Chemistry, Graduate School of Engineering, Kyushu University, 744 Motooka, Fukuoka 819-0395, Japan

[3] Division of Biotechnology, Center for Future Chemistry, Kyushu University, Japan

*e-mail: safrina_dyah@apps.ipb.ac.id

Abstract:

Phycocyanin, a natural blue pigment–protein complex derived from *Spirulina platensis*, has gained growing interest for its multifunctional role in skin health. This study presents an integrated approach combining green extraction, bioactivity assessment, and nanodelivery design to enhance phycocyanin's stability and functionality in cosmetic applications. Using natural deep eutectic solvents (NaDES), phycocyanin was efficiently extracted and purified under environmentally friendly conditions while maintaining its native structure. The purified pigment demonstrated strong antioxidant, anti-inflammatory, and photoprotective properties, effectively mitigating UV-induced oxidative stress and promoting skin cell recovery. To overcome its limited stability and poor skin permeability, two complementary delivery systems were developed. The water-based chitosan–phycocyanin nanoparticles improved resistance to light and temperature degradation while enhancing transdermal permeation. In parallel, oil-based nanocarriers—gel-in-oil (G/O) and solid-in-oil (S/O) nanodispersions—facilitated the penetration of phycocyanin through the stratum corneum without disrupting its structural integrity. Both systems offered efficient protection and delivery of the bioactive pigment through different skin environments. Overall, integrating green extraction with dual nanodelivery platforms provides a sustainable and versatile strategy for developing next generation nanocosmetics. This work highlights phycocyanin as a green-derived, skin-protective molecule and a model bioactive for innovative nanocarrier design in future cosmeceutical formulations.

METABOLIC ENGINEERING FOR MICROBIAL BIOPRODUCTION

Hiroshi Shimizu
Department of Bioinformatic Engineering,
Graduate School of Information Science and Technology,
The University of Osaka, 1-5 Yamadaoka, Suita, Osaka 565-0817, Japan
TEL: +81-6-6879-7446

Abstract:
Microorganisms have been industrially utilized in the fields of brewing, foods and chemicals production processes. Because the thousands of metabolic reactions simultaneously occur and many metabolic reactions are related to the target production and cell growth, development of the rational design method of metabolic pathway modification to optimize production of the target products are needed. In order to efficiently produce targets, carbon flow from a raw material to target compounds and well-coupling with cofactors balancing of ATP and NADPH should be considered.

In my presentation, recent advances in metabolic flux analyses are introduced, especially computational pathway modification design by flux balance analysis (FBA). Computational tools for searching for effective gene deletion targets and recruitment of heterologous genes are introduced. Adaptive laboratory evolution (ALE) is also applied to identify and eliminate the rate limiting step in the metabolic pathways. Improvement of enzyme function and conversion of enzyme function by artificial intelligence (AI) in metabolic engineering is also discussed.

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Keywords: Metabolic Engineering, bioproduction, FBA, ALE, AI

DEVELOPMENT OF YEAST-BASED SUSTAINABLE PROTEINS USING FUNCTIONAL AMINO ACID ENGINEERING

Hiroshi Takagi
Nara Institute of Science and Technology, Nara, Japan

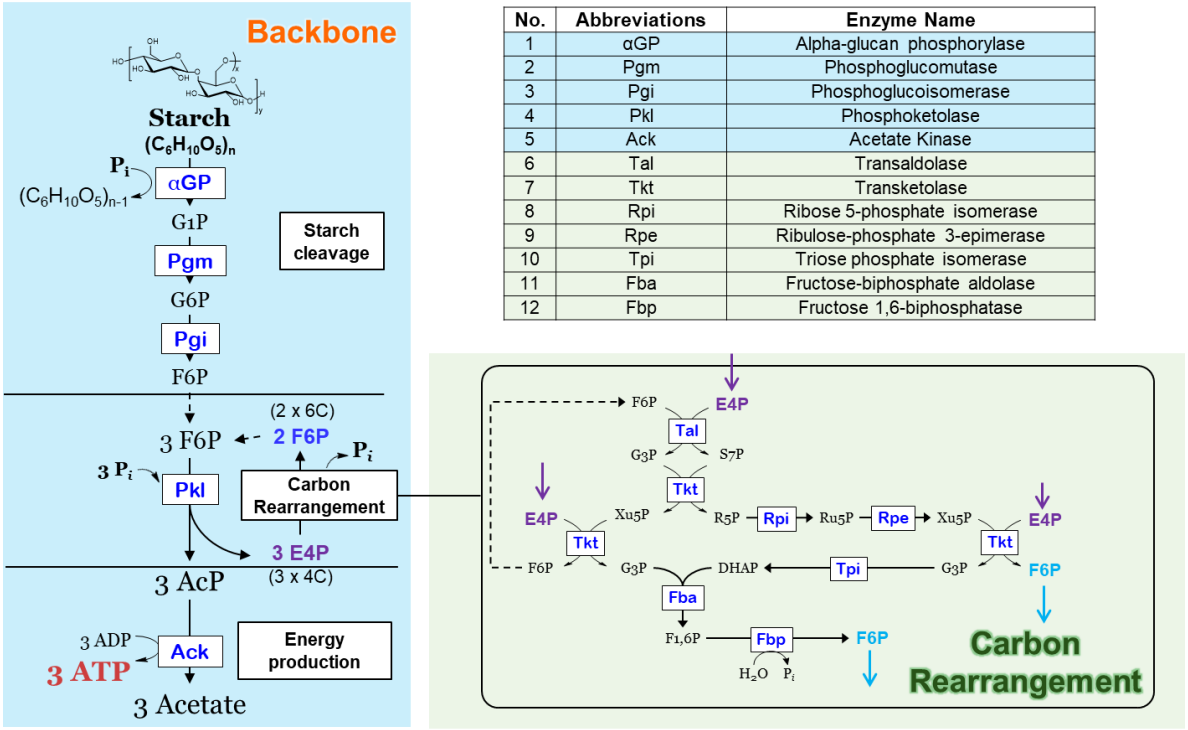
Abstract:
Sustainable proteins, including meat substitutes, are emerging as a promising solution to the food crisis exacerbated by global population growth, climate change, and ethical concerns regarding livestock production. These proteins, derived from plants, animal cells, insects, and microorganisms, face several technical challenges that hinder their market expansion. There are three types of microbial fermentation: traditional, biomass, and precision fermentation, which is gaining attention in food-tech because of its contributions to sustainability, gastronomy, and wellbeing. Our research focuses on the metabolic regulation and physiological roles of amino acids found in the yeast *Saccharomyces cerevisiae*. As for traditional fermentation, we have developed mutant strains of brewing yeast that overproduce or accumulate 'functional' amino acids (leucine, ornithine, proline, phenylalanine, *etc*.) and have successfully commercialized many alcoholic beverages with enhanced flavor, addition of a healthy image, and improved fermentation ability. In terms of biomass fermentation, to increase the added value of alternative proteins, we are now improving strains of Torula yeast (*Cyberlindnera jadinii* also known as *Candida utilis*), an excellent source of protein, with high levels of functional components (amino acids, nucleic acids, fatty acids, *etc*.) that contribute to meat taste, nutrition, and health. We are also optimizing culture conditions to increase these contents. Our current project includes developing prototypes of sustainable proteins using yeast cells and evaluating their characteristics to extract technical issues. Moreover, for the near future precision fermentation, the current CRISPR/Cas9 systems in *S. cerevisiae* cannot be considered a non-genetic modification technology because it requires the introduction of Cas9 and sgRNA into yeast cells using plasmid expression systems. We recently showed that the yeast genome can be edited without plasmid expression systems by using a commercially available protein transfection reagent and chemically modified sgRNAs. Our research will substantially contribute to the current understanding of genome engineering in yeast.

In Vitro RECONSTITUTION OF NON-OXIDATIVE GLYCOLYSIS WITH THERMOPHILIC ENZYMES

Kohsuke Honda,[1]* Gladwin Suryatin Alim,[1,2] Takuma Suzuki [1]
[1] International Center for Biotechnology, The University of Osaka, Japan
[2] Department of Chemistry, University of Basel, Switzerland
*e-mail: honda.kohsuke.icb@osaka-u.ac.jp

Abstract:
Chemical manufacturing through enzyme cascades, inspired by natural and engineered metabolic pathways, has emerged as a promising alternative to conventional fermentation-based manufacturing. One of the key challenges to improve the feasibility of *in vitro* reconstituted cascades is balancing the consumption and regeneration of essential cofactors, such as ATP/ADP and NAD^+/NADH, by integrating suitable enzyme modules.

To tackle this, we reconstituted the non-oxidative glycolysis (NOG) *in vitro* using 12 recombinant enzymes derived from thermophilic sources (Figure 1). Genes encoding the thermophilic enzymes were assembled in synthetic operons and co-expressed in a single recombinant *Escherichia coli* strain. Heat treatment of crude lysate of this stain enabled a one-step preparation of a thermostable enzyme cocktail constituting of NOG module. Through this module, we achieved an ATP regeneration turnover number exceeding 350, with maltodextrin and inorganic phosphate serving as inexpensive sacrificial substrates. Furthermore, by extending the NOG module with additional enzymes, we established novel *in vitro* metabolic pathways enabling semi-*de novo* ATP biosynthesis and UDP-glucose recycling. These results highlight the potential of thermophile-derived enzyme cascades as robust platforms for cofactor regeneration and synthetic biomanufacturing.



No.	Abbreviations	Enzyme Name
1	αGP	Alpha-glucan phosphorylase
2	Pgm	Phosphoglucomutase
3	Pgi	Phosphoglucoisomerase
4	Pkl	Phosphoketolase
5	Ack	Acetate Kinase
6	Tal	Transaldolase
7	Tkt	Transketolase
8	Rpi	Ribose 5-phosphate isomerase
9	Rpe	Ribulose-phosphate 3-epimerase
10	Tpi	Triose phosphate isomerase
11	Fba	Fructose-biphosphate aldolase
12	Fbp	Fructose 1,6-biphosphatase

Figure 1.
NOG module constructed in this study

Wolffia globosa MICROBIOME BENEFITS VITAMIN B12 PRODUCTION

Chakrit Bunyoo[1,2,4], Juthaporn Pholmakam[4,5], Karan Lohmaneeratana[3,4,5], Whitea Jasmine Salamet[1,4], Arinthip Thamchaipenet[3,4,5]*
[1]Interdisciplinary Graduate Program in Bioscience, Faculty of Science, Kasetsart University, Bangkok, Thailand
[2]Central Scientific Instrument Management Laboratory, Bureau for Research and Innovation Management, Chulabhorn Royal Academy, Bangkok, Thailand
[3]Department of Genetics, Faculty of Science, Kasetsart University, Bangkok, Thailand
[4]Duckweed Holobiont Resource & Research Center (DHbRC), Kasetsart University, Bangkok, Thailand
[5]Omics Center for Agriculture, Bioresource, Food and Health, Kasetsart University (OmiKU), Bangkok, Thailand
*e-mail: arinthip.t@ku.ac.th

Abstract:
Wolffia globosa, the fast-growing tiniest duckweed, is well-known as plant-based protein and future food applications for its richness in protein and nutritional values, particularly vitamin B12. Typically, microbial communities are closely associated with duckweed as holobionts and help plants to promote growth. Previous microbiome analysis of four duckweed species including *W. globosa* revealed alteration of microbial communities under natural and stress conditions. In this work, taxonomic assignment of microbiome from long-term storage *W. globosa* unveiled 'stable' core microbiome of members in the class of Actinomycetia, Alphaproteobacteria, Bacteroidia, and Gammaproteobacteria. Analysis of twenty metagenome-assembled genomes (MAGs) revealed complete metabolic pathways of nitrogen metabolism, beta-carotene, cobalamin (vitamin B12), gamma-aminobutyrate (GABA), stress tolerance, and degradation of benzene, toluene, and xylene. Subsequently, six out of MAGs have been isolated by culture-dependent methods namely, *Allorhizobium*, *Brevundimonas*, *Microbacterium*, *Novosphingobium*, *Pseudonocardia*, and *Sphingomonadales*. Some of them harbor the complete cobalamin biosynthetic pathway including biosynthesis of the tetrapyrrole precursor, corrin ring formation, and nucleotide loop assembly. The findings provide new insights into *W. globosa* 'stable' core microbiomes and highlight their potential roles in vitamin B12 production.

WE GOTTA START SOMEWHERE, RIGHT? A SMALL STEP OF CULTURED MEAT RESEARCH IN THAILAND

Tavan Janvilisri,[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
*e-mail: tavan.j@chula.ac.th

Abstract:
Cultured meat technology, involving the *in-vitro* cultivation of animal muscle and fat cells, offers a promising path towards sustainable and ethical protein production, necessitating foundational research in Thailand. This talk will outline our project aiming to address technical bottlenecks and build a scientific basis for this emerging industry. We successfully developed methods for isolating and maintaining porcine muscle-derived stem cells, confirming their myogenic potential. Key progress was made in reducing production costs by creating in-house recombinant porcine growth factors. Furthermore, we advanced the development of 3D scaffolding edible materials, supporting cell proliferation into spheroid aggregates and subsequent differentiation into muscle tissue. We also engineered a custom 3D bioprinter and explored controlled delivery systems using microgels for growth factors. While challenges remain—such as lower growth rates in serum-free media, stability issues with growth factors, and post-printing structural integrity of hydrogels—the project has been ongoing with the hope to set a pipeline for this technology. This work establishes a critical, albeit small, foundation in cell culture media, protein delivery, and bioprinting technology, paving the way for a future alternative protein industry in Thailand.

BIOLOGICS AND ITS APPLICATION IN SHRIMP

Supattra Treerattrakool
Center of Applied Shrimp Research and Innovation (CASRI), Institute of Molecular Biosciences, Mahidol University, Thailand
e-mail: tsupattra@gmail.com

Abstract:

Shrimp are important aquatic species in Thailand. Ovarian maturation is a vital process in shrimp **production, which is commonly induced by unilateral-eyestalk ablation of the female broodstock; the technique that leads to a reduction in gonad-inhibiting hormone (GIH). Although** eyestalk ablation can induce rapid maturation and continuous spawning in captive condition, but the spawners will become weakening and eventual die within 1-2 months, causing over-exploitation of broodstocks and directly affects shrimp production investment. Therefore, **our study focuses on manipulating GIH that controls in ovarian maturation by blocking GIH activity in shrimp without eyestalk ablation. Our research clearly demonstrates that** GIH monoclonal antibody (GIHmAb) can specifically inhibit GIH activity and induce ovarian maturation in shrimp at a greater extent than eyestalk ablation. This will definitely be of great benefit to shrimp industry of the country in terms of shrimp production, broodstock utilization and desirable for both ethical and economical bases**.**

Moreover, the giant freshwater prawn, *Macrobrachium rosenbergii* is commercially cultured in Asian countries. The males grow faster than females and can be harvested in a larger size, therefore is in a high market demand both in Thailand and for export. Because growth is a major concern for freshwater prawn culture, mono-sex culture is an alternative way to achieve higher average body weight at harvest, and thus higher yields. The secondary goals of our research are to develop effective strategies that can help enhance male giant freshwater prawn production that are foremost impediment to shrimp aquaculture development. We developed the biomolecules that can interfere the expression of a gene for an insulin-like androgenic gland hormone or IAG in *M. rosenbergii* through the RNAi technology. This strategy can induce complete sex reversal of a male prawn into a functional female (Neo-female) that is named after Mahidol University as the MU1 neo-female. The MU1 neo-female is capable of mating with normal males and predominantly produce male progeny with a minimal proportion of females.

The technologies developed by our group have been implemented on farms, yielding significant results and receiving favorable feedbacks from farmers. This will contribute significantly to shrimp aquaculture in terms of both the economic sustainability and the well-being of shrimp farmers.

AL-DNA AND THANARA SKIN MICROBIOME PRODUCTS

Asso. Prof. Dr. Naraporn Somboonna
Chulalongkorn University, and AL-DNA Co. Ltd., Thailand
e-mail: Naraporn.S@chula.ac.th

Abstract:
AL-DNA is a deep technology startup from Chulalongkorn University, incubated and supported by CU Enterprise, CU Sci Products and Services, and the Leaders Innovation Fellowship (LIF). The company specializes in advanced microbial analysis technologies for humans, animals, and the environment using deep sequencing (commonly referred to as microbiome analysis) as well as rapid and portable genetic testing (DNA/RNA) technologies. The company operates through three main business units: (1) microbiome-based products for both external and internal human use, with an emphasis on anti-aging solutions; (2) microbiome and probiotic analysis services and training; and (3) DNA/RNA detection kits and testing services, offering more than 36 patented and petty-patented testing solutions, with additional options available through customization. Presently, AL-DNA has developed multiple commercially-ready prototype methods, including detection of live bacterial, fungal, and foodborne pathogens in food, beverages and industry environments, SARS-CoV-2 (COVID-19), and African Swine Fever Virus (ASFV). These genetic detections are leveraged from but not limited to LAMP, RPA, multiplex LAMP, RT-mLAMP, RT-mRPA, paper-based methods, live genetic-LAMP, and nanoparticle detection; and some of the methods have been validated with real-world samples and documented under ISO16140-4 standards. These tests are portable and accessible at the point-of-care, requiring no expensive equipment, delivering results within one hour, and offering simple, user-friendly procedures with visual readouts. The costs are lower than PCR and real-time PCR, making them ideal for local diagnostics, mobile units, and onsite testing in various sectors.

Additionally, microbiome products focusing on probiotics and active ingredients for skin health are being developed under the commercial brand THANARA that differentiates itself in the market through its proprietary 4P-Biotics (Probiotics, Parabiotics, Prebiotics, and Postbiotics). Both **THANARA Anti-Aging & Sensitive Skin Serum** and **THANARA Anti-Aging & All Repair for All Skin Types Skincare SPF50/PA+++** focus to restore facial microbiome balance, reduce inflammation, hydrate, relieve dark spots or hyperpigmentation, and improve skin barrier and skin resilience.

IMMUNE BOOSTING COLD BREW COFFEE: FUTURE BEVERAGE TRENDS BUT MORE SUSTAINABLE

Jomkhwan Meerak
BIRTH2022 Co., Ltd., Chiang Mai, Thailand
e-mail: birth2022.jm@gmail.com

Abstract:
The coffee industry is facing many changes in the coming decades. Demand is expected to grow worldwide, especially for high-quality beans, even as the effects of climate change seriously threaten traditional supply routes. In addition, eco-friendly companies and solutions are essential in shaping a more responsible future for ecological impact. In fact, the 3rd wave coffee, as considered for its specialty flavors, gives way to the 4th and 5th wave for the market worldwide, which will become more important and new categories to challenge our notions of what "coffee" is. For this reason, Thai coffee industries face a significant global marketing challenge in developing high-quality coffee beans for novel, tasty, beneficial values and a sustainable future. Moreover, the development of innovative foods and beverages that can go beyond nutrients and energy is necessary to meet the requirements of consumers' wellness trend in an era of health risks from environmental issues and pandemics are prevalent. "BIRTH2022 Co., Ltd.", embarking on exploring the scientific method for helping synergy between the Thai coffee business and sustainability, we have been researching to produce functional coffee as the 1st immune boosting in the market. The research aligned with the 4th generation of global coffee business, which offers delightful flavor and aroma while also providing health benefits to consumers. By utilizing the combination of lactic acid bacteria and yeast for a novel fermentation process, the coffee bean revealed 3x higher levels of natural bioactive flavonoids but a 40% reduction of toxic compounds when compared to commercial ones in the current market. Moreover, medical research showed the possibility as a future beverage for the health and wellness trend. For instance, we developed the cold drip extraction machine to help extend the shelf life of cold brew coffee to 5X longer than others in the market, but with more concentration of flavors. For the next solutions of sustainability and environmental impact, we have been conducting research to ensure eco-friendly and sustainable living, especially for our farmers and communities. Overall, "byproducts and wastes" are undergoing deep research to utilize as high-value ingredients in the food and cosmetic industries. In addition, non-extracted waste, such as from fermentation, is formulated as the living biofertilizer and combined with soil probiotic bacteria to improve the quality of agricultural soil for high-quality organic crop production during climate change. In conclusion, we truly hope to work toward a more sustainable future in the coffee industry and serve the high-quality of your daily coffee cup for novel flavors, social and health impacts.

Keywords: functional coffee, fermented coffee, functional beverages, 4th wave coffee

MICROBIOME-BASED BUSINESS OPPORTUNITIES: WHAT ARE THE NEXT STEPS FOLLOWING A DECADE OF RESEARCH ON THE HUMAN GUT MICROBIOME?

Dr. Pinidphon Prombutara
Mod Gut Co., Ltd., Thailand
e-mail: pinidphon.p@modgut.com

Abstract:
The gut microbiome sector is experiencing rapid innovation; however, there is still a need for a deeper understanding of how products that modify the microbiome can meet consumer needs and identify opportunities throughout the technology value chain. Over the past decade, microbiome research has accelerated, becoming a central hub for innovation due to its potential impact on the agrifood and healthcare industries. Despite significant activity from startups, a notable gap remains in aligning scientific research with product development in the microbiome field.

Mod Gut Co., Ltd., a service-based company in Thailand focused on gut microbiome solutions, is highlighting emerging microbiome-related innovations and outlining opportunities for industry players in the healthcare sector to address unmet needs.

DEVELOPMENT OF SACCHAROMYCES CEREVISIAE STRAIN FOR ISOBUTANOL PRODUCTION FROM AN OSMOTOLERANT AND ETHANOL-PRODUCING YEAST

Jirasin Koonthongkaew
Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand
e-mail: jirasin.k@chula.ac.th

Abstract:
Isobutanol or isobutyl alcohol (IUPAC: 2-methylpropan-1-old) serves as an advanced biofuel alternative to ethanol. Isobutanol has recently emerged as a promising candidate for conversion into sustainable aviation fuel (SAF) using the alcohol-to-jet (ATJ) process. *Saccharomyces cerevisiae*, the conventional yeast utilized for ethanol synthesis, can synthesize a minor quantity of isobutanol via the metabolic pathway of the amino acid valine. Although recent studies demonstrated the strategies to enhance isobutanol synthesis by metabolic engineering, the altered strains were primarily derived from laboratory strains and predominantly face challenges in industrial-scale production. This study aims to develop an industrially feasible isobutanol strain of *S. cerevisiae* with little genetic alteration to resolve challenges in large-scale production. The original strain used in this study is the osmotolerant ethanol-producing *S. cerevisiae* strain D3C (isolate G2-3-2) isolated by Hoondee et al. (2016). Conventional mutagenesis was conducted on G2-3-2, yielding the isobutanol-tolerant mutant strain (named IbOH-1), which can tolerate up to 21 g/L of isobutanol. The genomic DNA analysis revealed that IbOH-1 harbored multiple mutations in genes associated with nitrogen starvation response, cell wall biosynthesis and integrity, stress resistance-related amino acid biosynthesis, glycerol accumulation biosynthesis, and the Hog pathway, which collectively contribute to tolerance against isobutanol toxicity. The *BAT1* gene was subsequently deleted using CRISPR/Cas9 to enhance isobutanol productivity. The synthesis of isobutanol from IbOH-1*bat1*Δ cells was examined in both nutrient-rich and nutrient-moderate fermentation media, with the optimization of glucose concentration in the fermentation media. The maximum isobutanol concentration achieved was 2.016 g/L, using nutrient-moderate yeast nitrogenous base (YNB) fermentation media with 150 g/L of glucose, supplemented with 8 g/L of peptone, 3 g/L of $(NH_4)_2SO_4$, 1 g/L of KH_2PO_4, 0.5 g/L of $MgSO_4 \cdot 7H_2O$, and 0.05 g/L of $FeSO_4 \cdot 7H_2O$.

Poster Presentation

Session I.
Bioinformatics and Systems Biology, Synthetic Biology

BIODEGRADATION PATHWAYS OF PHTHALATE ESTERS IN *Gordonia polyisoprenivorans* SPK-13

Pimdao Theerasin, and Prinpida Sonthiphand*
Department of Biology, Faculty of Science, Mahidol University,
Bangkok, Thailand
*e-mail: prinpida.son@mahidol.ac.th

Abstract:
Plastic waste not only generates microplastics but also releases chemical components that contaminate the environment and adversely affect the health of plants, animals, and humans. Among these chemicals, phthalate esters are extensively used as plasticizers that are recognized worldwide as environmental contaminants. Although various bacterial strains capable of degrading phthalate esters have been isolated, real-world applications require molecular insights to support effective environmental remediation. Using genome sequencing and functional analysis, this study investigated the degradation mechanisms of phthalate esters by the previously isolated *Gordonia polyisoprenivorans* SPK-13, a non-pathogenic bacterium with demonstrated efficiency in degrading multiple types of phthalate esters. The assembled genome of SPK-13 is 6,172,146 base pairs and contains genes involved in degradation, including esterases, lipases, and cutinases, as well as metabolic gene clusters such as *pcaBCDGH*, *catAC*, and *fadA*. These genomic features suggest that SPK-13 utilizes aerobic degradation pathways to mineralize phthalate esters, with phthalic acid and protocatechuate as the main intermediates.

IDENTIFICATION OF GENETIC MARKERS TO AID THE DISTINCTION OF *Bacillus subtilis* FROM OTHER CLOSELY RELATED SPECIES

Teerapat Khatkanta,[1] Saowalak Kalapanulak,[2,3] Susakul Palakawong Na Ayudthaya,[4] Weerayuth Kittichotirat[2,5]*

[1]Bioinformatics and Systems Biology for Driving Frontier BCG Economy Program, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

[2]Bioinformatics and Systems Biology Program, School of Bioresources and Technology, School of Information Technology, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

[3]Center for Agricultural Systems Biology (CASB), Systems Biology and Bioinformatics research laboratory, Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

[4]Thailand Institute of Scientific and Technological Research (TISTR), Pathum Thani, Thailand

[5]Systems Biology and Bioinformatics research laboratory, Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand

*e-mail: weerayuth.kit@kmutt.ac.th

Abstract:

Bacillus subtilis is widely recognized for its agricultural, industrial, and biotechnology applications. However, its high genetic similarity to other members within the *B. subtilis* group often hinders accurate identification, leading to potential misclassification and inappropriate strain usage. This study aims to address these challenges by characterizing the genetic diversity among *B. subtilis* strains, subspecies, and closely related species and identifying candidate molecular markers for precise taxonomic resolution. A pan-genome analysis of 87 *Bacillus* genomes using the Roary pipeline revealed 906 conserved core genes. Phylogenomic reconstruction utilizing these genes clarified evolutionary relationships within the group. Furthermore, the core genes were examined to identify nucleotide variant positions specific to *B. subtilis*, resulting in the discovery of 601 variants across 379 genes. These variants were further evaluated against identical nucleotide positions in other species using nucleotide BLAST to confirm their potential as diagnostic markers for reliably distinguishing *B. subtilis* from its close relatives. Collectively, our findings provide valuable insights into the genetic diversity of the *B. subtilis* group and propose candidate markers that could improve detection protocols. These advancements will enhance the accuracy of *B. subtilis* identification and minimize strain misapplication, ensuring the safe and effective application of *B. subtilis* across diverse fields.

PROBIOGENOMIC ANALYSIS AND ANTI-PROLIFERATIVE ACTIVITY OF PROBIOTIC AND POSTBIOTICS *Lactococcus lactis* BKKT-1: an *in silico* THERAPEUTIC PREDICTION

Papinwit Busayaboriboonchot[1], Pacharadanai Phanpipit[1], Engkarat Kingkaew[1,*], Napassakorn Kasemnukijkul[1], Supawadee Umthong[2, **]
[1]Department of Biology, School of Science, King Mongkut's Institute of Technology Ladkrabang, Bangkok 10520, Thailand
[2]Department of Biochemistry and Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand
*e-mail: engkarat.ki@kmitl.ac.th,
**e-mail: supawadee.u@chula.ac.th

Abstract:
Cervical cancer remains a major malignancy among women worldwide, with conventional cytotoxic therapies often associated with side effects that compromise quality of life. Probiotics are increasingly explored as adjunctive or alternative therapeutic agents due to their health-promoting and anticancer properties. Genomic analysis is central to probiotic research, as it enables the identification of genes linked to functionality, safety, and metabolite biosynthesis, thereby defining therapeutic potential. In this study, the whole genome of Lactococcus lactis BKKT-1 was analyzed using EzBioCloud, NCBI, KEGG, BAGEL4, VirulenceFinder, and PathogenFinder. The strain was confirmed to be non-pathogenic (probability 0.21) and free of virulence factors. Functional assays demonstrated strong gastrointestinal tolerance and 69.54% adhesion to Caco-2 cells, comparable to Lacticaseibacillus rhamnosus GG (72.12%). BAGEL4 analysis identified the nisin Z gene, encoding a bioactive peptide with antimicrobial, anticancer, and health-promoting potential. Importantly, the cell-free supernatant (postbiotics) of BKKT-1 inhibited HeLa cervical cancer cell proliferation by 68.31%, in contrast to 25% canosine, which achieved only 3.1% inhibition. These findings demonstrate that L. lactis BKKT-1 is a safe and functionally potent probiotic, with genomic traits supporting gastrointestinal resilience, epithelial adhesion, and nisin Z production. Collectively, genomic analysis validates its potential in cervical cancer prevention and therapy.

Keywords: *Lactococcus lactis*; Whole-genome sequencing; Bioinformatic analysis; Nisin Z; Anti-cancer activity

IMPACT OF HETEROLOGOUS *Beta Carotene Ketolase (bkt)* GENE EXPRESSION FROM *Hematococcus pluvialis* IN *Synechocystis* sp. PCC 6803 ON CAROTENOID PRODUCTION UNDER SALT STRESS

Benjamat Sukkokee,[1] Saowarath Jantaro,[1]*
[1]Laboratory of Cyanobacterial Biotechnology, Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand
* e-mail: saowarath.j@chula.ac.th

Abstract:

Synechocystis sp. PCC 6803 is a model cyanobacterium extensively studied for its photosynthetic capacity and potential in the sustainable bioproduction of high-value compounds, herein carotenoids. Among these, ketocarotenoids are particularly valuable due to their potent antioxidant properties. However, *Synechocystis sp. PCC 6803* naturally produces only limited types of carotenoids and lacks an efficient pathway for the biosynthesis of high value ketocarotenoids. In this study, we explored strategies to improve carotenoid biosynthesis via heterologous expression of the β-carotene ketolase gene (*bkt*) from *Haematococcus pluvialis* (or OX_BKT) in *Synechocystis* sp. PCC 6803. All strains were cultured in BG_{11} medium containing 0.25%, 1%, and 2% (w/v) NaCl. Unknown peaks that were undetectable in WTc were found in certain HPLC chromatograms of the OX_BKT strain at 1% and 2% NaCl. It is considered that the peaks are either new carotenoid species or free astaxanthin. In addition, exposure to high NaCl concentrations altered the carotenoid profile in both WTc and OX_BKT; **myxoxanthophyll** and **zeaxanthin** contents decreased, whereas **β-carotene** and **chlorophyll *a*** contents increased. These findings suggest that salt stress may change carotenoid metabolism and pigment composition and also induce the ***bkt*** gene expression to produce new carotenoid products in *Synechocystis* sp. PCC 6803.

DEVELOPMENT OF BETA-CLASS CARBONIC ANHYDRASES FROM *Roseateles terrae* HL11 FOR CO_2 CAPTURE

Panyada Wattanachai,[1] Hataikarn Lekakarn,[2] Katesuda Aiewviriyasakul,[1] Katewadee Boonyapakron,[1] Sornpornpun Pairoh,[1] Wuttichai Mhuantong,[1] Verawat Champreda,[1] Benjarat Bunterngsook[1,*]

[1] Enzyme Technology Research Team, Biorefinery Technology and Bioproduct Research Group, National Center for Genetic Engineering and Biotechnology, 113 Thailand Science Park, Khlong Luang, Pathum Thani 12120, Thailand

[2] Department of Biotechnology, Faculty of Science and Technology, Rangsit Campus, Thammasat University, Pathum Thani 12120, Thailand

*e-mail: Benjarat.bun@biotec.or.th

Abstract:

Roseateles terrae HL11 strain, isolated from soil attached to sago palm root, revealed the presence of genes encoding carbonic anhydrase enzymes. Regarding genome sequencing and functional gene annotation, one gene encoding β-class carbonic anhydrase (β-CA_2211) was identified from *R. terrae* HL11 which is responsible for biological enhancement of CO_2 capture application. This study aims to characterize function and CO_2 conversion activity of β-CA_2211 for its potential use in carbon capture, utilization and storage (CCUS) technology. The predicted three-dimensional structure of β-CA_2211 using homology modeling SWISS-Model using Eubacterial beta-carbonic anhydrase (PDB 2esf) as a template indicated that β-CA_2211 assembled into homo-tetrameric structure. Subsequently, the β-CA_2211 gene was successfully cloned into pET28a(+) and heterologously expressed in *Escherichia coli* BL21 (DE3). The recombinant protein was purified by using Ni-NTA affinity chromatography with the expected size approximately 26.38 kDa in SDS-PAGE gel. The enzyme exhibited optimum temperature was found to be 40°C and the activity assay through protonography confirmed hydratase activity of tetrameric form for CO_2 hydration assay. Furthermore, Wilbur–Anderson assays demonstrated outstanding catalytic performance of β-CA_2211 reaching 5,454.55±1,714.19 WAU/mg. These demonstrated high potential of the β-CA as biocatalyst for CO_2 sequestration.

DISCOVERY AND FUNCTIONAL CHARACTERIZATION OF RECOMBINANT ALPHA-CLASS CARBONIC ANHYDRASE DERIVED FROM ANAEROBIC UNCULTURED MICROBIAL CONSORTIUM

Sirikanya Jongprasertkul,[1] Apirak Chonphaiboon,[1] Nattachai Kasipan,[1] Hataikarn Lekakarn,[2] Panyada Wattanachai,[3] Benjarat Bunterngsook[3,*]

[1] Science Classrooms in University-Affiliated School Project, Thammasat UniversitySuankularb Wittayalai Rangsit School Center, Khlong Luang, Pathum Thani 12120, Thailand

[2] Department of Biotechnology, Faculty of Science and Technology, Rangsit Campus, Thammasat University, Pathum Thani 12120, Thailand

[3] Enzyme Technology Research Team, Biorefinery Technology and Bioproduct Research Group, National Center for Genetic Engineering and Biotechnology, 113 Thailand Science Park, Khlong Luang, Pathum Thani 12120, Thailand

*e-mail: Benjarat.bun@biotec.or.th

Abstract:

Carbonic anhydrases (CAs) are metalloenzymes that catalyze the reversible hydration of carbon dioxide, playing a pivotal role in CO_2 transport and sequestration. For practical applications in industrial processes, CAs must exhibit stability at high temperatures and under alkaline pH conditions. Therefore, the development of novel CAs with superior properties, along with technologies that enhance their stability, represents a critical technological gap that needs to be addressed. In this study, a novel α-class carbonic anhydrase (α-CA) was successfully identified using metagenomic approach in which genomic DNA was extracted from an anaerobic microbial community present in a biogas bioreactor. The identified α-CA designated as ApCA exhibited the highest amino acid sequence similarity (78% identity and 88% similarity) to an α-CA from *Allochromatium palmeri*, an anaerobic mesophilic bacterium. To improve its stability and facilitate immobilization, ApCA was heterologously expressed in *Escherichia coli* BL21(DE3) as ApCA-ferritin (ApCA-FN) chimeric protein fused with ferritin which is an iron-based nanocage protein. The ApCA-FN exhibited 15.31 U/mg at 50°C with high activity at pH ranging from 7.0-11.0 though colorimetric method using p-nitrophenyl acetate as a substrate. Therefore, this fusion strategy offers a simplified alternative to traditional immobilization methods, resulting in a ferritin-mediated carbonic anhydrase complex.

STRUCTURAL AND FUNCTIONAL INSIGHTS INTO A NOVEL ALDEHYDE DEFORMYLATING OXYGENASE FOR BIOFUEL APPLICATIONS

Nidar Treesukkasem, Surawit Visitsatthawong, Thanyaporn Wongnate*
School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC), Wangchan Valley, 555 Moo 1 Wangchan, Rayong, 21210, Thailand
*e-mail: thanyaporn.w@vistec.ac.th

Abstract:
Aldehyde Deformylating Oxygenase (ADO) is a ferritin like diiron protein that catalyzes aldehyde into corresponding C_{n-1} alkanes, major components of biofuels. In this study, we discovered the novel species from *Pseudomonas plecoglossicida* of ADO (*Ps*ADO) using the Enzyme Function Initiative-Enzyme Similarity Tool (EFI-EST). *Ps*ADO reveals a loop motif that contains a disulfide bond. An extended loop in *Ps*ADO features a novel substrate tunnel, enhancing both efficiency and thermostability. *Ps*ADO can enhance the activity to produce alkane, with a k_{cat} of 1.38 min^{-1}, 106 times higher than that of *Prochlorococcus marinus* MIT9313 (*Pm*ADO). Moreover, *Ps*ADO exhibits a markedly higher melting temperature (T_m) of 60 °C, compared to 41 °C for *Pm*ADO. AlphaFold 3 and CaverDock analyses demonstrated that deletion of the extended loop in *Ps*ADO led to a reduction in alkane production of up to 9.4-fold. Additionally, the N47A variant decreased tridecane formation by 1.25-fold, underscoring the critical role of these structural features in substrate accessibility. These findings emphasize *Ps*ADO's potential for biofuel applications, particularly in the efficient biosynthesis of long-chain alkanes suitable for jet fuel. With enhanced stability and catalytic efficiency, *Ps*ADO represents a promising candidate for industrial biotechnology and biofuel production.

Figure 1.
Structural comparison between the novel species of *Ps*ADO and *Pm*ADO to catalyze the aldehyde to alkane.

COMPLETE GENOME INSIGHTS INTO A Bacillus cereus GROUP ISOLATES FROM FOOD

Sawanya Potirungsee, [1] Phornphan Sornchuer, [2] Kritsakorn Saninjuk [1,3, *]
[1] School of Science, Mae Fah Luang University, Chiang Rai, Thailand
[2] Microbiology and Immunology, Department of Preclinical Science, Faculty of Medicine, Thammasat University, Klongluang, Pathum Thani 12120, Thailand.
[3] Microbial Products and Innovation Research Group, Mae Fah Luang University, Chiang Rai, Thailand
*e-mail:Kritsakorn.san@mfu.ac.th

Abstract:
Bacillus species are spore-forming, Gram-positive bacteria that are widely distributed indiverse ecological niches. The *B. cereus* group is particularly significant due to itsimplications for human health and food safety. Members of this group contaminate a variety of raw and processed foods and can survive heat treatments owing to the high resistance of their spores. *B. cereus* is an opportunistic pathogen capable of causing gastrointestinal illnesses, including diarrheal and emetic syndromes, as well as extra-intestinal infections. These conditions arise from the production of exotoxins such as hemolysin BL, non-hemolytic enterotoxin, and cytotoxin K, which are associated with diarrheal symptoms, and the emetic toxin cereulide, which induces nausea and vomiting. This clade exhibits notable medical and ecological diversity and is recognized for its resistance to multiple antibiotics, including β-lactam agents. Although tetracycline remains one of the most effective treatments, emerging resistance is increasingly reported. Furthermore, biofilm formation enhances persistence and virulence, posing challenges for both treatment and food safety. In this study, two *B. cereus* group isolates obtained from food in Thailand were subjected to whole-genome sequencing using Oxford Nanopore technology. Genomic analyses revealed features consistent with the *B. cereus* sensu stricto lineage. Comparative phylogenomic and average nucleotide identity (ANI) analyses positioned the isolates within the B. cereus clade, clustering closely with reference genomes such as *B. cereus* WPySW2 and AFA01. Both isolates harbored multiple virulence genes, including *nheA*, *nheB*, *nheC*, *entFM*, *cerA*, and *bceT*, indicating dual diarrheal and hemolytic pathogenic potential. These findings highlight the importance of understanding the pathogenicity, resistance mechanisms, and ecological adaptability of *B. cereus* for mitigating foodborne risks and informing public health interventions.

MICROBIOME BIOMARKERS FOR COLORECTAL CANCER DIAGNOSIS VIA METAGENOMIC ANALYSIS

Kasidet Taweepon[1], Tavan Janvilisri[2], Joy Scaria[3], Supeecha Kumkate[1], Phurt Harnvoravongchai[1]*
[1]Department of Biology, Faculty of Science, Mahidol University, Thailand
[2]Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand
[3] Department of Veterinary Pathobiology, Oklahoma State University, USA
*e-mail: phurt.har@mahidol.edu

Abstract:
Colorectal cancer (CRC) is a leading malignancy worldwide, contributing significantly to cancer-related deaths. Its progression is often linked to delayed diagnosis and limited therapeutic effectiveness, as tumors may develop resistance to treatment. Early-stage detection improves outcomes, emphasizing the need for reliable diagnostic tools. While various diagnostic approaches, including tumor profiling and gut microbiome analysis, have been proposed, universal CRC biomarkers remain unidentified. Most prior studies focused on specific microbes using single analytical metrics.

In this study, we utilized a metagenomic gut microbiome database to identify potential microbial biomarkers for CRC. Multiple analytical methods—including microbial diversity, differential abundance, and interaction network analyses—were applied to assess candidate microbes and their associations. No significant differences were found in the top ten abundant species among control, adenoma, and cancer groups. Both alpha and beta diversity were comparable across groups. Differential abundance analyses identified Prevotella copri as a potential CRC biomarker, showing a high LDA score and increased abundance in cancer samples. However, interactions between P. copri and other microbes remain unclear and require further investigation to clarify its role in colorectal carcinogenesis.

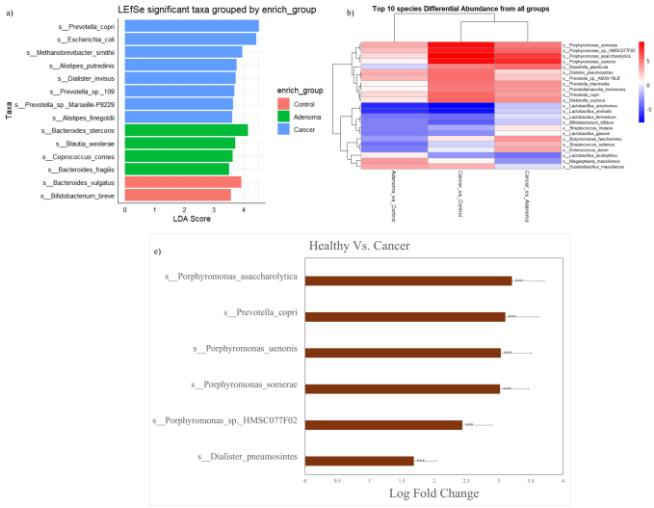


Figure 2.
Species-level biomarker discovery from differential abundance analyses using (a) LEfSe (LDA > 3.5), (b) DESeq2 (heatmap of log fold changes), and (c) ANCOM-BC (pairwise log fold changes; |logFC| > 1). Six species identified by ANCOM-BC passed prevalence and robustness filters. Significance: q < 0.05 (*), q < 0.01 (**), q < 0.001 (***).

Session II.
Medical Biotechnology & One Health

PERFORMANCE TESTING OF A URINE MICROALBUMIN DIP TEST STRIPS DEVELOPED FOR PRELIMINARY KIDNEY DISEASE SCREENING

Umaporn Pimpitak[1]*, Wanwisa Poonlapdecha[2] Anumart Buakeaw[1], Sirirat Rengpipat[2] and Kittinan Komolpis[1,2,3]

[1]The Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, 10330 Thailand

[2]Qualified Diagnostic Development Center, Chulalongkorn University, Bangkok, 10330 Thailand

[3]Food Risk Hub, Research Unit of Chulalongkorn University, Bangkok 10330, Thailand

*Corresponding author. E-mail: Umaporn.p@chula.ac.th

Abstract:

This study describes the development of a novel lateral flow dipstick assay for the rapid screening of chronic kidney disease (CKD). The assay utilizes gold nanoparticles as a signal and is based on competitive antigen-antibody binding for the detection of microalbumin in urine, a key indicator of CKD. This point-of-care test is designed for convenient initial screening, particularly for microalbuminuria. The qualitative colorimetric dipstick, with a cutoff value of 20 µg/mL, provides results based on visual inspection of the color change, eliminating the need for specialized personnel. The method is cost-effective, provides rapid results, and can be implemented in various healthcare settings. In a study of 237 urine samples, the dipstick assay showed agreement with a standard reference method in 229 samples (51 positive, 178 negative), while 8 samples yielded discordant results. Statistical analysis revealed a sensitivity of 87.93%, a specificity of 99.44%, and an accuracy of 96.62% for the urine microalbumin dipstick. These results suggest that this dipstick assay is a promising tool for CKD screening by monitoring urine albumin levels for microalbuminuria, enabling physicians to make timely decisions regarding patient care. Positive results should be further confirmed by standard laboratory testing.

MECHANISMS OF SSG1-MEDIATED LIFESPAN EXTENSION THAT APPEAR TO BE INVOLVED IN TRANSPORT OF *S*-ADENOSYLMETHIONINE IN BUDDING YEAST

Sayaka Kawasaki, Koji Masumura, Takafumi Ogawa, Masaki Mizunuma*
Graduate School of Integrated Sciences for Life, Hiroshima University
*e-mail: mmizu49120@hiroshima-u.ac.jp

Abstract:
Elucidation of the regulatory mechanisms of aging and lifespan is expected to contribute to prevention of age-related diseases and extension of healthy lifespan. Previously, we found that the *SSG1* (the spontaneous suppression of growth-delay in *sah1-1*) mutation in budding yeast extended lifespan with high accumulation of *S*-adenosylmethionine (SAM) in vacuole. The mutant expresses a C-terminally elongated Ssg1 protein at the vacuolar membrane due to a frameshift mutation. Given the high similarity of Ssg1 to the MATE (multidrug and toxic compound extrusion) family transporter, Ssg1 was predicted to be a transporter of SAM. Therefore, the aim of this study was to clarify the mechanisms of lifespan extension by characterizing the functions of Ssg1.

To investigate the role of Ssg1 in lifespan regulation, mutations were introduced toward amino acid residues predicted to be important for transport activity. These mutations abolished the high accumulation of SAM and lifespan extension. Furthermore, SAM transport activity was demonstrated with vacuolar membrane vesicles isolated from *SSG1*-overexpressing strains.

These results show for the first time that Ssg1 is a vacuolar membrane-localized SAM transporter and that its transport is involved in lifespan extension.

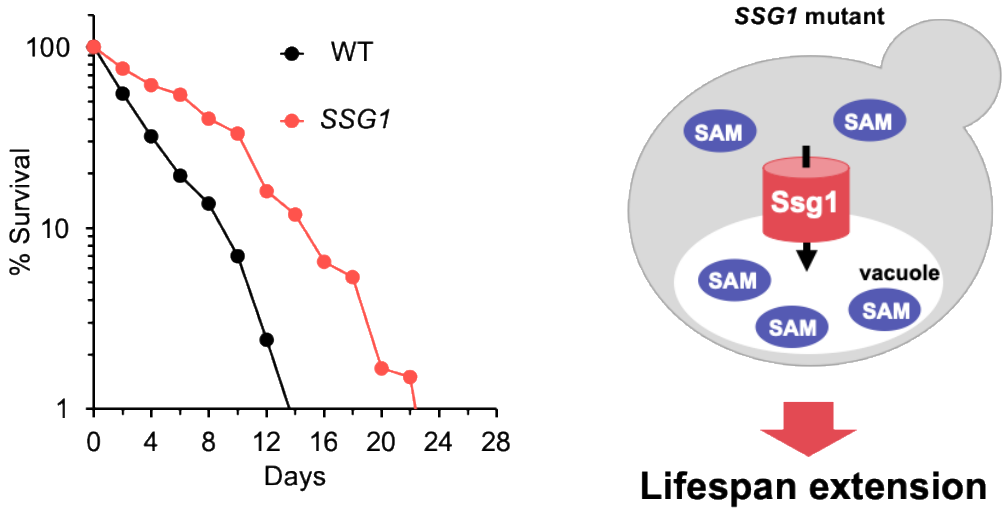


Figure 1.
Lifespan extension of the *SSG1* mutant

ANALYSIS OF THE OXIDATIVE STRESS RESISTANCE INDUCED BY *S*-ADENOSYL-L-HOMOCYSTEINE IN *Saccharomyces cerevisiae* AND *Caenorhabditis elegans*

Miyuko Kanaji, Takafumi Ogawa, Koji Masumura, Masaki Mizunuma*
Graduate School of Integrated Sciences for Life, Hiroshima University
*e-mail: mmizu49120@hiroshima-u.ac.jp

Abstract:
Elucidating the regulatory mechanisms of lifespan can provide practical applications for lifespan extension and aging-related diseases. We previously reported that supplementation with *S*-adenosyl-L-homocysteine (SAH), a metabolite in methionine metabolism, extended the lifespan of the yeast *Saccharomyces cerevisiae* and nematode *Caenorhabditis elegans*. In methionine metabolism, *S*-adenosyl-L-methionine (SAM) acts as a methyl donor in methylation reactions, whereas SAH competitively inhibits these reactions. Recently, we found that supplementation with SAH promotes tolerance to oxidative stress in yeast and in nematodes. Since longevity and stress resistance are closely related, SAH-induced oxidative stress resistance is expected to play an important role in longevity. Given that SAH supplementation leads to increased accumulation of SAH and SAM in yeast, we predicted that methyltransferases might be involved in the process of oxidative stress resistance. Among the methyltransferase deletion mutants, we screened for strain(s) that did not affect stress resistance induced by SAH in yeast. We obtained both mutant strains that exhibited sensitivity and resistance to oxidative stress, suggesting that multiple methyltransferases are involved in this mechanism. Furthermore, the *C. elegans* ortholog of the candidate methyltransferase identified in yeast also exhibited oxidative stress resistance when mutated, indicating that this mechanism may be conserved between yeast and nematodes.

MULTIFUNCTIONAL TERMINALIA CATAPPA-INCORPORATED SODIUM ALGINATE/CARBOXYMETHYL CHITOSAN HYDROGEL FOR ENHANCED BURN WOUND HEALING

Tudchaphong Chongsubthum[1], Isaran Kaewketa[1], Punyaporn Thongprasert[2], Thanyaluck Thanyacharoen[2], Walaipun Rukprasert[4], Worrapot Pengpa[4], Kriengsak Lirdprapamongkol[3], Patcharaporn Siwayaprahm[4], Piyachat Chuysinuan[2], Supanna Techasakul[2], Jisnuson Svasti[3]*
[1]Bangkok Christian College, Bangkok, Thailand
[2]Laboratory of Organic Synthesis, Chulabhorn Research Institute, Bangkok, Thailand
[3]Laboratory of Biochemistry, Chulabhorn Research Institute, Bangkok, Thailand
[4]Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand
*e-mail: tudchaphongtim@gmail.com, isarankk@gmail.com, piyachat@cri.or.th

Abstract:
The skin is the body's largest organ, serving as a critical barrier against infection and environmental stress. Burn injuries represent a significant public health concern, particularly in low- and middle-income countries, contributing to high morbidity, mortality, and economic burden. These injuries compromise the skin barrier, leading to prolonged inflammation, oxidative stress, microbial invasion, and delayed healing. There is increasing demand for advanced wound dressings that are non-toxic, promote regeneration, and reduce antibiotic reliance. This study developed a natural bilayer hydrogel wound dressing incorporated with *Terminalia catappa* (TC) leaf extract to provide antibacterial, antioxidant, and anti-inflammatory properties. The bilayer comprises a calcium-crosslinked sodium alginate (SA) and carboxymethyl chitosan (CMC) hydrogel for moisture retention and biocompatibility, and an electrospun polyvinyl alcohol (PVA)/polycaprolactone (PCL) nanofiber sheet that mimics the extracellular matrix and enhances mechanical strength. Compressive testing indicated that the 9.38% TC-loaded hydrogel had the lowest resistance (0.16 ± 0.04 N/mm^2) and modulus of elongation (0.66 ± 0.14 N/mm^2), reflecting high flexibility and deformability suitable for wound surfaces, whereas unmodified SA/CMC was the most rigid. FTIR analysis confirmed component integration: SA/CMC showed OH-stretching at 3300 cm^{-1}, and TC-loaded hydrogels (6.25–12.5%) displayed OH-stretching at 3249–3258 cm^{-1} and amide II bands at 1592–1599 cm^{-1}, indicating polyphenol-mediated crosslinking. TC extract exhibited C–O–C stretching at 1198 cm^{-1}, confirming ether linkages. Antimicrobial testing demonstrated strong activity against MRSA and *P. aeruginosa* (inhibition zones up to 28.00 ± 2.65 mm), while E. coli and *C. albicans* were inhibited under specific conditions. MICs ranged from 0.98–1.95 mg/mL for bacteria and 0.98–250 mg/mL for fungi. Antioxidant activity was highest in the 9.38% hydrogel, with 82.27 ± 0.35% (DPPH) and 92.63 ± 0.26% (ABTS) radical scavenging. Anti-inflammatory effects were evaluated in LPS-stimulated RAW 264.7 macrophages. NO levels were reduced from 32.8 ± 2 µM in stimulated cells to 18.6 µM with 12.50% TC extract at 5.00 mg/mL, slightly lower than the positive control (19 µM Vermelhotin), indicating strong dose-dependent suppression of inflammation without cytotoxicity. Biocompatibility and wound healing potential were confirmed in HaCaT cells. Collectively, these results demonstrate that the TC-loaded bilayer hydrogel is a safe, multifunctional, and effective dressing, combining flexibility, antioxidant and antimicrobial activity, and anti-inflammatory properties, making it a promising solution for enhancing burn wound repair, particularly in resource-limited settings.

PCL/COLLAGEN/ALGINATE 3D SCAFFOLD INCORPORATING PHLOROTANNIN FOR BONE TISSUE REGENERATION: ASSESSMENT OF SUB-CHRONIC TOXICITY

Tae-Hee Kim [1,2]* Hyun Kyoung Yang [3], Jin Young Park [4], Jae Yong Jung [5], Do-Hyung Kim [6]
[1]Research Center for Marine-Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in Universities, Pukyong National University, Busan 48513, Republic of Korea
[3]University College, Pukyong National University, Busan, 48513, Republic of Korea
[4]Major of Electrical, Electronics, and Software Engineering, Pukyong National University, Busan, 48548, Republic of Korea
[5]Marine-Bionics Convergence Technology Center, Pukyong National University, Busan, 48513, Republic of Korea
[6]Department of Aquatic Life Medicine, College of Fisheries Sciences, Pukyong National University, Busan, 48513, Republic of Korea
*e-mail: taehee@pknu.ac.kr

Abstract:
The development of effective scaffolds for bone regeneration is crucial due to the growing demand for innovative strategies to repair bone defects and accelerate the healing process. In this study, a polycaprolactone/2% fish collagen/2% alginate (P/FC/A) 3D scaffold incorporating 5% phlorotannin was developed to enhance bone tissue regeneration. Although the regenerative efficacy of the P/FC/A scaffold has been demonstrated in vitro and in vivo, its sub-chronic toxicity in animal models has not been fully investigated, raising concerns regarding its safety for clinical applications. To address this, we assessed the sub-chronic toxicity of the P/FC/A scaffold over a 12-week period using New Zealand White rabbits (10 six-month-old males and 10 ten-month-old females). A total of 20 rabbits were randomly divided into two groups (n = 10 per group): an experimental group implanted with the P/FC/A scaffold and a negative control group implanted with a high-density polyethylene scaffold. Comprehensive assessments, including measurements of body and organ weights, hematological and serum biochemical parameters, and histopathological examinations of major organs (liver, kidney, spleen, heart, and lung), revealed no significant differences between groups. Furthermore, no adverse effects were observed in P/FC/A-implanted group. These findings demonstrate the non-toxic nature and favorable safety profile of the P/FC/A scaffold, supporting its potential suitability for clinical use in bone regeneration.

ITS-BASED IDENTIFICATION OF COMMON POACEAE SPECIES FOUND AROUND BANGKOK

Lilian Haidvogl[1,2], Umaporn Siriwattanakul[2,3], Wanichaya Chaiwimol[3], Wisuwat Songnuan[2,3,4,*]

[1]Graduate Program in Toxicology, Faculty of Science, Mahidol University, Bangkok, Thailand
[2]Systems Biology of Diseases Research Unit, Faculty of Science, Bangkok, Thailand
[3]Department of Plant Science, Faculty of Science, Mahidol University, Bangkok, Thailand
[4]Center of Excellence on Environmental Health and Toxicology (EHT), Bangkok, Thailand
*e-mail: wisuwat.son@mahidol.ac.th

Abstract:
Poaceae species—the main contributors to pollen allergy within Thailand—have almost identical pollen, often only differing significantly in size, so grains cannot be discriminated at species level visually. Exact taxonomical identification of grasses, necessary for research, is only achieved by experts when the entire plant, including inflorescence, is available. As this is often unobtainable, and sequencing can be time-consuming, other ways to verify a sample's classification must be found. Here, we demonstrate a way of aiding in the identification of 15 common grass species found around the Bangkok area, based on PCR amplification of its conserved internal transcribed spacer (ITS) region. Using eight different primers, a unique amplification pattern was created for each species, allowing to distinguish between the grasses of the Panicoideae and Chloridoideae families. While the close resemblance of all collected ITS sequences does not allow for precise characterization, directed PCR amplification may be used as an immediate species indicator, before the sequencing results return and verify the identification. However, the scarcity of ITS sequences for Thai grasses limits further improvement of this method. It is therefore important to also expand relevant databases to aid development of better processes, improving speed and quality of research.

MICROFLUIDIC BACTERIA-NOSE CHIP EMPLOYING *Corynebacterium accolens* FOR BREATH VOC DIAGNOSTICS

Po-Hui Wu[1], Yan-Yu Chen[1]*
[1]Department of Chemical Engineering, National Chung Hsing University, No. 145, Xingda Rd., South Dist., Taichung, 40227, Taiwan (R.O.C.).
*e-mail:
annayyc0707@nchu.edu.tw

Abstract:
The preliminary study developed a bench-scale inverse-membrane bioreactor that employed the nasal commensal *Corynebacterium accolens* as a biosensing element for detecting volatile organic compounds (VOCs) in human breath. While biologically informative, the system required large gas volumes and long residence times, limiting portability and clinical efficiency. To address these limitations, the bioreactor was miniaturized into a microfluidic "bacterial nose" chip. The chip was fabricated by bonding multilayer polydimethylsiloxane (PDMS) sheets, cast from a 3D-printed mold. This miniaturization significantly reduced sample consumption by over 90%, shortened diffusion paths, and enabled multiplexed analysis on a single substrate. A PETE membrane, pre-colonized with *C. accolens*, was embedded within a dedicated sensing chamber, while adjacent microchannels delivered humidified air or calibration gases to sustain a stable gas-liquid interface that mimics the nasal cavity. *C. accolens*, commonly found in healthy nasal microbiota, shows desiccation tolerance and expresses lipase pathways responsive to VOCs. The system's feasibility was demonstrated by monitoring lipid levels, biomass, dissolved oxygen, and headspace acetone in response to clinically relevant acetone concentrations. This study highlights the potential of using nasal commensals in a portable, disposable, and non-invasive VOC detection platform for point-of-care diagnostics.

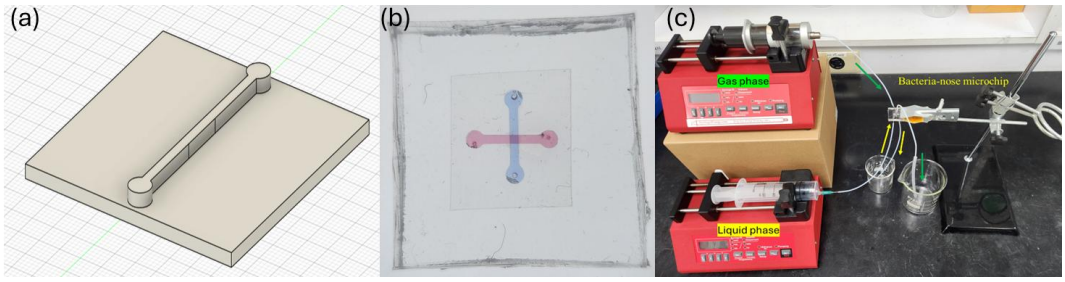


Figure 1.
(a) 3D printing channel; (b) Bacteria-nose microchip; and (c) Mimic nasal environment for sensing.

ENHANCING SCOLIOSIS DETECTION USING AI: INTEGRATING DEEP LEARNING INTO THE MEDICAL FIELD

Pittayud Aursukitwattana,[1]* Pakwalan Kiewwichai[2]
[1]Denla British School, Thailand
[2]King Mongkut's International Demonstration School, Thailand
*e-mail: Fringyronaldo@gmail.com

Abstract:
In the past, the study of biological conditions such as scoliosis relied heavily on physical detection through human eyes, with limited access to advanced technology. This often made it difficult for doctors to accurately identify and differentiate between each type of scoliosis, which are thoracic, thoracolumbar, and lumbar. Nowadays, with advancements in artificial intelligence, a deep learning image classification model can assist in recognizing these spinal curvatures more quickly and accurately. The model that is being used is the Xception model, trained using spinal X-ray images. The model achieved a validation accuracy of 68% and a test accuracy of 96%. This can potentially be introduced as a tool to aid in the detection of scoliosis. In the future, doctors can possibly compare their manual classification of scoliosis types with the model's predictions and discussed spinal.

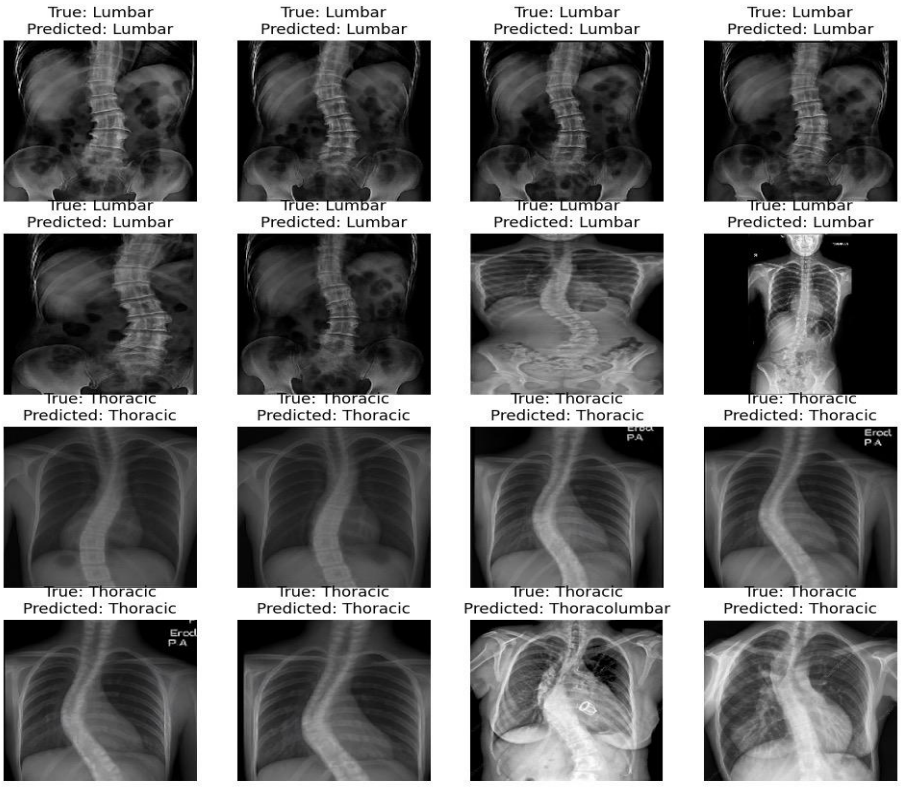


Figure 1.
Example of model predictions

EVALUATION OF CHONDROCYTE CULTURE FORMATS FOR ENHANCING EARLY CARTILAGE MATRIX FORMATION

Matthuros Sonthisathaporn[1], Nattanan T-Thienprasert[1] and Chomdao Sinthuvanich[1*]
Department of Biochemistry, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand
*e-mail: chomdao.si@ku.th

Abstract:
Osteoarthritis (OA) is a chronic disease primarily affecting individuals over 60 years old, with a higher prevalence in females. The global incidence of OA is continuously rising due to aging populations and increasing rates of obesity and injury. Unlike other tissues, damaged cartilage has limited self-healing capabilities due to its avascular nature, low cell count, and abundant extracellular matrix (ECM). Current treatments for OA include surgical interventions such as drilling, subchondral abrasion, microfracture, and Autologous Chondrocyte Implantation (ACI). However, these approaches face challenges such as issues with cell handling and scaffold imperfections. This study aims to explore optimal *in vitro* culture conditions that support cartilage matrix production for potential application in cell-based therapies. Gene expression of Piezo2, ACAN, Col2A1 as well as glycosaminoglycan (GAG), DNA, and hydroxyproline content, were analyzed to identify which culture method best preserves the chondrocyte phenotype and promotes early-stage cartilage matrix synthesis. The results showed that the monolayer culture was superior in maintaining crucial gene expression. This culture also demonstrated enhanced extracellular matrix efficiency, as evidenced by significantly higher GAG/DNA and hydroxyproline/DNA ratios. These results suggest that monolayer culture provides a promising environment for *in vitro* cartilage matrix synthesis, paving the way for future injectable cell-based therapies for OA in both humans and animals.

UV-RESPONSIVE GALLIC ACID CONJUGATED CHITOSAN METHACRYLOYL HYDROGEL: SYNTHESIS AND APPLICATION FOR DIABETIC WOUND TREATMENT

Dong-Joo Park,[1,2] Se-Chang Kim,[2,3] Won-Kyo Jung[1,2,3,*]
[1]Major of Biomedical Engineering, Division of Smart Healthcare Major of Biomedical Engineering and New-senior Healthcare Innovation Center (BK21 Plus), Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
Chronic wounds are often aggravated by excessive inflammation and oxidative stress caused by trauma, burns, infections, and metabolic disorders. Therefore, creating biomaterials that can locally regulate the detrimental impact of overproduced reactive oxygen species (ROS) and prolonged inflammatory responses is critically important. In this work, we developed a novel hydrogel with improved therapeutic potential by combining fish gelatin methacryloyl (FGelMA), an emerging alternative to mammalian-derived gelatin, with gallic acid conjugated chitosan methacryloyl (GA-CSMA). The hydrogels were fabricated using a UV photocrosslinking method and its morphology, rheological properties, swelling behavior, and degradation profiles were systematically investigated. The GM/G-CM hydrogels demonstrated potent radical scavenging activity against DPPH and ABTS, while *in vitro* studies confirmed excellent cytocompatibility, proliferation, migration and angiogenesis. Furthermore, it inhibited the production of nitric oxide (NO), tumor necrosis factor-α (TNF-α), and Interleukin-1β (IL-1β) while enhancing the production of Interleukin-10 (IL-10) in lipopolysaccharide (LPS)-stimulated RAW264.7 macrophages. Finally, in a diabetic mouse model with chronic wound conditions, the hydrogel exhibited anti-inflammatory and angiogenic effects. These results suggest that the GM/G-CM hydrogel, with its enhanced anti-inflammatory and antioxidant properties, can potentially be utilized as a wound dressing to improve hard-to-heal chronic wounds.

OPTIMIZING A SPLIT LENTIVIRAL DELIVERY SYSTEM FOR CRISPR/CAS9-BASED GENE KNOCKOUT IN MESENCHYMAL STEM CELLS

Lanlalit Pongsasakulchot,[1] Kanok Keerati-Opasawat,[1] Natcha Gahawong, [1] Waracharee Srifa[1,*]

[1]Department of Biochemistry, Faculty of Medical Science, Naresuan University, 65000, Thailand

*e-mail: waracharees@nu.ac.th

Abstract:

Pooled CRISPR knockout (KO) screens enable large-scale functional analysis of genotypic-phenotypic relationships for cell line models, leading to insights into cellular functions and disease development. However, applying this approach to primary human cells remains challenging due to limited culture sizes and windows, as well as low delivery efficiency of CRISPR components. Here, we explored a CRISPR-based KO approach compatible with pooled screens using a split lentiviral system for the sequential delivery of sgRNA- and Cas9-expressing vectors in mesenchymal stem cells derived from human exfoliated deciduous teeth (SHED). Our results show that serial transduction using common CRISPR screening lentiviral vectors is compatible with SHED, with up to 76% guide RNA vector delivery efficiency and 56.8% Cas9 vector co-delivery efficiency in serial transduction. The delivery efficiency directly correlated with lentiviral doses with stable expression for both vectors. Gene knockout was validated at the *HBB* locus, resulting in an average indel mutations of 28%. Notably, knockout efficiency is considerably lower than Cas9 delivery efficiency, highlighting Cas9 vector delivery and CRISPR component expression as key limiting factors. These findings establish a proof-of-concept framework for split lentiviral CRISPR/Cas9 delivery in primary MSCs and provide a foundation for future pooled CRISPR screening in MSC models.

EXPLORING FISH GELATIN BIOACTIVE HYDROGEL FOR ENHANCED DIABETIC WOUND HEALING

Nayab,[1,2] Dong-Joo Park,[1,2] Won-Kyo Jung[1,2,3,*]
[1]Major of Biomedical Engineering, Division of Smart Healthcare Major of Biomedical Engineering and New-senior Healthcare Innovation Center (BK21 Plus), Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
Non-healing diabetic wounds remain a significant clinical challenge, often leading to severe complications and threatening patients' lives. Natural biomaterial-based hydrogel dressings have emerged as effective alternatives to accelerate wound repair. In this study, a bioactive hydrogel was developed from fish gelatin (FG), a sustainable substitute for mammalian gelatin, combined with oxidized hyaluronate (OHy) through a Schiff base reaction. The resulting FG–OHy hydrogel exhibited adequate mechanical stability and self-healing properties. In vitro assays demonstrated cytocompatibility and suppression of inflammatory mediators, including NO, IL-1β, TNF-α, and PGE2, in lipopolysaccharide (LPS)-stimulated RAW 264.7 macrophages. Furthermore, the hydrogel reduced intracellular reactive oxygen species (ROS), thereby alleviating oxidative stress. In vivo studies using diabetic mouse models confirmed enhanced wound closure, re-epithelialization, and collagen deposition, alongside upregulated expression of angiogenesis and anti-inflammatory markers such as CD31, CD206, and Arg1. These findings highlight the advanced therapeutic potential of fish gelatin-based hydrogels, positioning them as a promising alternative for diabetic wound management.

SCREENING, PURIFICATION AND WHOLE-GENOME ANALYSIS OF BACTERIOCIN PRODUCED BY *Lactococcus lactis* WWW1-2 WITH POTENTIALS AGAINST *Aeromonas hydrophila*

Woratep Jumi[1], Engkarat Kingkaew[1,*], Papinwit Busayaboriboonchot[1], Pasit Phatcharachaitas[1], Weerapong Woraprayote[2,3,**]
[1]Department of Biology, School of science, King Mongkut's Institute of Technology Ladkrabang, Bangkok, 10520, Thailand
[2]Department of Biochemistry, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, 10700, Thailand
[3]Siriraj Metabolomics and Phenomics Center, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, 10700
*e-mail: engkarat.ki@kmitl.ac.th
**e-mail: weerapong.wor@gmail.com

Abstract:
The growing incidence of antibiotic resistance in *Aeromonas hydrophila* poses a significant threat to aquaculture. *A. hydrophila* is commonly regarded as a pathogen of fish and other aquatic animals, and it also has the potential to infect humans. The main clinical symptoms include gastrointestinal disorders and wound or soft tissue infections. This underscores the urgent need for alternative antimicrobial agents. Bacteriocin-producing lactic acid bacteria (LAB) represent a promising strategy owing to their combined antimicrobial and probiotic properties. In this study, strain WWW1-2 was isolated from wastewater and identified by whole-genome analysis as *Lactococcus lactis*. The probiotic potential of this strain was systematically evaluated. It exhibited strong tolerance to acidic (pH 4.0) and bile conditions (0.3% oxgall), along with notable adhesion to Caco-2 intestinal epithelial cells. Safety assessments revealed no hemolytic activity and the absence of virulence-associated genes, indicating its non-pathogenic character. Bacteriocin production by *L. lactis* WWW1-2 was further characterized. The bacteriocin was purified using a three-step procedure involving Amberlite XAD-16 resin extraction, SP Sepharose ion-exchange chromatography, and C-18 reverse-phase chromatography. The purified compound displayed potent inhibitory activity against *A. hydrophila* B1AhB1, with a titer of 6,400 AU/mL. Overall, these results demonstrate that *L. lactis* WWW1-2 combines safety, probiotic attributes, and strong bacteriocin-mediated antimicrobial activity, highlighting its potential as a viable and effective alternative to conventional antibiotics for the control of aquatic pathogens.

Keywords *Aeromonas hydrophila*, Lactic acid bacteria, Genomic analysis, Antimicrobial peptide, Probiotic

OCT-4 ACTIVATING COMPOUND 1 ENHANCES DEVELOPMENTAL COMPETENCE AND PLURIPOTENCY OF PORCINE SCNT EMBRYOS

Thida Praeksamut[1], Phattarawadee Noita[1] and Rangsun Parnpai[1,*]
[1] Embryo Technology and Stem Cell Research Center, School of Biotechnology, Institute of Agricultural Technology, Suranaree University of Technology, Nakhon Ratchasima, THAILAND
*e-mail: rangsun@g.sut.ac.th

Abstract:
Somatic cell nuclear transfer (SCNT) is an assisted reproductive technique involving a donor cell is transferred into an enucleated oocyte. Its efficiency remains low due to abnormal nuclear reprogramming. Previous studies have shown that SCNT blastocysts exhibit aberrant expression of *OCT-4* and related genes. *OCT-4* transcription factor is crucial for embryonic development, maintaining pluripotency, and regulating primordial germ cell formation. On the other hand, DNA methylation plays an important role in mammalian embryogenesis, such as gene imprinting, X chromosome inactivation, and genome stability. In the cloning technique, SCNT-derived embryos are highly methylated compared with in vitro fertilized embryos. Therefore, abnormal SCNT embryos may be caused by an incomplete reprogramming of DNA methylation. Enhancing *OCT-4* expression in SCNT embryos may improve their reprogramming efficiency. In this study, we investigated the optimal concentration and effects of OCT-4 Activating Compound 1 (OAC1) that was reported to induce the expression of *OCT-4* and *NANOG* in bovine SCNT embryos. Comparisons were made with porcine embryos derived from *in vitro* fertilization (IVF). The results of this study indicated that treatment with OAC1 at a concentration of 1.5 µM significantly increased the blastocyst formation rate and total cell numbers in SCNT embryos ($p < 0.05$). Furthermore, OAC1 enhanced the expression of *OCT-4*, *SOX2*, and *NANOG* specifically at the 8-cell stage, but did not significantly affect gene expression at other developmental stages. Regarding DNA methyltransferase (*DNMT*), IVF embryos exhibited lower expression levels than SCNT embryos during early development, with expression levels increasing from the 8-cell to the blastocyst stages involving re-methylated occurs and new genomic imprints are established by activating the methylation. In conclusion, OAC1 appears to exert beneficial effects on embryonic development in SCNT embryos by promoting *OCT-4* and related genes expression and reprogramming through modulation of DNA methylation.

ASSESSMENT OF THE ANTIOXIDANT AND ANTI-INFLAMMATORY PROPERTIES OF HUMAN PLACENTAL EXTRACT IN HUMAN MESENCHYMAL STEM CELLS

Kanda Rungboon, Nipha Chaicharoenaudomrung, Natchadaporn Sorraksa, Phongsakorn Kunhorm, and Parinya Noisa*
School of Biotechnology, Institute of Agricultural Technology, Suranaree University of Technology
*Corresponding e-mail: kandakdrb@gmail.com

Abstract:
Cellular senescence is a major human concern, caused by both natural aging and external environmental factors. Among these factors, if the body accumulates oxidative stress in the body weakens physiological functions, leading to cellular deterioration, organ dysfunction, and aging. As a result, people have increasingly turned to dietary supplements and commercial cosmetics to maintain their health and beauty. However, one major problem with most products may have long-term side effects and increase the risk of chronic diseases. Human placental extract (HPE) has gained increasing attention in scientific and clinical fields as a promising natural supplement whose advantages include being naturally sourced and having few side effects. It's rich in nutrients, cytokines, and growth factors that contribute to its antioxidant properties, restore cells, and delay cellular senescence. Therefore, this study aimed to evaluate the effects of HPE at optimal concentrations under both normal and oxidative stress conditions through 3-[4,5-dimethyl-2-thiazolyl]-2,5-diphenyl-2H-tetrazolium bromide (MTT) assays, 2',7' dichlorodihydrofluorescein diacetate (DCFH-DA) assays, and gene expression analysis through reverse transcription (RT)-PCR. The results suggested that HPE significantly decreased the production of intracellular reactive oxygen species (ROS) compared to the untreated control under stress conditions. Mechanistically, RT-PCR analysis revealed that HPE significantly enhanced antioxidant defense mechanisms by upregulating the expression of key antioxidant genes superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPX) in a dose-dependent manner. This collective gene regulation demonstrated that HPE effectively strengthened the cellular antioxidant system, leading to a decrease in ROS production and subsequent delay of cellular senescence. These findings strongly supported the potential of HPE as a safe and scientifically validated natural compound for mitigating oxidative stress and combating age-related cellular deterioration in supplements and cosmeceuticals.

NOVEL INSIGHTS INTO THE ROLE OF VESICLE- AND MONOLAYER-DERIVED EXTRACELLULAR VESICLES FROM BOVINE OVIDUCT EPITHELIAL CELLS IN ENHANCING EMBRYO QUALITY In Vitro

Apisit Polrachom[1,1], Kamolchanok Tonekam[2], Worawalan Samruan[3], Traimat Boonthai[5,2] and Rangsun Parnpai[6*]

[1]Embryo Technology and Stem Cell Research Center, School of Biotechnology, Institute of Agricultural Technology, Suranaree University of Technology, Nakhon Ratchasima 30000, Thailand

[2]Biological Science Program, Faculty of Science, Burapha University, Chon Buri 20131, Thailand

*e-mail: rangsun@g.sut.ac.th

Abstract:

This study investigated the effects of extracellular vesicles (EVs) derived from bovine oviduct epithelial cells (BOECs) on the development of bovine embryos during in vitro culture (IVC). EVs play an essential role in mimicking the oviductal microenvironment by transferring bioactive molecules such as proteins and RNAs, thereby facilitating intercellular communication and embryo development. In this experiment, EVs were isolated from two BOEC culture systems: a monolayer culture (BOEC-M-EVs) and a vesicle-forming culture (BOEC-V-EVs). These EVs were supplemented into the IVC medium at concentrations of 2×10^6, 4×10^6, and 8×10^6 particles/mL, while non-supplemented embryos served as controls. Supplementation with BOEC-M-EVs significantly increased total blastocyst cell numbers at all concentrations tested (132.8 ± 3.6, 147.6 ± 5.6, and 148.2 ± 1.7) compared with the control group (108 ± 5.2, $P < 0.05$). Similarly, BOEC-V-EVs enhanced total cell numbers at 4×10^6 and 8×10^6 particles/mL (149.0 ± 1.7 and 158.6 ± 3.2, $P < 0.05$). Both EV types improved blastocyst quality at higher concentrations, consistent with the upregulation of IFNτ, a gene essential for maternal recognition of pregnancy in ruminants. These findings demonstrate that BOEC-derived EVs support embryo development by recreating physiological cues of the oviduct and suggest their promising application for enhancing in vitro embryo production and reproductive efficiency in cattle.

Keywords: ruminant species, reproduction, oviduct epithelial cells, *In vitro* fertilization

DEVELOPMENT OF DIGITAL DROPLET PCR (ddPCR) ASSAY FOR RAPID DETECTION OF G6PD VIANGCHAN MUTATIONS IN THAI POPULATIONS

Akawich Wangsiriwech[1]*
[1]Concordian International School Grade 12
*e-mail: akawichwangsiriwech@gmail.com

Abstract:
G6PD Viangchan (c.871G>A, p.Val291Met) is the most prevalent G6PD deficiency variant in Thailand, contributing to severe hemolytic anemia upon exposure to oxidative stress. Conventional diagnostic methods such as UV spectrophotometry assays are unable to detect heterozygous carriers, whilst Fluorescence spot tests (FST), have low quantitative accuracy.

A digital droplet PCR (ddPCR) assay targeting G6PD Viangchan using variant-specific TaqMan probes was developed, aiming to improve accuracy and diagnostic time. Following thermal optimization, samples underwent ddPCR analysis and genotype calls were validated against sequencing-confirmed diagnoses.

Among 13 clinical samples, 11 generated results whilst 2 failed due to insufficient DNA. The assay demonstrated 100% sensitivity (95% CI: 29.2%-100%), 100% specificity (95% CI: 63.1%-100%), and 100% positive predictive value.

Results identified three homozygous wild type females, one homozygous mutant female, three hemizygous wild type males, and two hemizygous mutant males. Two samples showed wild type with minimal mutant contamination.

The limited sample size of 13 creates a wide confidence interval, warranting a larger validation study to confirm robustness. The assay is currently limited to Viangchan. However, through multiplex ddPCR panel, the assay may offer comprehensive rapid single-screening of the prevalent G6PD deficiencies in Southeast Asian populations.

Keywords: G6PD, Viangchan, ddPCR, validation

ESTABLISHMENT OF THE GLYCOPROTEIN CD147 KNOCKOUT IN A HUMAN LEUKEMIA CELL LINE (K562) USING LENTIVIRUS-BASED CRISPR/CAS9 SYSTEM.

Wannakan Jaikamlue[1], Kumpanat Pomlok[2], Suparat Lithanatudom[3], Jiraprapa Wipasa[4], Pathrapol Lithanatudom[1, *]

[1] Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, 50200, Thailand

[2] Department of Microbiology, Faculty of Science, Silpakorn University, Nakhon Pathom, 73000, Thailand

[3] Program in Genetics, Faculty of Science, Maejo University, Chiang Mai 50290, Thailand

[4] Research Institute for Health Sciences, Chiang Mai University, Chiang Mai, 50200, Thailand

[*]e-mail: pathrapol.l@cmu.ac.th

Abstract:

Cluster of differentiation 147 (CD147) is a plasma membrane-bound glycoprotein that functions as an adhesion molecule. While CD147 has been proposed as a promising biomarker in cancer and a potential antitumor targeting solid tumors/adherent cell model, its role in leukemia (suspension cells) has not been extensively studied. Therefore, this study aimed to establish the CD147-knockout leukemia models in a human leukemia cancer cell line (K562) using CRISPR-Cas9 technology. In this study, we successfully generated 6 stable cell lines bearing CD147-depletion namely KO1, KO6, KO8, KO9, KO10 and KO13. Flow cytometry analysis confirmed KO6 was the most significant reduction in CD147 expression. Besides, morphological analysis revealed that the CD147-depleted cells were relatively larger in size with an increased level of debris as compared to controls. We hypothesize that the type of cell death is most likely a necrotic-like cell death since the cell morphology after CD147-knockout are primarily associated with cellular enlargement and swelling. Taken together, we concluded that disruption in CD147 expression in K562 cells was detrimental to cell survival, thus, further studies should be conducted to explore the role of CD147-knockout in greater details, particularly focusing on the molecular mechanisms underlying the cellular aberration of CD147-depleted K562 cells.

Session III.

Industrial & Environmental Biotechnology, & Alternative Energy

FLUOROMETRIC DETECTION OF IRON(III) IONS AND HEMOGLOBIN USING O-TOLUIDINE BASED CARBON DOTS

Woo Tae Hong,[1] Sung Jun Park,[2] Jae Yong Jung,[2] Jin Young Park,[3] Hyun Kyoung Yang[2,3,4*]
[1]Industry-University Cooperation Foundation, Pukyong National University, Busan 48513, Republic of Korea
[2]Marine-Bionics convergence technology center, Pukyong National University, Busan 48513, Republic of Korea
[3]Major of Electrical, Electronics, and Software Engineering, Pukyong National University, Busan, 48548, Republic of Korea
[4]University College, Pukyong National University, Busan, 48513, Republic of Korea
*e-mail: hkyang@pknu.ac.kr

Abstract:
The fluorometric detection or iron(III) ions (Fe^{3+}) is required in environmental detection, anemia diagnosis, and criminal investigation. In order to improve their performance, water soluble properties, facile synthesis, cheap detection cost, and high quantum yield is highly demanded to luminescent materials for fluorometric detection. In this study, the morphological, structural, luminescent characteristics of carbon dots (CDs) and their fluorometric detection of Fe^{3+} and hemoglobin were researched. The CDs based on o-toluidine were synthesized via hydrothermal process. The CDs exhibits two-dimensional honeycomb lattice with hydrophilic properties. Moreover, the CDs behave blue dominant emission under 240 nm light excitation. Their luminescence intensity was decreased by adding Fe^{3+} and hemoglobin concentration, which is related with fluorescence resonance energy transfer between CDs and analytes. Compared with other heavy metal ions, this phenomenon has high selectivity due to the energy transfer between hydroxyl group of CDs and Fe^{3+} ions, as shown in Figure 1. The limit of detection of Fe^{3+} and hemoglobin were calculated to be 0.133 mM and 72 nM, respectively. These results indicate that the CDs can be applied as a luminescent material in fluorometric detection of Fe^{3+} and hemoglobin for environmental detection, anemia diagnosis, and criminal investigation.

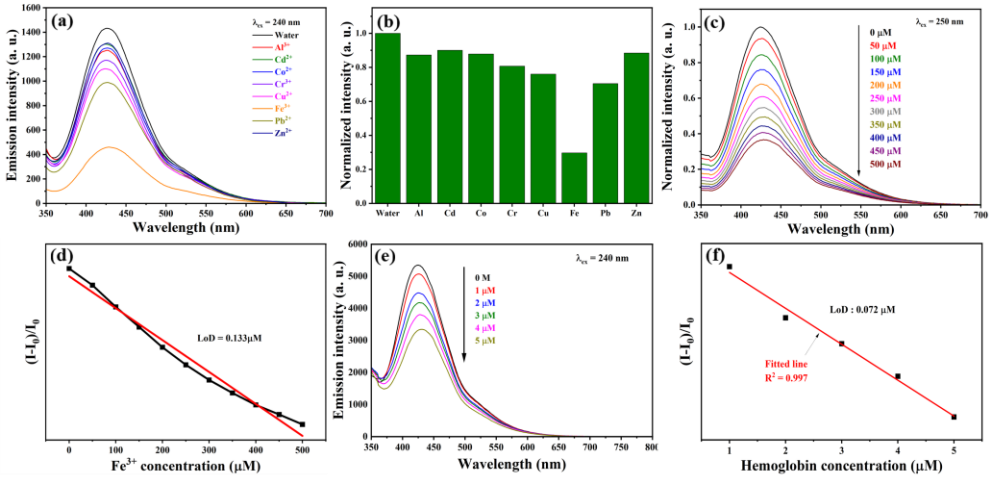


Figure 1.
Comparison of (a) luminescence spectra and (b) luminescence intensity of CDs-heavy metal ion system for various heavy metal ions, (c) luminescence spectra and their (d) correlation graph between concentration of Fe^{3+} ions and quenching ratio ($(I-I_0)/I_0$), (e) luminescence spectra and (f) correlation graph between hemoglobin concentration and quenching ratio.

CRISPR/Cas9-DRIVEN GENE KO OF β-GLUCAN SYNTHASE GENE *fks*s IN SELECTIVE LIGNIN-DEGRADING FUNGUS, *Gelatoporia subvermispora*

Junko Sugano, Moriyuki Kawauchi, Yoichi Honda*
Graduate School of Agriculture, Kyoto University, Japan
*e-mail: honda.yoichi.5n@kyoto-u.ac.jp

Abstract:
Gelatoporia (*Ceriporiopsis*) *subvermispora*, a selective white-rot basidiomycete, synthesizes an extracellular polysaccharide, sheath, between its hyphae and wood substrate. Sheath is proposed to have a special role in wood degradation by this fungus. However, the biosynthesis mechanism for the cell surface polysaccharides in *G. subvermispora* is still unclear. β-1,3-glucan is suggested to be a major component of the agaricomycete cell wall, as well as sheath. The present study investigated the function of *fks* encoding fungal membrane protein that synthesizes β-1,3-glucan in the cell surface structure formation in *G. subvermispora*.

G. subvermispora was predicted to have two distinct *fks* genes, *fks1* and *fks2*, by phylogenetic analysis. *fks1* and *fks2* disruptants were obtained by CRISPR/Cas9 genome editing. Growth tests and India ink staining indicate that both disruptants demonstrated a reduction in radial growth and the width of sheath layer, respectively, with more apparent reduction in the *fks1* disruptants. TEM observation suggests that the cell wall of the wild type may have a two-layer structure. The boundaries between each layer were vague in the *fks1* disruptant, while in the *fks2* disruptant, the two-layer structure disappeared, and the cell wall became thinner. The results imply that Fks1 and Fks2 play distinct roles in the cell surface structure formation of *G. subvermispora*.

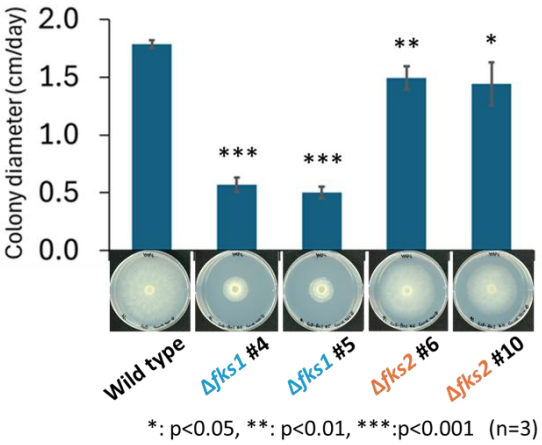


Figure 1.
Effect on growth by *fks* disruption

SYNERGISTIC N-CAPROIC ACID PRODUCTION VIA CO-CULTURE OF *Enterococcus faecalis* isolate VT-H1 AND *Clostridium kluyveri*

Suttavadee Junyakul,[1]**Thanyaporn Wongnate**[1,*]
[1]School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC),Rayong 21210, Thailand
*e-mail: thanyaporn.w@vistec.ac.th

Abstract:
The microbial production of medium-chain fatty acids (MCFAs) through chain elongation offers a sustainable route for converting short-chain fermentation products into high-value bio-based chemicals. *Enterococcus faecalis* isolate VT-H1, previously characterized for its high hydrogen production and its ability to generate acetic and butyric acids, presents a promising candidate for integration into chain elongation systems. In this study, we developed a co-culture platform combining *E. faecalis* isolate VT-H1 and *Clostridium kluyveri*, leveraging their complementary metabolic capabilities to enhance n-caproic acid biosynthesis. The co-culture system was evaluated under controlled conditions with 130 mM ethanol supplementation. Optimal performance was achieved at pH 7.0 and 37 °C, producing 127.89 mM of n-caproic acid, corresponding to a yield of 2.51 g caproic acid per g ethanol consumed, while also utilizing acetate and butyrate supplied by *E. faecalis*. The presence of *E. faecalis* VT-H1 supported precursor supply (acetate and butyrate) while simultaneously sustaining anaerobic redox balance through hydrogen production, which likely facilitated more efficient metabolism in *C. kluyveri*. Beyond its biotechnological significant, n-caproic acid has substantial industrial and economic relevance as a versatile platform chemical, serving as a precursor for antimicrobials, biofuels, plasticizers, and fragrance compounds, thereby providing strong incentives for sustainable bioprocess development. These findings highlight the feasibility of integrating hydrogenogenic and chain-elongating microbial strains to drive MCFAs production, paving the way for future scale-up and application of co-culture platforms in waste-to-chemical valorization strategies.

EVALUATING *Chlorella* sp. GROWTH IN SOLAR PANEL SHADED GREENHOUSES

Nien-Hua Chen Tai,[1] Chieh-Ting Lin,[1] Yan-Yu Chen [1,*]
[1]Department of Chemical Engineering, National Chung Hsing University, No. 145, Xingda Rd., South Dist., Taichung, 40227, Taiwan (R.O.C.)
*e-mail : annayyc0707@nchu.edu.tw

Abstract:
Microalgae are promising organisms for CO_2 fixation due to their rapid growth and efficient photosynthesis. However, outdoor cultivation is often challenged by fluctuating and excessive sunlight, which can cause photoinhibition and limit microalgal growth. This study employed semi-transparent organic photovoltaic (OPV) panels, which transmit partial light while generating electricity but also reduce excessive sunlight, therebuy optimize the photon conversion efficiency (PCE). We investigated the growth of *Chlorella* sp. under two light conditions: one shaded by OPV panels and one exposed to sunlight. Cultures were grown in 1000-mL serum bottles, continuously aerated with air. Daily measurements included OD_{685}, light intensity, and temperature. Results showed shaded group slower increase in OD_{685} but higher PCE. Despite receiving only 30% PPFD of the sunlight group, the OPV-shaded culture maintained 70% growth rate, Moreover, OPV shading reduced culture temperature fluctuations by 3-5 ℃ compared to full sunlight, which likely alleviated heat stress, contributed to maintaining relatively high growth despite reduced light availability. This study demonstrates the feasibility of cultivating microalgae in OPV-integrated greenhouses, combining renewable energy generation with microalgae culture. Future work will aerate cultures with CO_2, calculate CO_2 fixation based on inlet and outlet CO_2 concentrations, and also investigate differences between PV and OPV.

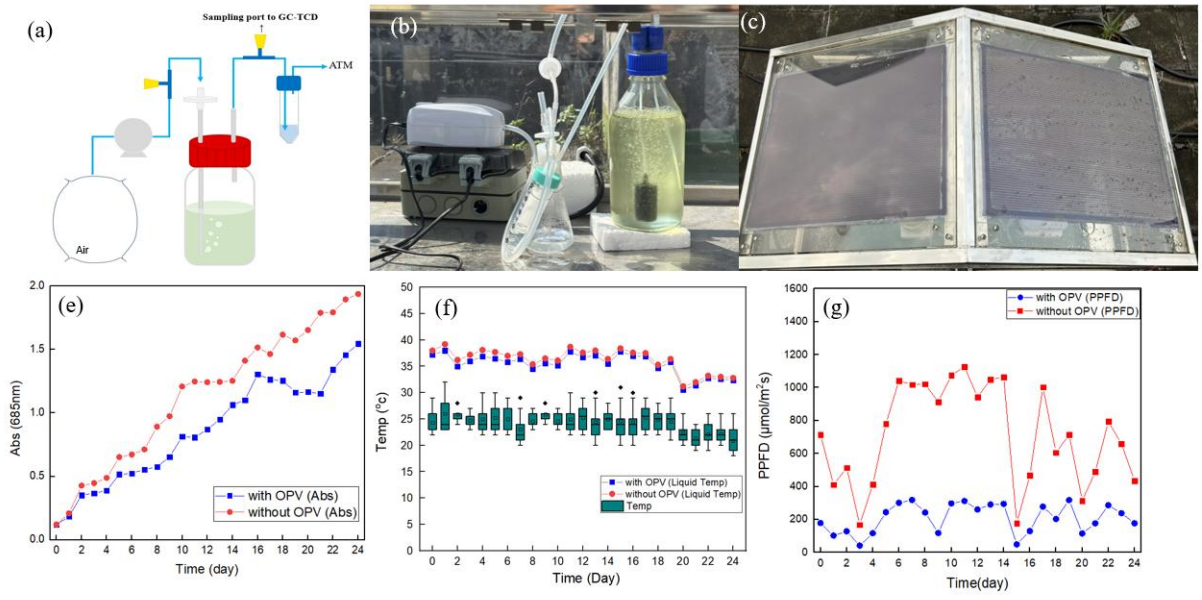


Figure 1.
(a) Experimental setup schematic. (b) Photo of the actual cultivation system. (c) Semi-transparent OPV solar panels on greenhouse roof. (e) OD_{685} v.s. Time. (f) Midday maximum liquid temperatures in the bottles compared with ambient air temperature. (g) PPFD profiles under with and without OPV shading

EVALUATION OF MOSS GROWTH AND ITS EFFECTIVENSS IN CARBON DIOXIDE UPTAKE

Jyun-Yan Kuo,[1] Yan-Yu Chen[1,*]
[1]Department of Chemical Engineering, National Chung Hsing University, No. 145, Xingda Rd., South Dist., Taichung, 40227, Taiwan (R.O.C.)
*e-mail: annayyc0707@nchu.edu.tw

Abstract:
Physcomitrium patens was evaluated as a photosynthetic, carbon-fixing platform due to its high chlorophyll content, which enables it to grow well in low light. Three 20-mL liquid-culture methods were tested, including magnetic stirring, orbital shaking and air bubbling, to determine the most effective method of cultivating moss. Orbital shaking provided the optimal balance of gentle mixing and efficient mass transfer. This method yielded the best growth results and was selected for scaling up to 200 mL. Subsequently, the cultures were supplied with 2% (v/v) CO_2 under two reactor configurations: a fully submerged aqueous phase and a direct gas-phase contact chamber. Gas analysis by GC-TCD verified CO_2 removal in both systems. However, the moss fixed CO_2 at rates of 0.029 mg/OD/h and 0.066 mg/OD/h in the liquid and gas phases, respectively, which is approximately twice the rate in the liquid phase. This demonstrates the advantage of minimising gas-liquid transfer resistance and maximising tissue exposure to CO_2. The dry cell weight of the moss before and after the reactions will be determined in order to estimate the rate at which CO_2 is stored in biomass and to evaluate performance under various CO_2 concentrations.

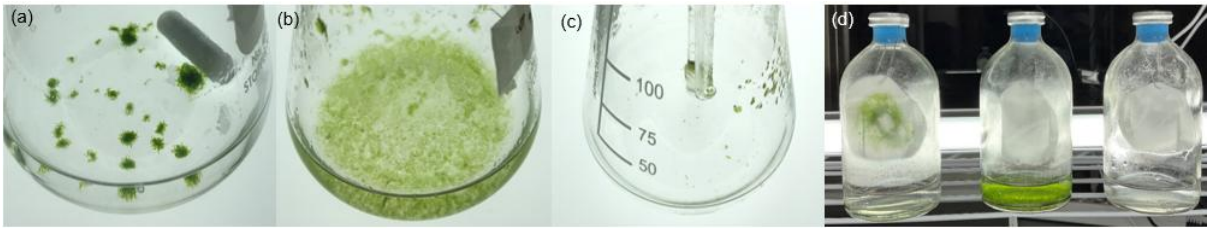


Figure 1.
Cultivation by using (a) magnetic stirring, (b) orbital shaking, and (c) air bubbling. (d) Gas-phase and liquid-phase bioreactors for evaluating CO_2 fixation rates.

UNLOCKING THE POTENTIAL OF ANAEROBIC DIGESTION FOR TROPICAL COMMUNITIES: THE SUZDEE SYSTEM'S APPROACH TO BIOGAS AND BIOFERTILIZER PRODUCTION

Charndanai Tirapanampai[1], Thamonwan Woraruthai[1], Thipwan Jiemanukunkij[1], Suchada Sawatraksa[1], Patchaneewan Witdyawudthikul[1], Sasithorn Rungjaroenchaiwat[1], Cheerapat Suphawatkon[1], Pattama Senthong[2], Ruchareka Wittayawuttikul[1], Pimchai Chaiyen[1] and Thanyaporn Wongnate[1*]

[1] School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC), Rayong 21210, Thailand

[2] Faculty of Science and Industrial Technology, Prince of Songkla University, Surat Thani Campus, Muang, Surat Thani, Thailand 84000, Thailand

* Corresponding author. E-mail address: thanyaporn.w@vistec.ac.th (T. Wongnate).

Abstract:

This study presents the implementation and performance evaluation of the "SUZDEE (Sustainable Zero Waste Digestant for Well-Being)" anaerobic digestion (AD) system in Thailand for food waste (FW) management (Figure 1). The SUZDEE system is a small-scale, decentralized AD unit designed for household and community use. Each unit comprises a 1,000-L digester operated under mesophilic conditions, with daily FW loading (1-5 kg/day) and manual mixing to maintain process stability. Biogas was captured through gas-tight tubing and quantified using a gas flow meter, while digestate was collected periodically and analyzed for nutrient composition to ensure its suitability as a biofertilizer. Over the course of one year, 29 systems were deployed across 14 Thai provinces, collectively processing 15,335 kg of FW. The systems produced 747 m^3 of biogas (equivalent to 15,579 MJ) and 13,941 L of nutrient-rich biofertilizer, generating an estimated 8,282 USD in community value while reducing greenhouse gas emissions by 10,475 kgCO_2 equivalent. Social return on investment (SROI) analysis demonstrated an additional social value of 9,979 USD, corresponding to an SROI ratio of 1.0914. A community survey further indicated high levels of user satisfaction (average score of 4/5) across ease of operation, odor management, and fertilizer utilization. The implementation of SUZDEE systems supports the United Nations Sustainable Development Goals (SDGs) 11 and 12, which emphasize sustainable cities, communities, and consumption. These findings highlight the feasibility of scaling up SUZDEE or similar AD systems in tropical low-income regions, enabling circular economy pathways through resource-efficient and waste-to-wealth strategies.

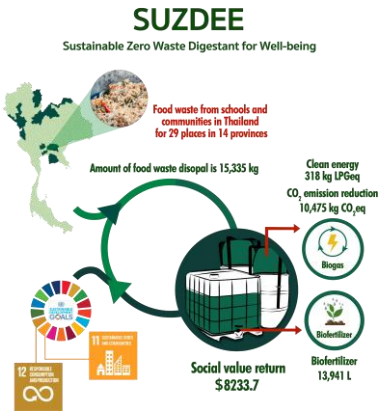


Figure 1.

ENHANCED BIOHYDROGEN PRODUCTION FORM FOOD WASTE USING IMMOBILIZED *Enterococcus faecalis* ISOLATE VT-H1

Sasithorn Rungjaroenchaiwat Thamonwan Woraruthai and Thanyaporn Wongnate*
School of Biomolecular Science & Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC), Wangchan Valley, Rayong 21210, Thailand
*Corresponding author e-mail: thanyaporn.w@vistec.ac.th

Abstract:
The development of cost-effective and sustainable biohydrogen production is vital for renewable energy. This study evaluates immobilized *Enterococcus faecalis* isolate VT-H1 for hydrogen production from food waste under mesophilic conditions. Microbial cells were entrapped in calcium alginate beads, and the effects of alginate concentration and cell density were optimized. Scanning electron microscopy confirmed stable immobilization and cell growth within the matrix, enhancing hydrogen production kinetics. Optimal conditions (2% w/v alginate, OD_{600} of 1.0) yielded a maximum hydrogen production rate of 0.040 mol H_2/mol glucose·h with a shortened lag phase. Immobilized cells retained high hydrogen yields over three reuse cycles, confirming operational stability. Compared with suspended-cell cultures, the immobilized system achieved superior performance with both sucrose and real food waste, reaching 101.3 mL H_2/gVS at 20 gVS/L. Volatile fatty acid analysis showed butyrate as the main metabolite linked to optimal yields, while excessive substrate led to VFA accumulation and reduced efficiency. Techno-economic assessment indicated improved cost-efficiency from inoculum reusability despite slightly lower batch yields. These findings establish immobilized *E. faecalis* VT-H1 as a promising biocatalyst for scalable, economically viable hydrogen production from food waste, integrating renewable energy generation with sustainable organic waste management in a circular bioeconomy framework.

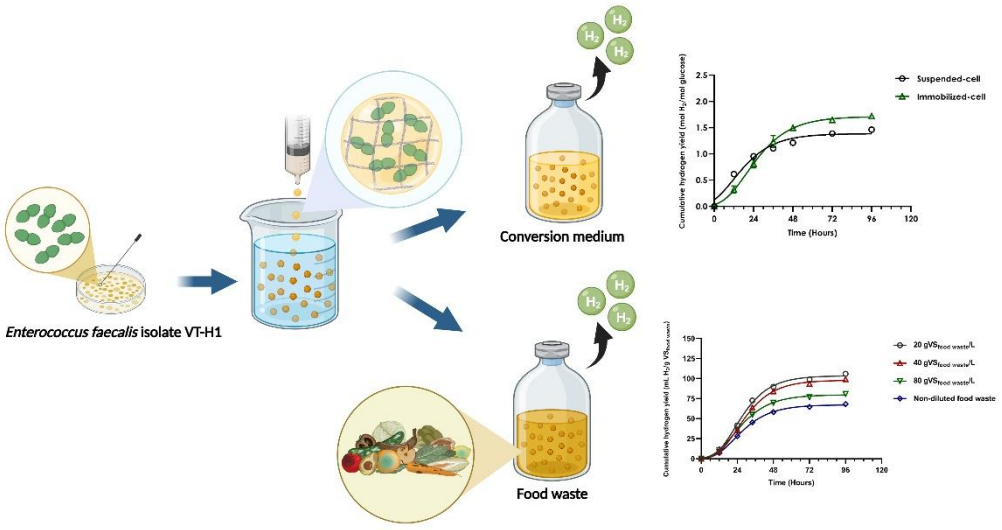


Figure 1.
Schematic diagram of this study

INTEGRATED APPROACHES FOR LDPE BIODEGRADATION IN SOIL USING MICROBIAL AND PHYSICOCHEMICAL STRATEGIES

Chanokporn Muangchinda,[1] Kallayanee Naloka,[1] Onruthai Pinyakong[1,2,*]
[1]Center of Excellence in Microbial Technology for Marine Pollution Treatment (MiTMaPT), Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand
[2]Center of Excellence on Hazardous Substance Management (HSM), Bangkok 10330, Thailand
*e-mail: onruthai.p@chula.ac.th

Abstract:
Low-density polyethylene (LDPE), widely used in single-use products, is highly resistant to natural degradation, leading to its accumulation in the environment. This study developed a synthetic bacterial consortium comprising *Gordonia sihwensis* LS1, *Amycolatopsis thermoflava* 3B14, and *Mesorhizobium* sp. 1B3 to enhance LDPE biodegradation in soil. Visible light provided by a 24W LED lamp (220 V, 60 Hz) and a deep eutectic solvent (DES), prepared by mixing choline chloride and glycerol in a 1:2 molar ratio, were applied individually or in combination with bioaugmentation. After 60 days, the combined treatment achieved the highest degradation, with 7.88% LDPE weight loss and a half-life of 504 days, compared to 1.66%-5.87% weight loss and half-lives of 685-2,482 days in other treatments. Scanning electron microscopy and Fourier-transform infrared spectroscopy revealed surface roughness and reduced spectral intensities, indicating polymer breakdown. 16S rRNA gene amplicon sequencing showed that consortium members persisted in soil without affecting the indigenous microbial communities. Genomic analysis identified genes associated with LDPE degradation, as well as genes for biofilm formation and biosurfactant production, which may facilitate degradation. These findings demonstrate the consortium's potential for accelerated LDPE degradation and underscore the effectiveness of integrating microbial and physicochemical strategies for mitigating plastic pollution in soil.

ISOLATION AND CHARACTERIZATION OF *Enterococcus faecalis* VT-H2 FOR ENHANCED BIOHYDROGEN PRODUCTION FROM PALM OIL MILL EFFLUENT

Cheerapat Suphawatkon Thamonwan Woraruthai Charndanai Tirapanampai Thanyaporn Wongnate*
School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology, Rayong 21210, Thailand
*e-mail: thanyaporn.w@vistec.ac.th

Abstract:
This study aimed to isolate and comprehensive characterization of *Enterococcus faecalis* VT-H2 from palm oil mill effluent (POME), integrating hybrid genome sequencing, pan-genome analysis, growth optimization, and fermentation performance. Morphological and genomic analyses revealed that VT-H2 harbors a streamlined 2.69 Mb genome lacking plasmids but enriched with carbohydrate-active enzymes, hydrogenase components, and polysaccharide transport systems, underscoring its metabolic versatility. Comparative pan-genomics with VT-H1 highlighted strain-specific enrichment in glycosyl hydrolases and uptake pathways. The annotated genome contained key polysaccharide-degrading enzymes such as endoglucanase (EC 3.2.1.4) and β-glucosidase (EC 3.2.1.21), supporting efficient hydrolysis of cellulose and hemicellulose into glucose, providing a genomic basis for enhanced lignocellulose utilization. Physiological assays confirmed robust growth across mesophilic conditions (30-40 °C) and resilience to variable pH, while fermentation trials demonstrated hydrogen production of up to 44.8 mL H_2/g VS from raw POME. Notably, alkaline conditions favored higher cumulative yields, whereas near-neutral conditions enhanced production rates, highlighting trade-offs between yield and kinetics. Together, these results position VT-H2 as a metabolically adaptable and industrially robust strain for valorizing agro-industrial residues into hydrogen. Beyond strain-specific insights, this study illustrates the power of genome-informed microbial selection for optimizing waste-to-energy bioprocesses and lays the groundwork for scalable, low-cost biohydrogen production platforms.

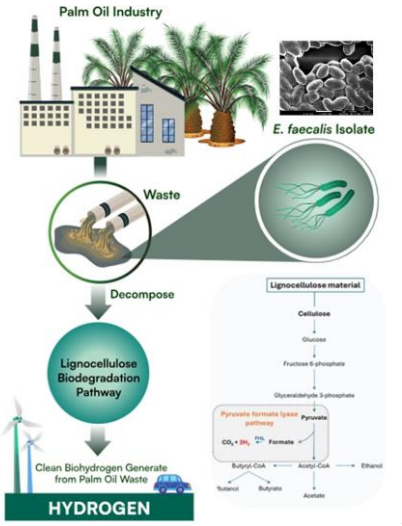


Figure 1.
Overview of this study

BIODEGRADATION OF CO-OCCURRING POLYETHYLENE MICROPLASTICS AND DI(2-ETHYLHEXYL) PHTHALATE BY *Ancylobacter* sp. PD-4

Sakaoduoen Bunsangiam,[1] Chatsuda Sakdapetsiri,[2] Onruthai Pinyakong[1, 3]*
[1]Center of Excellence in Microbial Technology for Marine Pollution Treatment (MiTMaPT), Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand
[2] Department of Plant Pathology, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom, Thailand
[3]Research Program on Remediation Technologies for Petroleum Contamination, Center of Excellence on Hazardous Substances Management (HSM), Bangkok, Thailand
*e-mail: Onruthai.p@chula.ac.th

Abstract:
The co-occurrence of polyethylene microplastics (PE MPs) and di(2-ethylhexyl) phthalate (DEHP) results from their widespread use in agricultural plastics, with both being simultaneously released during film degradation and fertilizer application. PE MPs disrupt soil ecosystems and accumulate through food chains, while DEHP is an endocrine disruptor linked to developmental and reproductive toxicity, posing ecological and human health concerns. This study investigated the combined effects of PE MPs and DEHP on soil microbial communities and identified microorganisms capable of degrading both pollutants. Soil microcosm experiments showed that co-exposure delayed PE MP degradation but did not significantly alter microbial community composition. Fifteen bacterial strains were isolated, with *Ancylobacter* sp. PD-4 exhibiting the highest efficiency, removing 14.7% of PE MPs after 60 days and degrading 60.7% of DEHP within 7 days. Scanning electron microscopy and elemental analysis confirmed polymer surface damage and an increased oxygen-to-carbon (O/C) ratio. Genomic and metabolomic analyses revealed potential degradative enzymes, including laccase, alkane monooxygenase, and phthalate dioxygenase, and highlighted distinct metabolic pathways for each pollutant. These findings establish *Ancylobacter* sp. PD-4 as a promising candidate for developing bioremediation strategies to address complex plastic and plasticizer contamination in agricultural environments.

ENHANCEMENT OF PHOSPHITE-DEPENDENT BIOCONTAINMENT STRATEGY THROUGH ENGINEERING OF THE SUBSTRATE SPECIFICITY OF A PHOSPHORUS TRANSPORTER

Akari Miwa, Naoki Momokawa, Gamal Nasser Abdel-Hady, Akio Kuroda, Ryuichi Hirota*
Unit of Biotechnology, Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan
*e-mail: hirota@hiroshima-u.ac.jp

Abstract:
Advances in genetic and metabolic engineering have enabled the development and application of various genetically modified microorganisms. However, their potential release into natural environments poses biosafety and biodiversity concerns. To address this issue, genetic biocontainment strategies have recently attracted considerable attention to prevent the uncontrolled proliferation of engineered microbes outside enclosed facilities. Previously, we established a biocontainment strategy based on the dependency on phosphite (Pt), a phosphorus compound rarely detected in natural environments. This strategy was implemented by introducing the exogenous Pt/hypophosphite (HPt)-specific transporter *htxBCD*, together with the phosphite dehydrogenase *ptxD*, while disrupting all endogenous phosphorus transporters. Although this strategy is highly effective, it may be compromised by anthropogenic Pt release from agricultural applications and industrial wastewater. In this study, we developed a more stringent biocontainment strategy based on HPt-dependency owing to the greater scarcity and environmental instability of HPt compared to Pt (Fig. 1A).

To confer HPt-dependency, we engineered the substrate-binding protein (HtxB) of the HtxBCD transporter via site-directed mutagenesis, resulting in two single mutants (W52A and D206A) capable of selectively transporting HPt but not Pt (Fig.1B). We then disrupted all phosphorus transporters in *E. coli* MG1655 and introduced the genes for the engineered HPt-specific transporter HtxB*CD, PtxD, and HPt dioxygenase HtxA. The engineered strain exhibited strict HPt-dependency. Furthermore, in an escape mutation assay using 3.1×10^{10} cells, no escape mutants capable of utilizing an alternative phosphorus source were detected, confirming the effectiveness and robustness of HPt-dependency as a biocontainment strategy.

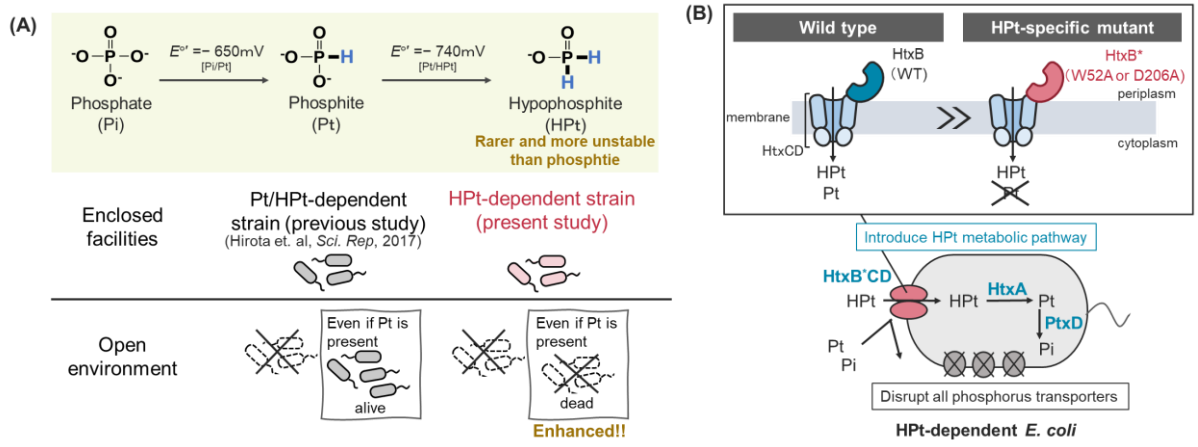


Figure 1.
The concept of this study. A) Comparison between the Pt-dependent and HPt-dependent biocontainment strategies. B) Simplified schematic of the HPt-dependent biocontainment strategy.

A SUSTAINABLE CONVERSION PLATFORM FOR BIO-BASED A-HYDROXYACETIC ACID: FROM RECYCLED ETHYLENE GLYCOL TO GREEN CLEANING AND ETCHING APPLICATIONS

Subhankar Dhar[1] and Liang-Jung Chien[1]*
[1] Department of Chemical Engineering, Ming Chi University of Technology, New Taipei City, Taiwan
*e-mail: LJCHIEN@mail.mcut.edu.tw

Abstract:
Green chemistry and circular economy have become key focuses in chemical and bioprocess industries, yet developing efficient, non-food-based production platforms for bio-based chemicals and expanding their applications remains a challenge. In this study, we developed a high-efficiency bio-based α-hydroxyacetic acid (GA) conversion platform using ethylene glycol as the feedstock through engineered *Gluconobacter* sp. This platform reduces reliance on food crops and enables the use of recycled raw materials, achieving an 86.74% conversion rate and a final GA concentration of 39.84 g/L. For downstream applications, GA (1 M) combined with SLS (0.1% w/v, equivalent to 3.5 mM) achieved a 96% removal rate of oxide layers and oil residues from copper, aluminum, and stainless steel with 90% less corrosivity compared to conventional cleaning agents. For etching applications, GA (1 M) + H_2O_2 (3% w/v, equivalent to 0.88 M) was effective for copper and aluminum, while GA + $FeCl_3$ (0.5 M) enabled selective etching of stainless steel. Biodegradability was evaluated through biochemical oxygen demand (BOD) testing, chemical oxygen demand (COD) testing, and simulated wastewater treatment degradation tests, with GA concentration monitored by HPLC. Results demonstrated an 82% degradation within 28 days, whereas conventional acidic cleaners showed negligible biodegradability. This work demonstrates the feasibility of combining a GA conversion platform with eco-friendly downstream applications, providing an innovative solution for green chemistry and sustainable processing.

EFFICIENT AZEOTROPIC CONDENSATION STRATEGY FOR SUSTAINABLE PRODUCTION OF POLY(GLYCOLIC ACID) FROM GLYCOLIC ACID

Maroof Ali[1] and Liang-Jung Chien[1]*
[1] Department of Chemical Engineering, Ming Chi University of Technology, New Taipei City, Taiwan
*e-mail: LJCHIEN@mail.mcut.edu.tw

Abstract:
Poly(glycolic acid) (PGA) is a biodegradable polymer with growing relevance in packaging and biomedical applications. Compared with conventional plastics such as PET, PP, and PE, PGA combines high tensile strength, superior gas barrier performance, and complete biodegradability, making it an attractive, sustainable alternative. Here, PGA was synthesized via azeotropic condensation of glycolic acid using methanesulfonic acid as catalyst and o-xylene/Dean–Stark for continuous water removal. The process at 130–180 °C for 6 h yielded a purified white solid. Characterization confirmed successful polymer formation: FTIR showed a strong carbonyl band at ~1741 cm^{-1}, ^1H NMR displayed methylene resonances at δ 4.6–4.8 and 4.2–4.4 ppm without residual –COOH peaks (>97% conversion), and XRD revealed semi-crystalline features (up to 53% crystallinity). Thermal analysis indicated decomposition above 280 °C with <2 wt% residue (~98% purity), Tg ~36 °C, and Tm ~215 °C. This efficient route provides a foundation for scalable, high-quality PGA production, supporting future development of greener materials for sustainable packaging and advanced biomedical devices.

Keywords: Poly(glycolic acid)、Azeotropic condensation polymerization、Biodegradable polymer

CONSOLIDATED BIOPROCESSING FOR THE PRODUCTION OF VALUABLE CHEMICALS FROM SEAWEED PROCESSING RESIDUES – DEVELOPMENT OF MANNAN-UTILIZING *Halomonas elongata* –

Sae Tanaka,[1] Aoi Kaji,[1] Hideki Nakayama,[2] Kiyotaka Hara,[3] Fumiyoshi Okazaki[1]*
[1]Graduate School of Bioresources, Mie University, Japan
[2]Graduate School of Integrated Science and Technology, Nagasaki University, Japan
[3]Graduate School of Integrated Pharmaceutical and Nutritional Sciences, University of Shizuoka, Japan
*e-mail: okazaki@bio.mie-u.ac.jp

Abstract:
Halomonas elongata is a halophilic Gram-negative bacterium capable of growing across a wide range of salt concentrations, from 0.3% to 21%. As an adaptation to salt stress, it accumulates water-soluble functional molecules known as compatible solutes within the cell. Therefore, *H. elongata* is a promising production host for valuable compounds such as ectoine, with high-salt-content seaweed biomass serving as the feedstock. Among such resources, nori represents a promising target for valorization due to the generation of defective products caused by discoloration and processing residues. This study aimed to establish a value-added production system from nori processing residues using an integrated bioprocess approach. Specifically, we attempted to confer β-1,4-mannan utilization capability to *H. elongata* through cell surface engineering. To achieve surface display of β-1,4-mannanase, heterologous mannan-degrading enzymes derived from bacteria were employed, with the outer membrane-associated lipoprotein P5 from *H. elongata* serving as the anchor (Figure 1). Fusion genes encoding P5, the target enzyme, and either an HA or FLAG tag were constructed and stably integrated into the *H. elongata* genome via transposon-mediated insertion. As a result, recombinant *H. elongata* cells successfully degraded alkali-heat-treated nori processing residues, producing β-1,4-mannooligosaccharides as the main products, while a minor amount of D-mannose was also released.

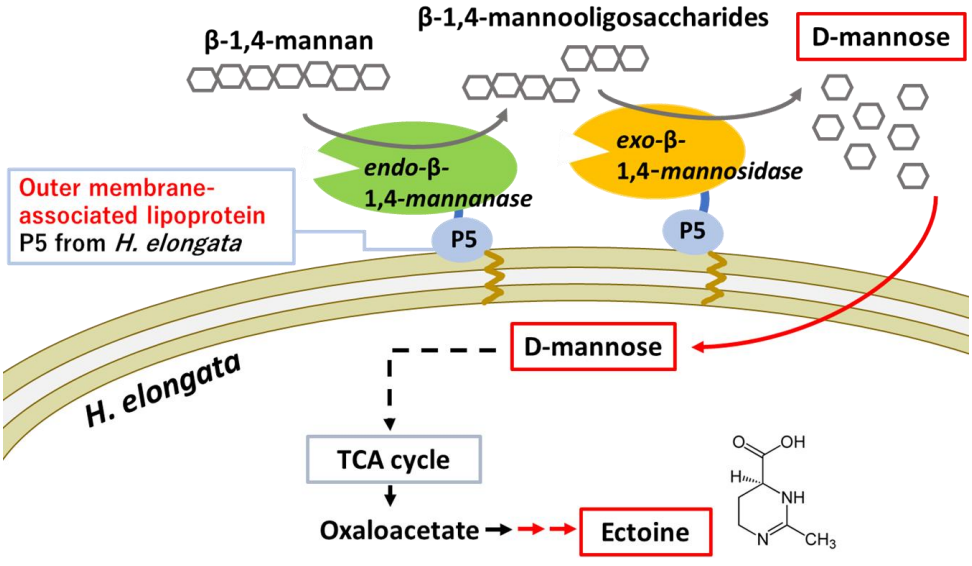
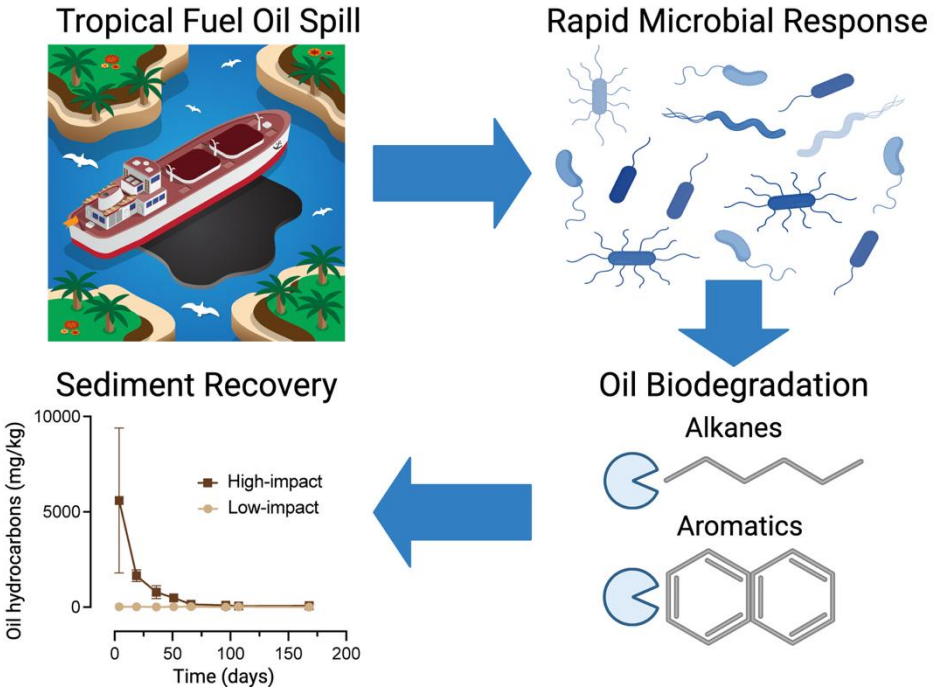


Figure 1.
Schematic representation of mannan utilization by recombinant *Halomonas elongata* through cell-surface display technology.

TROPICAL INTERTIDAL MICROBIOME RESPONSE TO THE '*2024 MARINE HONOUR OIL SPILL'*

Christaline George, Stephen B Pointing
Department of Biological Sciences, National University of Singapore, Singapore 117558
*e-mail: christaline.george@nus.edu.sg

Abstract:
Marine fuel oil (MFO) spills in tropical coastal environments are under-characterized. Microbial and geochemical responses to the June 2024 Marine Honour MFO spill on Singapore's intertidal sediments were analyzed over 185 days. Using metagenomics and hydrocarbon profiling, microbial community shifts and hydrocarbon degradation were quantified across visibly oiled (high-impact) and clean (low-impact) sites. Total petroleum hydrocarbon (TPH) levels peaked at 1,810–9,408 mg/kg in high-impact sites, declining to 1,349–1,965 mg/kg within 17 days. Comparatively, low-impact sites ranged from 16.9–20.9 mg/kg and declined to undetectable levels. Microbiomes adapted to the spill through increased diversity and abundance of hydrocarbon-degradation genes. *Oleiobacter* sp., *Macondimonas* sp., and *Marinobacter* sp., were key alkane degraders, while *Cycloclasticus* sp., *Alteromonas* sp., and novel *Immundisolibacteraceae* drove aromatic degradation. In contrast, *Alcanivorax sp.* and and *Colwellia* sp. recovered from Deepwater Horizon crude oil spill in oceanic water and cold deepwater were absent. Rubredoxin *(rdx)* and Dioxygenases *(paaB and pcaJ)* were the most abundant alkane and aromatic degradation genes, respectively, across samples. Oil deposition influenced microbial succession and hydrocarbon-degrading gene profiles, reflecting early toxicity in heavily oiled areas. Persistence of hydrocarbon degradation genes in sediments suggested long-term functional priming. The study provides novel genome-resolved insight into positive microbial response to MFO pollution and baseline data for oil spill response strategies in Southeast Asia and beyond.



SUGARCANE LEAF DERIVED-BIOCHAR ACID CATALYST FOR EFFICIENT ISOSORBIDE PRODUCTION FROM SORBITOL

Chonthicha Nilapornkul,[1] Pongtanawat Khemthong,[2] Bunyarit Panyapinyopol,[1] Wasawat Kraithong,[2] Pawan Boonyoung,[2] Saran Youngjan,[2] Jakkapop Phanthasri,[2] Kamonwat Nakason,[1,*]
[1]Department of Sanitary Engineering, Faculty of Public Health, Mahidol University, Bangkok, Thailand
[2]National Nanotechnology Center (NANOTEC), National Science and Technology Development Agency (NSTDA), Pathumthani, Thailand
*e-mail: kamonwat.nak@mahidol.ac.th

Abstract:
Isosorbide is a high-value chemical used in food, pharmaceuticals, and plasticizers, commonly produced via acid-catalyzed sorbitol dehydration. While homogeneous acid catalysts are effective, they pose challenges such as corrosion, difficult separation, and environmental concerns. To address these issues, this study developed a heterogeneous acid catalyst from sugarcane leaves (SCL). The catalyst was synthesized through carbonization at 500 °C under CO_2 for 1 h, followed by sulfonation at 200 °C for 6 h using concentrated sulfuric acid. Its physicochemical properties were characterized using CHNS analysis, BET surface area, acidity, TGA/DTG, SEM, TEM, FTIR, and XPS. The resulting catalyst showed excellent properties, with a surface area of 154 m^2/g, total acidity of 4.18 mmol/g, and sulfonic acid content of 2.31 mmol/g. Isosorbide synthesis was conducted at 200–240 °C for 6–27 h with catalyst loadings of 0–35 wt.%. Optimal yield (54.23 mol%) and selectivity (60.96%) were achieved at 220 °C for 21 h with 25 wt.% catalyst. Recyclability tests confirmed the catalyst's stability and reusability. These findings demonstrate that SCL-derived biochar is a promising, eco-friendly catalyst for dehydration reactions, advancing sustainable chemical production.

Keywords: Sorbitol conversion, Agricultural residues, Sugarcane leaf, Double dehydration, Isosorbide

DISTRIBUTION AND DIVERSITY OF CHEMOLITHOAUTOTROPHIC PHOSPHITE-OXIDIZING BACTERIA IN COASTAL AND MARINE ENVIRONMENTS

Takafumi Yamanaka, Linh Thi Thuy Cao, Akio Kuroda, Ryuichi Hirota*
Graduate School of Integrated Sciences for Life, Hiroshima University, Japan
*e-mail: hirota@hiroshima-u.ac.jp

Abstract:
Phosphite (HPO_3^{2-}) is a reduced inorganic phosphorus compound rarely detected in natural environments (Fig. 1A). Even when detected, it is generally found at nanomolar concentrations. Nevertheless, chemolithoautotrophic bacteria utilizing energy from phosphite oxidation, termed dissimilatory phosphite-oxidizing microorganisms (DPOM), were recently reported. DPOM oxidize phosphite via the *ptx-ptd* gene cluster, including AMP-dependent phosphite dehydrogenase (PtdF) and NAD-dependent phosphite dehydrogenase (PtxD), producing ATP and reducing equivalents that support autotrophic growth with CO_2 as sole carbon source (Fig. 1B). To date, only two isolated strains and two enrichments have been described, and their distribution, abundance, and ecological significance remain poorly understood.

In this study, we investigated the distribution and diversity of DPOM using enrichment cultures from sediments collected in brackish and marine environments in Japan. Shotgun metagenomic analysis enabled genome reconstruction and phylogenomic assessment of their diversity. DPOM were detected in 35 samples from 16 sites, and 13 metagenome-assembled genomes (MAGs) were reconstructed. These MAGs represent novel species within *Desulfotignum* or novel species—and potentially novel genera—within UBA1062 (class *Desulfomonilia*). The broad environmental distribution of DPOM suggests that phosphite could be more prevalent than currently recognized. These findings reveal critical implications for phosphorus cycling and highlight the potential for alternative phosphorus resources.

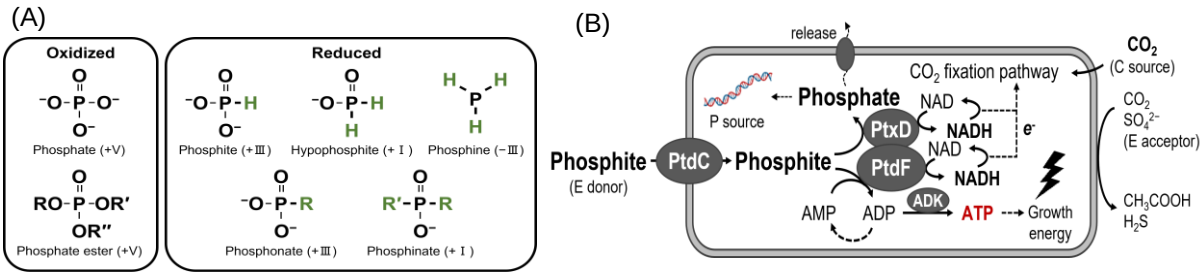


Figure 1.
(A) Phosphorus compounds in different oxidation states. The top row shows inorganic species; the bottom row shows organic species. The roman numerals in parentheses indicate the oxidation state of phosphorus. (B) Metabolic overview of dissimilatory phosphite oxidation. DPOM oxidizes phosphite via PtdF, producing ATP and reducing equivalents through NADH generation by PtdF and PtxD. This energy metabolism supports chemolithoautotrophic growth with CO_2 as the sole carbon source. PtdC, phosphite transporter; PtdF, AMP-dependent phosphite dehydrogenase; PtxD, NAD-dependent phosphite dehydrogenase; ADK, adenylate kinase.

VALUE-ADDED PRODUCTION OF BIOSURFACTANT BY AN ALKALIPHILIC CONSORTIUM USING MIXED AGRO-INDUSTRIAL RESIDUES

Anawin Junsawang,[1] Suphannika Intanon,[2] Witchaya Rongsayamanont,[3] Nichakorn Khondee[1,*]

[1]Department of Natural Resources and Environment, Faculty of Agriculture, Natural Resources and Environment, Naresuan University, Phitsanulok, Thailand

[2]Department of Agricultural Science, Faculty of Agriculture, Natural Resources and Environment, Naresuan University, Phitsanulok, Thailand

[3]Faculty of Environment and Resource Studies, Mahidol University, Nakhon Pathom, Thailand

*e-mail: nichakornk@nu.ac.th

Abstract:

The use of microbial consortia and agro-industrial residues offers a promising approach for sustainable and cost-effective biosurfactant production, as it combines synergistic microbial interactions with valorization of low-cost waste substrates. This study employed an alkaliphilic consortium of *Brevibacterium casei* NK8 and *Microbacterium paraoxydans* NK22, cultivated at pH 10 using agro-industrial residues as substrates. Defatted rice bran (DR), extracted defatted rice bran (EDR), and crude rice bran oil (CRO) were used as carbon sources, while spent yeast (SY) was utilized as a nitrogen source. Two experimental groups were evaluated: (1) 7% (w/v) DR, 11% (w/v) SY, and 3% (v/v) CRO; and (2) 7% (w/v) EDR, 11% (w/v) SY, and 0.5% (v/v) CRO. The DR-based formulation resulted in 1.55 g/L of biosurfactant, with viable cell counts of 1.46×10^8 and 8.66×10^8 CFU/mL for NK8 and NK22, respectively. In contrast, the EDR-based formulation produced 5.26 g/L of biosurfactant, with cell counts of 4.65×10^7 and 3.64×10^7 CFU/mL for NK8 and NK22, respectively. Moreover, compared to conventional biosurfactant media such as Horikoshi medium, the DR- and EDR- based formulation reduced medium costs up to 62.06% and 90.07%, respectively. These results indicate that the EDR-based formulation is more suitable for biosurfactant production, offering a cost-effective and sustainable strategy for converting agro-industrial residues into high-value biosurfactants.

UPCYCLING OF SOY SAUCE INDUSTRY BYPRODUCT INTO ECTOINE BY THE MODERATELY HALOPHILIC BACTERIUM, *Halomonas elongata*

Hanna Mitsunaga[1], Pulla Kaothien-Nakayama[1], Ryo Kawamoto[2], Katsuyuki Miyoshi[2], Hiroyuki Tamino[3], Hideki Nakayama[1,2,*]

[1] Graduate School of Integrated Science and Technology, Nagasaki University, 1-14 Bunkyo-machi, Nagasaki City, Nagasaki 852-8521, Japan

[2] Graduate School of Fisheries and Environmental Sciences, Nagasaki University, 1-14 Bunkyo-machi, Nagasaki City, Nagasaki 852-8521, Japan

[3] Maruisyouyu Company, Limited, 1-1-5 Nishi, Nakano City, Nagano 383-0021, Japan

*e-mail: nakayamah@nagasaki-u.ac.jp

Abstract:

Our goal is to develop technology to upcycle high-salinity soy sauce cake, a byproduct of the soy sauce industry, into ectoine, a high-value cosmetic ingredient, using the ectoine-producing halophilic bacterium *Halomonas elongata* OUT30018. We first prepared soy sauce hydrolysate (SH) by hydrolyzing soy sauce cake with 2.5%, 5%, or 10% w/v sodium hydroxide (NaOH), then neutralized it with hydrochloric acid (HCl), and added sodium chloride (NaCl) to prepare SH media containing 1.5 M NaCl. Growth tests showed that *H. elongata* OUT30018 grew best in medium prepared from SH treated with 5% w/v NaOH, with cells accumulating ectoine at levels comparable to those grown in synthetic media with the same NaCl concentration. To increase ectoine yield, we deleted the *doeA* gene, which encodes the ectoine-degradation enzyme, and the *ectD* gene, which encodes the ectoine-hydroxylation enzyme, from the *H. elongata* genome to create Δ*doeA* and Δ*ectD* single-deletion mutants, along with a Δ*doeA*Δ*ectD* double-deletion mutant. We are currently conducting growth tests to assess how these gene deletions affect ectoine yield in the mutant strains.

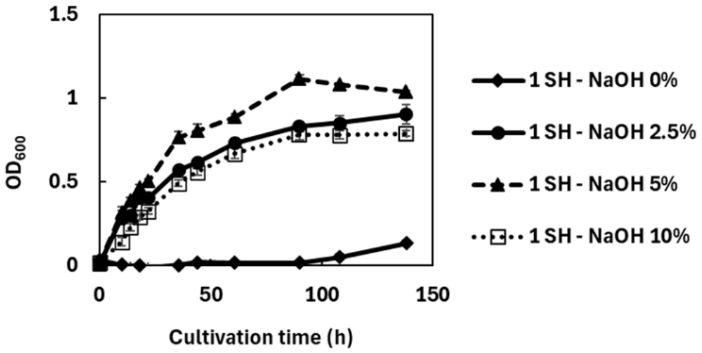


Figure 1.

Growth curve of the *H. elongata* OUT30018 in soy sauce hydrolysate (SH) media prepared from soy sauce cake hydrolyzed with 2.5%, 5%, or 10% w/v NaOH.

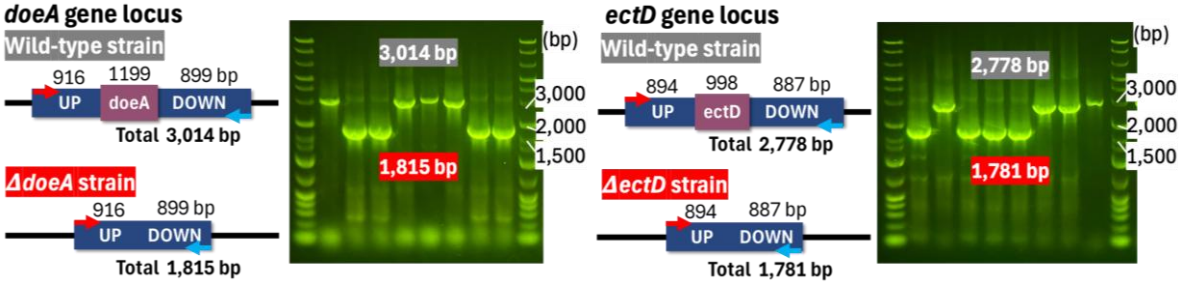


Figure 2.

Screening of the *H. elongata* Δ*doeA* (left panel) and Δ*ectD* (right panel) strains by colony PCR amplifying the *ectD* or *doeA* gene loci on the genomes.

EFFECTS OF REDOX MEDIATORS ON THE REMOVAL OF PHENOLICS AND COLOR FROM PALM OIL MILL EFFLUENT BY LIGNINOLYTIC PEROXIDASE-PRODUCING WHITE-ROT FUNGI

Wanitchaya Bunkoed,[1] Tunyawat Jinawong,[2] Anukool Kietkwanboot,[3] Nattawut Boonyuen,[4] Oramas Suttinun[1,*]

[1]Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla 90110, Thailand

[2]Department of Civil and Environmental Engineering, Faculty of Engineering, Prince of Songkla University, Hat Yai, Songkhla 90110, Thailand

[3]Faculty of Science and Technology, Hatyai University, Hat Yai, Songkhla, Thailand

[4]National Center for Genetic Engineering and Biotechnology (BIOTEC) , Khlong Luang, Pathum Thani 12120, Thailand

*e-mail: oramas.s@psu.ac.th

Abstract:

The presence of phenolics with low and high molecular masses, such as phenolic acids, tannins and lignin, is one of the contributors to a recalcitrant brownish color of palm oil mill effluent (POME). White-rot fungi capable of producing extracellular ligninolytic enzymes are effective degraders of these compounds. Two white-rot fungi exhibiting manganese (MnP) and lignin peroxidases (LiP), namely *Trametes hirsuta* AK04 and *Lentinus squarrosulus* LL12, were tested with three mediators including acetosyringone (AC), veratryl alcohol (VA), and $MnSO_4$, at varying concentrations (0.01-1 mM). The presence of all mediators markedly enhanced the ability of strain LL12 to remove phenolics (23-46%) from 521 mg/L and color (41-79%) from 9,339 units compared to the control (7% and 12%). The effect of each mediator depended on its concentration. The addition of AC at 0.01 mM resulted in the highest phenolics and color removal. The high redox potential of AC and its nature as a phenolic compound derived from lignin derivatives may contribute to its compatibility with LiP produced by the strain LL12. In contrast, only the addition of $MnSO_4$ led to a slightly higher removal of phenolics (41%) and color (24%) than the control (35% and 20%) by strain AK04. The different results between the two enzymes might be attributed to the differences in their redox potential and catalytic mechanisms. Gallic acid was the major individual phenolic detected in the treated POME (2 6 -33 mg/L) with (41-5 4 %) removal. Other phenolics were found in very low levels (< 3 mg/L).

ISOLATION AND SCREENING OF BACTERIA FOR BIOSURFACTANT PRODUCTION AND OILY SLUDGE DEGRADATION IN PETROLEUM WASTEWATER

Natcha Ruamyat,[1] Ekawan Luepromchai,[2] Witchaya Rongsayamanont,[3] Nichakorn Khondee,[1,*]

[1] Department of Natural Resources and Environment, Faculty of Agriculture, Natural Resources and Environment, Naresuan University, Thailand

[2] Microbial Technology for Marine Pollution Treatment Research Unit, Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand

[3] Faculty of Environment and Resource Studied, Mahidol University, Thailand

*e-mail: nichakornk@nu.ac.th

Abstract:

Oily wastewater and oily sludge from petroleum industries are important environmental issues due to the difficulty of treatment and disposal. This research investigated isolating potential bacteria for bioconversion of oily sludge to useful biosurfactants. This study classified oily wastewater and oily sludge as grease trap and water separate tank from D-LOF pond (wastewater D-LOF, D-LOF SP, oily sludge D-LOF SUR, and D-LOF SP); the grease tap pond carrier oily sludge accumulated with leaves transferred from D-LOF pond (wastewater D-DUMP, oily sludge D-SUMP SUR, and D-SUMP BOTT); and surface and machine cleaning before coming to the Open API site and storage tank (wastewater C-LOF and holding basin). The supernatant, which was transferred twice, demonstrates a high potential for oil displacement of 36.8 ± 0.3% from wastewater C-LOF containing oily sludge D-LOF SP. Moreover, the reduced contact angle capability measures 95.6 ± 1.4 degrees for wastewater C-LOF containing D-SUMP SUR sludge. This shows the differences in potential biosurfactant activities to be produced by bacteria from various sources of oily wastewater and oily sludge. The amount of isolated bacteria was highest in oily wastewater C-LOF mixed with oily sludge D-LOF SP, which was caused by the source of wastewater being in contact with a high concentration of oily sludge for a long period of time. Moreover, oily sludge D-LOS SP was transferred several times, and contact with air and light affected the chemical composition. That is affecting the ability of bacteria to tolerate high concentrations and expediting the degradation of oily sludge. A total of 10 isolates from effective sources of oily wastewater and oily sludge were investigated for the potential of production and activities of biosurfactant (surface tension) and oil degradation after 4 days of incubation. The 10 isolates demonstrate effective isolates 36, 38, 39, 40, and C2 produced biosurfactant ranging from 0.17 ± 0.01 g/L to 0.37 ± 0.14 g/L. Moreover, surface tension efficiency ranges from 45.02 ± 0.62 mN/m to less than 40.22 ± 0.53 mN/m and exhibits the highest oil degradation values between 21 ± 0.62% and 30 ± 0.41%. The analysis of 16S rRNA sequencing and MALDI-TOF mass spectrometry led to the identification and classification of selected effective bacteria. The isolates identified are as follows: isolate 36 is *Cellulosimicrobium cellulans*, isolate 40 is *Staphylococcus epidermidis*, and isolates 39, 41, C2, and C8 are *Bacillus cereus*. The benefits from this study show that isolated bacteria can be applied in various fields of petroleum industries from the potential of produced biosurfactants and oily sludge degradation. Furthermore, the technologies (biodegradation EOR SRB etc.) from the use of isolated bacteria were friendly and did not produce secondary pollutants after processing.

GENETIC IMPROVEMENT AND CHITINOLYTIC ENZYME PRODUCTION OF *Stenotrophomonas maltophilia* Mc_E05 ISOLATED FROM TERMITE EXOSKELETON

Chinnaphat Meeto,[1] Kittipong Chanworawit,[1] Pinsurang Deevong[1,*]
[1]Department of Microbiology, Faculty of Science, Kasetsart University, 10900, Bangkok, Thailand
[*]e-mail: fsciprd@ku.ac.th

Abstract:
Chitin is a crystalline polysaccharide polymer and difficult to decompose. The seafood industry produces large amounts of chitin waste, which rapidly accumulates in the environment. Accumulation of the chitin wastes leads to a range of pollutant effects on soil, water, and air. Chitinases play an important role in industry, agriculture, and the environment. These hydrolytic enzymes catalyze and degrade chitin materials to produce monomer and oligomer units. The chitinolytic bacterial isolate Mc_E05 used in this study was obtained from the exoskeleton of the termite *Microcerotermes* sp. and the 16S rRNA gene sequence analysis revealed that it was closely related to *Stenotrophomonas maltophilia*. The present study aimed to improve the chitinase production of the potential isolate using mutagenesis. The genetic improvement using ultraviolet (UV) irradiation and ethyl methane sulfonate (EMS) treatment enhanced the chitinolytic ability of bacteria. Based on the 10% survival rate of bacteria, almost thousand colonies were detected for their chitinase production using point inoculation on the nutrient agar (NA) supplemented with 1% colloidal chitin. Bacterial mutants with increased chitinase activity were collected and used for subsequent experiments. The selected mutants were determined the enzymatic activity using the 3,5-dinitrosalicylic acid (DNS) method. The mutant E05-UV2 exhibited the maximum chitinolytic activity of 142.30 ± 7.31 mU/mL (approximately 170% increased from wild-type) after 96 h of incubation, while the mutant E05-EMS2 exhibited the maximum chitinolytic activity of 85.45 ± 2.44 mU/mL (approximately 62% increased from wild-type) after 72 h of incubation. The result indicated that UV mutagenesis was effective for increasing the chitinase activity of *S. maltophilia.* Moreover, all treatments with UV irradiation showed significantly higher efficiency than those of EMS mutagenesis. The present study successfully improved the chitinolytic activity of the isolated termite gut bacterium, *S. maltophilia,* through mutagenesis. The resulting mutants and their chitinases provide valuable potential for applications in biotechnology and environmental bioremediation.

CIRCULAR PRODUCTION OF BACTERIAL CELLULOSE THROUGH VALORIZATION OF PALM OIL MILL EFFLUENT BY *Komagataeibacter* sp. CV06

Naruemon Bunkaew,[1] Wilanee Chunglok,[1] Oramas Suttinun,[1]*
[1]Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai Campus, Songkhla, 90110, Thailand
*e-mail: oramas.s@psu.ac.th

Abstract:
Circular production of bacterial cellulose (BC) was carried out through valorisation of palm oil mill effluent (POME). Fourteen vinegar and kombucha samples were used to isolate BC producers on CARR agar. A total of twenty-one bacterial isolates were isolated, and six of them exhibited acetic acid bacterial properties on Hestrin-Schramm medium. Among them, the isolate CV06, obtained from myrobalan cider vinegar, yielded the highest BC production of 3.5 g/L on the 7th day. This isolate was identified as *Komagataeibacter* sp. by 16S rDNA sequencing. The acetic acid (AA) produced in the growth medium was further reused in the POME hydrolysis to release more fermentable sugars before being used as alternative media for BC fermentation. The POME-to-growth media ratios were adjusted between 1:9 and 4:6 (v/v) to obtain the final AA concentrations ranging from 0.18% to 0.54% in the hydrolytic mixture. The sugar content in POME hydrolysates increased from 80 to 101 g/L when the AA concentration in the mixture increased above 0.18%. In addition, the fermentation inhibitors, including acetic acid (0.32-0.96%) and phenolics (0.38-1.05 g/L) were detected. The conditions with AA concentrations between 0.36% and 0.48% yielded the maximum BC production of 5.0 g/L after 21 days.

REDUCING SUGAR EXTRACTION FROM OVER-ROASTED COFFEE BEANS AND COFFEE SILVERSKINS

Sukon Tantipaibulvut*, Patchanida Nuttipongpairoj, Areerat Khumpoln, Kanjanakorn Piyarat, Sukanya Yot-aon, Jirayut Euanorasetr, Sukanya Phuengjayaem
Laboratory of Biotechnological Research for Energy and Bioactive Compound, Department of Microbiology, Faculty of Science, King Mongkut's University of Technology Thonburi, Bangkok 10140, Thailand
*e-mail: sukon.tan@kmutt.ac.th

Abstract:
Significant amounts of waste are generated by the coffee industry, among them, coffee silverskin (CS) and over-roasted coffee beans (OCB) are the most abundantly generated during the beans roasting. In this study, this material was proximately analyzed and subsequently submitted to an acid hydrolysis aiming to extract reducing sugar. Reactions were performed to verify the effects of the variables H_2SO_4 concentration, temperature, and reaction time, on the efficiency of hydrolysis. After acid treatment, the hydrolysate was adjusted to the appropriate pH using sodium hydroxide solution. The conditions that gave a significant highest amount of reducing sugar were 90°C, 5% H_2SO_4, and 3 hours, which yielded 14.57±0.23 g sugar/L for OCB and 8.37±0.20 g sugar/L for CS. Treatment the material at 70°C for either 1 hour or 3 hours gave no significantly different amount of reducing sugar obtained for both CS and OCB, especially at 1% to 3% H_2SO_4. The hydrolysate from acid treatment of OCB and CS can be used as substrate for lactic acid and bioethanol production.

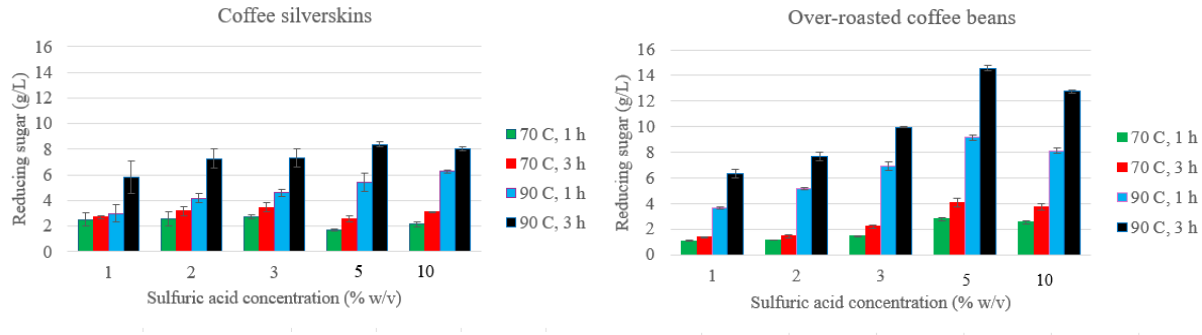


Figure 1.
Reducing sugar in the hydrolysate of coffee silver skins (left) and over-roasted coffee beans (right) after acid treatment at various conditions

CHARACTERIZATION OF UV-MUTATED *Kluyveromyces marxianus*: ISOBUTANOL TOLERANCE AND XYLOSE UTILIZATION

Krittaporn Thungmuthaswade[1], Navaphorn Pinrenu[2], Thanyalak Vorawongsakul[2], Jirasin Koonthongkaew[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Phayathai Rd., Pathumwan, Bangkok 10330, Thailand
[2]Department of Biotechnology, Faculty of Science, Chulalongkorn University, Phayathai Rd., Pathumwan, Bangkok 10330, Thailand
*e-mail: Jirasin.K@chula.ac.th

Abstract

Isobutanol has been of interest as a second-generation biofuel because it possesses higher energy density, lower vapor pressure, and potential as a platform chemical to produce materials with additional value, including isobutylene and biojet fuels, which are better than traditional ethanol. However, one of the main obstacles to reaching high fermentation titer is its acute toxicity to microorganisms, with concentrations above 8–10 g/L often reported as inhibitory to yeasts. To date, reports on the isobutanol tolerance of *Kluyveromyces marxianus* remain scarce. In this study, the wild-type strain *K. marxianus* G3-10(2) was mutated with ultraviolet (UV) irradiation and screened in culture media containing a high concentration of isobutanol. The obtained mutant 2(3) was evaluated for isobutanol tolerance in YPD medium with the addition of 10-14 g/L isobutanol. The mutant exhibited consistently stronger growth than the wild type, showing 1.2-fold, 1.1-fold, and 1.3-fold higher OD_{600} values at 72 h under 10, 12, and 14 g/L isobutanol stresses, respectively. Microscopic and colony morphology observations showed that both the mutant and wild-type strains exhibited oval budding cells and creamy, circular colonies. A spot assay at pH 4 and 7, with cultures grown at 30°C and 37°C, also confirmed the greater tolerance of the mutant, particularly at neutral pH at 30°C. In addition, a xylose utilization test revealed that both strains were able to metabolize xylose as the sole carbon source, with the mutant strain showing better cell growth compared to the wild-type strain. These observations show that UV mutagenesis can effectively improve *K. marxianus* mutants having high isobutanol tolerance and enhanced pentose utilization. Although the strains have not been tested for isobutanol production, the mutant represents a promising host platform for future metabolic engineering toward efficient isobutanol biosynthesis.

FACTORS INFLUENCING ON DEVELOPMENT OF TREHALOSE PRODUCTION BY *Saccharomyces cerevisiae*

Warissara Chotiwanee,[1] Sitanan Thitiprasert,[2,3] Nuttha Thongchul[2,3]*
[1]Program in Biotechnology at Faculty of Science, Chulalongkorn University, Thailand
[2]Center of Excellence in Bioconversion and Bioseparation for Platform Chemical Production, Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, Thailand
[3]Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, Thailand
*e-mail: Nuttha.T@chula.ac.th

Abstract:
Trehalose is a non-reducing disaccharide comprising two glucose units that are linked by an α,α-1,1-glycosidic linkage, exhibits remarkable versatility across various industries applications. The most unique characteristic of trehalose is that its function as an osmolyte compound that protects against numerous environmental stresses in a wide range of microorganism and plants. Conventional industrial trehalose production employs a sequential enzymatic process utilizing maltooligosyltrehalose synthase (EC 5.4.99.15) followed by maltooligosyltrehalose trehalohydrolase (EC 3.2.1.141), with starch serving as the primary substrate. Nevertheless, recent advances in sustainable biotechnology have stimulated the development of microbial trehalose biosynthesis pathways, thereby diversifying production methodologies. This study aims to design the fermentation process of trehalose production using *Saccharomyces cerevisiae*, leveraging its inherent capacity for trehalose synthesis under stress conditions. Based on the concept that trehalose could protect the yeast cells against environmental stresses, osmotic stress and high temperature control were examined. Additionally, the influence of yeast cell age on trehalose synthesis was determined to identify the optimal growth phase of yeast cells. A two-phase fermentation approach was applied for trehalose production by *S. cerevisiae* in shaken flask scale. *S. cerevisiae* was initially grown in cell production medium, containing 100 g/L glucose to produce high cell density and ethanol. The late-log phase cells were transferred into trehalose induction medium containing 100 g/L glucose and various ethanol concentrations, which were cultivated under at 45 °C. The experimental results demonstrated that supplementation with 25 g/L ethanol during the production phase significantly enhanced both extracellular and intracellular trehalose accumulation compared to alternative conditions. The extracellular trehalose production was 0.330 ± 0.010 g/L with a yield of 0.003 ± 0.000 g/g and a productivity of 0.055 ± 0.002 g/L·h, while the intracellular trehalose production was 0.180 ± 0.002 g/L, which corresponding to 0.429± 0.003 g trehalose/g cell. These findings indicate that stress conditions, particularly osmotic and thermal stress, can effectively improve trehalose production in *S. cerevisiae*.

LIQUID NITROGEN-ASSISTED LYOPHILIZATION OF *Saccharomyces cerevisiae* AND SPORES OF *Penicillium* sp.

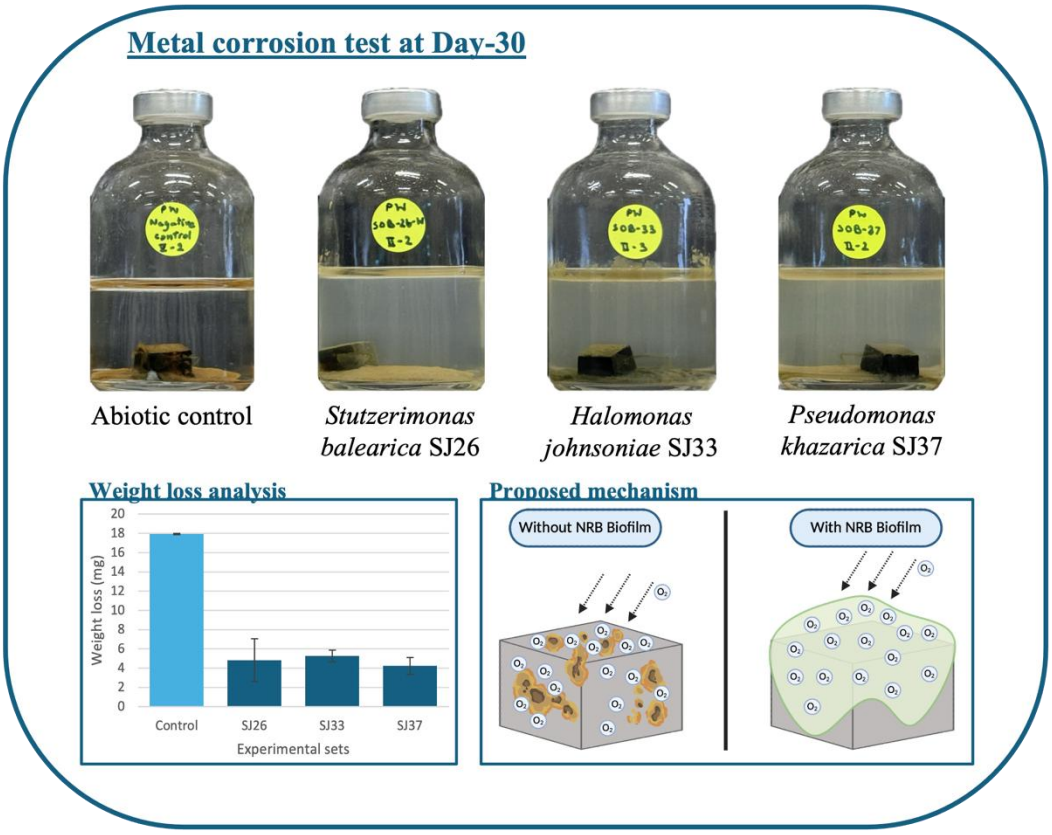
Nanthorn Paorach[1], Napatsapond Ponglerdtanadej[1], Sasipa Srisuk[1] and Kobchai Pattaragulwanit[1]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand
*e-mail:Nanthorn.p@chula.ac.th

Abstract:
Lyophilization, or freeze-drying, is the most widely used method for the long-term preservation of microorganisms. The principle of this method involves the sublimation of water from frozen samples under reduced pressure. The process consists of three main steps: freezing, primary drying, and secondary drying. Although lyophilization is well-established for preserving microorganisms, it is both time and energy intensive, particularly during the freezing and primary drying stages. This study aimed to develop a novel approach to lyophilization by using liquid nitrogen to replace these two time-consuming steps in the freeze-drying of yeast and fungal spores. Three cryoprotectants: 10% (w/v) monosodium glutamate, 10% (w/v) skim milk, and a combination of both were tested for lyophilizing *Saccharomyces cerevisiae* MSCU0360 and spores of *Penicillium* sp. MSCU0047. The liquid nitrogen-assisted lyophilized yeast and fungal spores remained viable after preservation for at least three months (96% and 92%, respectively), which were comparable to those of standard lyophilized cell (95% and 90%, respectively), regardless of the cryoprotectant and storage temperatures (4 or -20 ºC) used. This study successfully developed a liquid nitrogen-assisted lyophilization method that significantly reduces the time required for conventional lyophilization, while maintaining high survival and storage performance.

NITRATE REDUCING BACTERIA FROM OIL SLUDGE AND THEIR POTENTIAL ROLES ON METAL CORROSION INHIBITION

Luxnapol Marturunkakul, Chutima Rotchum, Ekawan Luepromchai*
Microbiology and Microbial Technology Program, Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand, 10330
*e-mail: ekawan.l@chula.ac.th

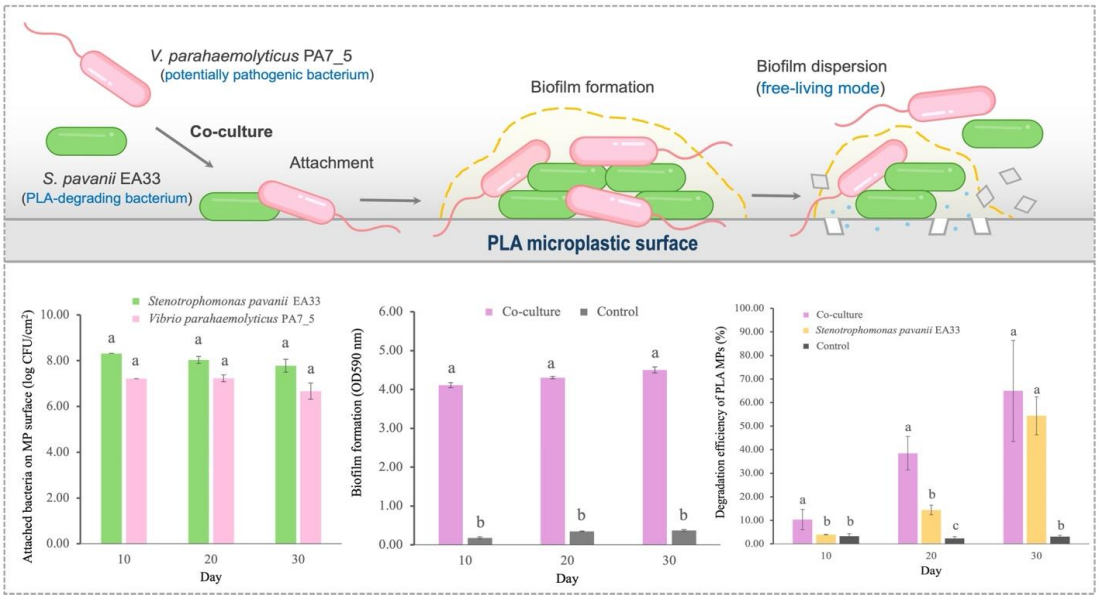
Abstract:
Microbiologically influenced corrosion (MIC) is a chronic problem that leads to economical loss in oil and gas industries. Although sulfate-reducing bacteria (SRB) are a major MIC promoter, roles of other bacterial groups on corroded surface such as nitrate-reducing bacteria (NRB) are equally important. Using six assorted media, eight potential NRB isolates (*Citrobacter cronae* SJ1, *Pseudomonas aeroginosa* SJ5, *Stutzerimonas balearica* SJ26, *Halomonas johnsoniae* SJ33, *Pseudomonas kurunegalensis* SJ21P, *Brucella cytisi* SJ21T, *Stutzerimonas stuzeri* SJ29 and *Pseudomonas khazarica* SJ37) were enriched from oil sludge. An aerobic metal corrosion experiment was then conducted in simulated produced water containing selected bacterial strains and L80-1 carbon steel coupons. After 30-day, the abiotic control decreased the metal weight by 17.9 mg/coupon, whereas strain SJ26, SJ33 and SJ37 decreased the metal weight by 4.8, 5.2 and 4.2 mg/coupon, respectively. The low metal weight loss was corresponded with the formation of biofilm, which suggested that these bacteria protected the metal surface from abiotic oxidation. *H. johnsoniae* SJ33 also produced significant ammonia indicating the reduction of nitrate, which was probably due to the anoxic condition in the bacterium biofilm. In conclusion, the NRB under aerobic condition were non-corrosive and inhibited metal corrosion. Further study will investigate the interactions between NRB and SRB on MIC.



EFFECT OF POTENTIALLY PATHOGENIC AND PLASTIC-DEGRADING BACTERIAL CO-CULTURE ON POLYLACTIC ACID MICROPLASTICS

Nutthamon Boonlum[1], Chonchanok Muangnapoh[1], and Ekawan Luepromchai[1,2]*
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Thailand
[2]Center of Excellence in Microbial Technology for Marine Pollution Treatment (MiTMaPT), Chulalongkorn University, Thailand
*e-mail: ekawan.l@chula.ac.th

Abstract:
Compostable plastics such as polylactic acid (PLA) can generate microplastics (MPs) due to their incomplete degradation and deterioration. PLA MPs can persist in the environment and create new ecological niches for microorganisms. Previous studies have shown that pathogenic bacteria are often among the pioneer colonizers on microplastic surfaces due to their biofilm-forming ability. Biofilm formation also alters the physicochemical properties of microplastics, thereby promoting the subsequent colonization and activity of other microbial groups. This study therefore investigated the synergistic effects of potentially pathogenic and plastic-degrading bacteria on PLA MPs when cultured as monocultures and co-cultures. The PLA MPs used in this study were prepared from PLA cup waste and cut into fragments of approximately 3 × 3 mm (< 5 mm in diameter). Initially, growth, colonization, and biofilm formation of four bacterial strains (Stenotrophomonas pavanii EA33, Bacillus pumilus STUV10, Vibrio parahaemolyticus PA7_5, and Staphylococcus saprophyticus PF11_E1) on PLA MPs were compared. PLA MPs in liquid medium enhanced growth and biofilm formation of all bacteria compared with the control without PLA MPs. The co-culture of S. pavanii EA33 (PLA-degrading bacterium) and V. parahaemolyticus PA7_5 (potentially pathogenic bacterium) showed synergistic enhancement of PLA MP degradation. The weight loss of PLA MP in co-culture was 39% at day 20, while only 14% was degraded in the monoculture. Morphological observations confirmed progressive erosion, cracking, and fragmentation of PLA MPs. In addition, V. parahaemolyticus PA7_5 showed better growth in co-culture (~8 log CFU/mL) than that of monoculture (~7 log CFU/mL). Overall, this study indicated the dual roles of PLA MPs as degradable substrates and carrier for pathogens. The findings will be used to determine the fate of PLA microplastics and pathogens in natural ecosystems.



Session IV.
Biodiversity, Natural Products and Applications

CULTURABLE ENDOPHYTIC FUNGI FROM *Rhodomyrtus tomentosa* LEAVES IN SOUTHERN THAILAND: DIVERSITY, DISTRIBUTION, AND ANTIMICROBIAL POTENTIAL

Arisara Ma,[1] Lakkhana Kanhayuwa Wingfield[1,*]
[1]Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla, 90110 Thailand
*e-mail: Lakkhana.k@psu.ac.th

Abstract:
Rhodomyrtus tomentosa (Aiton) Hassk., a medicinal plant valued for its antibacterial properties, was investigated for the first time to assess the distribution, diversity, and antimicrobial potential of its culturable endophytic fungi in 13 provinces of southern Thailand. Leaf samples were collected during the rainy season (May–August 2023), and endophytes were isolated and identified using a combination of morphological characters and molecular sequencing of the ITS, LSU, and TEF1-α regions. Phylogenetic analysis of 29 representative morphotypes classified them into 12 genera: *Chaetomium*, *Colletotrichum*, *Daldinia*, *Endomelanconiopsis*, *Fusarium*, *Gnomoniopsis*, *Lasiodiplodia*, *Neopestalotiopsis*, *Nigrospora*, *Phyllosticta*, *Preussia*, and *Pseudopestalotiopsis*. The most abundant genera were *Neopestalotiopsis* (RF 29.46%), *Endomelanconiopsis* (RF 17.24%), *Colletotrichum* (RF 13.72%), and *Phyllosticta* (RF 12.43%). Species richness (Margalef = 3.74; Menhinick = 0.32) and diversity (Shannon = 1.98; Simpson = 0.83) indices indicated relatively low fungal diversity. While some taxa were widespread across the region, others showed province-specific distributions, likely reflecting climatic, geographical, and geological variation. *Colletotrichum* and *Neopestalotiopsis* occurred in all provinces, whereas *Pseudopestalotiopsis* and *Gnomoniopsis* were restricted. Antimicrobial assays demonstrated that four of 13 morphotypes inhibited at least one bacterial pathogen, with *Chaetomium cupreum* strain KBSK-V1 exhibiting activity against both Gram-positive and Gram-negative bacteria. These findings highlight *R. tomentosa* leaf endophytes as a potential reservoir of bioactive fungi with pharmaceutical relevance.

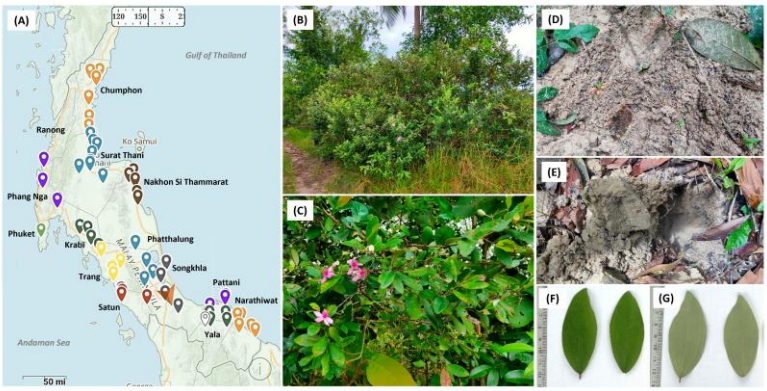


Figure 1.
Location of the sampling sites and habitats of the *Rhodomyrtus tomentosa* plants. Map of the locations of sample plots (A); *R. tomentosa* community (B) and individual characteristics (C); Physical characteristics of the bulk soil (D, E); Characteristics of the mature leaves (F; front, and G; back).

COMPARTMENTAL MODELLING FOR OPTIMAL FERMENTATION OF *Perilla frutescens* (L.) BRITT.

Bor-Yann Chen[1*], Keng-Wei Liu[1*], Chung-Chuan Hsueh[1], Po-Wei Tsai[2], Cheng-Yang Hsieh[1]
[1]Department of Chemical and Materials Engineering, National I-Lan University, Yi-Lan 260, Taiwan
[2] Department of Food Science, National Taiwan Ocean University, Keelung 202, Taiwan
*(Emails): boryannchen@yahoo.com.tw; bychen@niu.edu.tw

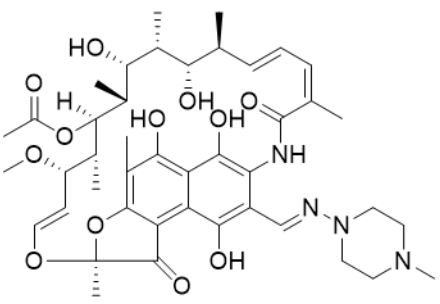
Abstract:
Since *Perilla frutescens* owns sedative and anti-inflammatory properties, it is popularly used as medicinal diets of all time. As prior studies indicated, *P. frutescens* leaves are abundant in polyphenolic contents with high antioxidant activities, which can effectively resist various viruses. Literature also mentioned that dominant phenolic acid compounds of perilla fermentation (e.g., rosmarinic acid (RA)) could be converted to crucial metabolites (e.g., ferulic acid, caffeic acid, and *p*-hydroxybenzoic acid). However, detailed transient dynamics of these target phenolic acids in *Perilla* sp. remained open to be explored for system optimization. Evidently, operation strategies to enhance production or utilization of associated metabolite(s) would be top-priority issue for further applications. To achieve maximal performance of fermentation, the effective microbial screening for perilla fermentation is apparently significant to achieve overall optimization.

This first-attempt model study adopted systematic evaluation to determine optimal acclimation for maximal RA-degrading performance of lactic acid bacteria (LAB) isolated from dominant consortia in stinky tofu via serial acclimation. With 8 cycles of serial acclimation, fifth cycle-fermentation using 500 mg L^{-1} perilla concentration could achieve the maximal RA-degrading efficiency (4.39×10^{-7} cfu^{-1} mL hr^{-1}) via compartmental modelling. The RA-utilizing efficiency was even achieved 1.3 fold of the world highest record. Apparently, due to negligible accumulation of inhibitory intermediate-ferulic acid (0.912-2.07 mg L^{-1}), maximizing the degradation performance of LAB was reached. This study clearly revealed that significant reduction of ferulic acid would be the performance-determining step for maximal RA degradation. Species-identification upon optimal microbial community pointed out that the dominant species was *Lactobacillus curvatus*, which is very different from the RA-producing microbes (e.g., *Bifidobacteria* and *Saccharomyces* spp.).

ANALYSIS OF THE CONCENTRATION-DEPENDENT EFFECTS OF THE ANTIBIOTIC RIFAMPICIN ON ACTINOMYCETES

Miran Hasegawa,[1] Takeshi Hosaka[1,*]
[1] Graduate School of Science and Technology, Department of Biomedical Engineering, Shinshu University, Japan
*e-mail: thosaka@shinshu-u.ac.jp

Abstract:
Antibiotics are chemical compounds produced by microbes that inhibit the growth of other microbes. An intriguing phenomenon not captured by this definition is that low concentrations of antibiotics, particularly those below the minimum inhibitory concentration (MIC), can benefit microbial growth. Rifampicin, a clinically important antibiotic, blocks bacterial RNA polymerase. In this study, we observed a concentration-dependent positive physiological effect of rifampicin on actinomycetes. We used *Streptomyces lividans* 66 as the model organism. When cultured at 30℃ on ISP2 agar medium with an ETEST® strip containing rifampicin, aerial mycelium and spore formation were markedly promoted by rifampicin at approximately 0.1–0.8 × MIC (Figure 1). In a separate experiment, *S. lividans* 66 was grown on Mannitol Soya Flour agar containing rifampicin at concentrations below the MIC, and spores were collected. Purified spores (2×10^7 CFU) were then inoculated onto ISP 2 agar with 5 × MIC rifampicin and incubated at 30°C to isolate rifampicin-resistant mutants. As a result, rifampicin-resistant mutants emerged at a high frequency (7.1×10^{-7} mutants per spores) from spores obtained under culture conditions with 0.1 × MIC rifampicin. This presentation highlights these phenomena and their applicability for potentiating actinomycetes possessing various industrial utilities.



Rifampicin

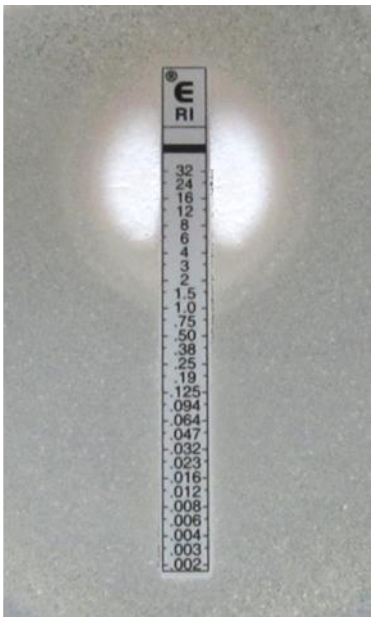


Figure 1.
Morphology of *Streptomyces lividans* 66 when grown with the antibiotic rifampicin.

ASSESSMENT OF HEAVY METAL AND FUNGICIDE TOLERANCE IN THE PLANT GROWTH-PROMOTING STRAIN *Daldinia eschscholtzii* MFLUCC20-0215 AND THREE FUNGAL STRAINS ISOLATED FROM *Litsea cubeba* (Lours.) Pers.

Khanitha Sawangwatthanagun,[1] Nareerat Vareedam,[1] Dusit Athinuwat,[2] Siraprapa Mahanil[1*]
[1]School of Science, Mae Fah Luang University, Thailand
[2]Faculty of Science and Technology, Thammasat University, Thailand
*email: Siraprapa.bro@mfu.ac.th

Abstract:
Fungi can be utilized to detoxify heavy metals or fungicides. This mycoremediation process offers a sustainable method for rehabilitating polluted areas. In this study, we evaluated the metals and fungicide tolerance of fungal endophytes isolated from *Litsea Cubeba (Lours) Pers.* and *Daldinia eschscholtzii* MFLUCC20-0215, which has previously been reported for its ability to promote plant growth. The *D. eschsholtzii* MFLUCC20-0215, *Diaporthe eugeniae* LCL03, *Colletotrichum fructicola* LCL05, and *Fusarium solani* LCL09 exhibited high tolerance to 500 ppm of arsenic acid (H_3AsO_4) and Lead (II) Nitrate ($Pb(NO_3)_2$) as shown by a tolerance index of 0.82 to 1.00. These four endophytic fungi were moderately tolerant to 1,000 ppm of Omethoate (tolerance index between 0.47 to 0.78) and low tolerance to 1,000 ppm of Cypermethrin (tolerance index between 0.19 to 0.57). The data from this study suggested that the colony morphology of fungal strains was not affected by the presence of lead and arsenic, which could lead to the ability to degrade these metals. The removal efficiency assessments and degradation assays are required to confirm the bioremediation capabilities. However, this study demonstrates their potential to remediate heavy metal and fungicide-contaminated soil, especially arsenic, which currently poses a significant environmental concern in Northern Thailand.

BIOTRANSFORMATIONS OF WHITE TEA BY *Lactococcus lactis* PKC-1: ENHANCED ANTIMICROBIAL AND ANTIOXIDANT ACTIVITIES

Pasit Phatcharachaitas[1], Engkarat Kingkaew[1, *], Napassakorn Kasemnukijkul[1], Nipon Sonhom[2, **], Woratep Jumi[1]
[1]Department of Biology, School of Science, King Mongkut's Institute of Technology Ladkrabang, Bangkok 10520, Thailand
[2]89/1 Sakdibhornssup Foundation Building, Ratchaprarop Road, Makkasan Subdistrict, Ratchathewi District, Bangkok 10400, Thailand
*Corresponding author: Engkarat Kingkaew
E-mail: engkarat.ki@kmitl.ac.th
**Co- Corresponding author: Nipon Sonhom
Email: nipon.sonhom@ssup.co.th

Abstract:
White tea is a natural source of polyphenols and flavonoids with antioxidant and antimicrobial properties. This study investigated the impact of fermenting white tea with *Lactococcus lactis* PKC-1 in five different media. Antimicrobial activity, total phenolic content (TPC), and antioxidant capacity were measured using the Spot-on-lawn assay, Folin–Ciocalteu method, and DPPH assay, respectively. Fermentation in media 4 and 5 significantly enhanced antimicrobial activity ($p < 0.05$). In medium 4, inhibition of *Pseudomonas aeruginosa* ATCC 9027 increased from 100 to 400 AU/mL, while in medium 5, inhibition of *Escherichia coli* ATCC 8739 rose from 200 to 800 AU/mL. Although TPC declined in most media, medium 5 showed a modest but significant increase (8.10 ± 0.89 to 8.71 ± 0.82 mg GAE/g, $p < 0.05$). Antioxidant capacity also improved in medium 5, from 80.93 ± 0.89% to 83.10 ± 0.82% ($p < 0.05$). Media 4 (monosodium glutamate, glucose, malt extract, Tween 80) and 5 (monosodium glutamate, malt extract, ammonium sulfate, Tween 80) yielded the strongest overall effects. These results demonstrate that fermentation with *L. lactis* PKC-1 can enhance the functional qualities of white tea, supporting its potential use in nutraceutical, food, and cosmetic products.

Keywords: White tea; *Lactococcus lactis*; Fermentation; Antimicrobial activity; Antioxidant capacity; Whole-genome analysis

Cratoxylum formosum EXTRACT ATTENUATES INFLAMMATION IN LPS-ACTIVATED MACROPHAGES BY REDUCING IL-6 EXPRESSION

Tuangtong Vongpipatana,[1,*] Talayboon Pooyoi,[1] Kotchakorn Srikhong[1]
[1]Department of Biochemistry, Faculty of Science, Kasetsart University, 50 Ngamwongwan Rd, Lat Yao, Chatuchak, Bangkok 10900, Thailand
*e-mail: fscittv@ku.ac.th

Abstract:
Inflammation is the defensive process against harmful stimuli. Although inflammation is beneficial for body protection, long-lasting inflammation is the cause of various diseases. Therefore, inflammation must be controlled for an appropriate period of time. It is well known that plants are an important source of bioactive compounds, which have many activities, including antioxidant activity, antimicrobial activity, and anti-inflammatory activity. *Cratoxylum formosum* is a native plant in Southeast Asia, and it has been reported that the ethanolic extract has bioactive compounds for reducing free radicals. In this study, we aim to reveal the effects of aqueous extract from fresh *C. formosum* leaves on anti-inflammation using lipopolysaccharide (LPS)-activated Macrophages as a model for inflammation. We found that crude *C. formosum* extract at 15.63, 62.50, and 250.0 µg/ml significantly decreased nitric oxide production in LPS-activated macrophages in a dose-dependent manner. Quantitative RT-PCR analysis was performed to determine the expression level of pro-inflammatory cytokines. The expression of IL-6 mRNA was inhibited in LPS-activated macrophages treated with 250.0 µg/ml of *C. formosum* crude extract. These results indicate that the aqueous extract from fresh *C. formosum* leaves is able to reduce inflammation and provide information for an alternative way to treat inflammation-associated diseases in the future.

FUNCTIONAL CHARCTERIZATION OF PlyCYU ENDOLYSIN AGAINST *Streptococcus agalactiae*

Sakunrat Ubonprasert,[1] Wachiraporn Wachiradusit,[1] Wichai Pornthanakasem,[1] Jeerus Sucharitakul,[2] Kittikhun Wangkanont,[3,4] Penchit Chitnumsub,[1] Ubolsree Leartsakulpanich[1,*]
[1]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Khlong Luang, Pathum Thani, Thailand
[2]Department of Biochemistry, Faculty of Dentistry, Chulalongkorn University, Bangkok, Thailand
[3]Center of Excellence for Molecular Biology and Genomics of Shrimp, Department of Biochemistry, Faculty of Science, and [4]Center of Excellence in Molecular Crop, Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
*e-mail: ubolsree@biotec.or.th

Abstract

The escalating threat of antimicrobial resistance (AMR) demands new antimicrobial agents. Bacteriophage-derived endolysins offer promising alternatives due to their rapid bactericidal activity, host specificity, and low likelihood of resistance development. In this study, we characterized the functional domains of PlyCYU, an endolysin from a *Streptococcus suis* prophage. Bioinformatic analysis predicted two catalytic domains—an N-terminal amidase-5 and a C-terminal glucosaminidase (Lyz2)—connected by two CW_7 cell wall binding motifs. Different variants have been constructed, and biochemical and biophysical assays have been employed to understand the role of each putative catalytic domain. The functional relationships of these domains in PlyCYU were demonstrated. Insights obtained are beneficial for designing novel effective endolysins with desired properties.

METABOLOMICS-BASED COMPARATIVE STUDY AND EVALUATION OF BIOLOGICAL ACTIVITIES IN TWO BROWN ALGAE

Jun-Hyung Lee,[1,2] Nam-Gyun Kim,[1,2] Won-Kyo Jung[1,2,3,*]
[1]Major of Biomedical Engineering, Division of Smart Healthcare Major of Biomedical Engineering and New-senior Healthcare Innovation Center (BK21 Plus), Pukyong National University, Busan 48513, Republic of Korea
[2]Marine Integrated Biomedical Technology Center, The National Key Research Institutes in University, Busan 48513, Republic of Korea
[3]Research Center for Marine Integrated Bionics Technology, Pukyong National University, Busan 48513, Republic of Korea
*e-mail: wkjung@pknu.ac.kr

Abstract:
This study aimed to identify species-specific biomarkers by focusing on polyphenol-based comparative metabolite profiling of two brown seaweed species, Ishige foliacea and Ishige okamurae, both of which are known for their high biological activity. Brown seaweeds are a treasure trove of diverse secondary metabolites, with polyphenols in particular recognized as a key group of compounds contributing to physiological activities such as antioxidant and anti-inflammatory effects. Despite this, systematic comparisons of polyphenol composition across closely related species remain limited. To address this gap, comprehensive metabolite profiling was conducted using LC–MS, GC–MS, and MS/MS. The acquired datasets were processed with Progenesis QI software to ensure robust peak alignment, normalization, and metabolite annotation. Principal Component Analysis (PCA) and Partial Least Squares Discriminant Analysis (PLS-DA) clearly distinguished the two species, while Variable Importance Scores (VIP) and heatmap visualization highlighted key differentiating metabolites. Notably, the targeted polyphenolic compounds diphlorethohydroxycarmalol (DPHC) and isophoroglucin A (IPA) were isolated via HPLC-based purification, and their physiological relevance was validated through antioxidant activity assays. These findings underscore the biological significance of DPHC and IPA as representative biomarkers, thereby providing a rationale for emphasizing these compounds. Furthermore, by clarifying the distinct polyphenolic profiles of I. foliacea and I. okamurae, this study establishes evidence-based criteria to differentiate the two species. Overall, the integration of non-targeted metabolomics, multivariate statistics, and biomarker validation presents a robust framework for advancing the functional exploration of marine-derived polyphenols, with implications for drug discovery and functional food development.

CHITINASE PRODUCTION BY *Aeromonas caviae* EW02 NEWLY ISOLATED FROM GIANT MUD CRAB POND AND POTENTIAL TO DEGRADE CHIRONOMID EGG MASSES (*Chironomus plumosus*)

Chirath Pitakkhuamdee,[1] Kittipong Chanworawit,[1] Piyangkun Lueangjaroenkit,[1] Pinsurang Deevong[1,*]
[1]Department of Microbiology, Faculty of Science, Kasetsart University, 10900, Bangkok, Thailand
*e-mail: fsciprd@ku.ac.th

Abstract:
Chitin is a naturally occurring polymer that is a fundamental structural component of crustacean shells and insect exoskeletons. This slow-decomposing polymer accumulates in the environment, contributing to pollution. In addition to bioremediation, the structural polymer of chitin has been broken down by chitinolytic bacteria and chitinase enzymes as a green alternative agent for biocontrol. Chironomids or non-biting midges (Chironomidae) are associated with several problems, including allergic reactions in humans, contamination of food and water supplies, impacts on health, nuisance, and economic damage. Chironomid eggs are embedded in a gelatinous matrix composed of glycoproteins and chitin. In the present study, chitinolytic bacterial isolates were obtained from a water sample in a giant mud crab pond using a microbial enrichment method. A semi-quantitative assay of chitinase production performed using the drop assay revealed that bacterial isolate EW02 exhibited the highest chitinase production value of 1.61 ± 0.09 in Luria–Bertani (LB) agar supplemented with 0.5% colloidal chitin. Based on 16S rRNA gene sequence analysis, the isolate EW02 was closely related to *Aeromonas caviae* (99.93% identity). In the chitinase activity assay, the chitinolytic EW02 exhibited the highest chitinase activity of 1.49 ± 0.04 U/ml at 48 h of incubation. After partial purification by ammonium sulfate precipitation and dialysis, the specific activity of chitinase was increased to 3.64 U/mg protein with a 4.17-fold purification. Moreover, both the bacterial cell suspension and the dialyzed chitinase from EW02 significantly inhibited chironomid egg hatching, with inhibition rates of 86.67 ± 5.78% and 26.67 ± 5.78%, respectively. The findings suggest that chitinolytic *A. caviae* EW02 newly isolated from crab pond has potential as a green biocontrol agent for the control of chironomids collected from natural water environments.

BIOSYNTHESIS AND STATISTICAL OPTIMIZATION OF POLYHYDROXYALKANOATE (PHA) PRODUCTION BY A NEWLY ISOLATED MARINE BACTERIUM NF3-3

Piyawan Kunriya, Antika Boondaeng, Waraporn Apiwatanapiwat, Chanaporn Trakunjae*
Kasetsart Agricultural and Agro-Industrial Product Improvement Institute, Kasetsart University, Bangkok 10900, Thailand
*e-mail: aapcpt@ku.ac.th

Abstract:
The accumulation of plastic waste has become a critical global environmental issue, emphasizing the urgent need for sustainable alternatives. Bioplastics, such as polyhydroxyalkanoates (PHAs), offer an eco-friendly solution due to their microbial origin and biodegradability, making them suitable for biomedical and packaging applications. This study aims to synthesize and optimize PHA production by the newly isolated marine bacterium NF 3-3. Preliminary one-factor-at-a-time experiments revealed that glucose and ammonium sulfate were the most suitable carbon and nitrogen sources, respectively. Under these conditions, strain NF 3-3 achieved a PHA production of 2.29 g L^{-1}. Further optimization using response surface methodology (RSM) in flask-scale cultivation resulted in a maximum PHA yield of 3.35 g L^{-1}, representing a 1.5-fold increase compared to the unoptimized condition. Remarkably, the presence of the 3-hydroxyvalerate (HV) monomer was also detected under the RSM optimized condition (14.20 g L^{-1} glucose, 0.92 g L^{-1} ammonium sulfate, and 7.11 g L^{-1} sodium chloride). These findings demonstrate the successful application of RSM in enhancing PHA production by the marine bacterium. Furthermore, the produced copolymer emerges as a promising candidate for diverse biomedical applications, as the incorporation of the HV monomer provides improved flexibility, toughness, and biocompatibility compared to the homopolymer polyhydroxybutyrate (PHB).

COFFEE SILVERSKIN AS A BIOREFINERY FEEDSTOCK: INTEGRATED PRODUCTION OF PHENOLICS, BIOACTIVE PEPTIDES, AND PREBIOTIC XYLOOLIGOSACCHARIDES

Wilasinee Jirarat,[1] Kamon Yakul,[1] Wanaporn Tapingkae,[2] Thanongsak Chaiyaso[1,*]
[1]Division of Biotechnology, Faculty of Agro-Industry, Chiang Mai University, Chiang Mai, 50100, Thailand
[2]Department of Animal and Aquatic Sciences, Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand
*e-mail: thanongsak.c@cmu.ac.th

Abstract:
Coffee silverskin (CS), the major by-product generated during the coffee roasting process, represents a sustainable biorefinery feedstock due to its high levels of phenolic compounds, proteins, and xylan-hemicellulose. This study developed an integrated biorefinery approach to valorize CS through the simultaneous production of phenolics, bioactive peptides, and prebiotic xylooligosaccharides (CS-XOS). The extraction of phenolic compounds was optimized using a hydrothermal (HT) process by varying CS loading (2.5–10%, w/v), temperature (110–130°C), and time (5–30 min) under a one-factor-at-a-time (OFAT) design. The optimal condition (5% CS loading, 125°C, 25 min) yielded the highest total phenolic content (TPC) of 55.59 ± 0.12 µmole GAE/g CS. These phenolics are known for their potent antioxidant activity and can significantly contribute to the functional value of CS-derived products. Protein recovery was performed using conventional alkaline extraction (CAE) under optimized conditions (1.0 M NaOH, 90 °C, 30 min), resulting in a protein yield of 80.64 mg/g CS. Enzymatic hydrolysis of the extracted proteins using protease_SE5 produced low-molecular-weight peptides (0.302 ± 0.01 mg/mL), including FLGY, FYDTYY, and FDYGKY. These peptides exhibited *in vitro* antioxidant activity (0–50%) and notable bioactivities, such as ACE-inhibitory (26–79%) and DPP-IV-inhibitory (0–19%) activities, while showing no cytotoxic effects, suggesting their potential as nutraceutical ingredients. Following protein recovery, the alkaline-extracted solid residue (ACSS), rich in xylan-hemicellulose, was employed for CS-XOS production. Hydrolysis using recombinant endo-xylanase yielded 52.5 ± 0.08 mg CS-XOS per gram of ACSS. Prebiotic evaluation demonstrated that CS-XOS effectively enhanced the growth of probiotic lactic acid bacteria strains, with maximum specific growth rates (µmax) ranging from 0.100 to 0.122 h^{-1}, comparable to commercial XOS. Overall, this integrated biorefinery approach provides a sustainable strategy for agro-industrial waste valorization. Simultaneous production of phenolics, bioactive peptides, and CS-XOS maximizes the value of CS while reducing waste. The co-produced compounds might serve as potential functional food and nutraceutical ingredients, with possible contributions to economic growth and environmental sustainability in line with the principles of the bio-circular-green economy (BCG).

ENDOLYSIN PlyCYU: CHARACTERIZATION AND ANTIMICROBIAL POTENTIAL AGAINST *Streptococcus agalactiae* CAUSING BOVINE MASTITIS

Wachiraporn Wachiradusit,[1] Sakunrat Ubonprasert,[1] Wichai Pornthanakasem,[1] Warangkhana Songsungthong,[1] Channarong Rodkhum,[2] Penchit Chitnumsub,[1] Ubolsree Leartsakulpanich[1]*
[1]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Khlong Luang, Pathum Thani, Thailand Bangkok, Thailand
[2]Center of Excellence in Fish Infectious Diseases (CE FID), Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand
*e-mail: ubolsree@biotec.or.th

Abstract:
Streptococcus agalactiae, a multidrug-resistant pathogen involved in bovine mastitis, causes substantial economic losses in the dairy industry. Bacteriophage-derived endolysins are novel antimicrobials known to specifically hydrolyze bacterial cell walls. Here, we identified a putative endolysin named PlyCYU, which contains two putative catalytic domains—an N-terminal amidase_5 and a C-terminal glucosaminidase (Lyz2)—along with two CW_7 family cell wall-binding motifs. PlyCYU was expressed in *E. coli* and purified using Ni-Sepharose chromatography. Biochemical and antibacterial activity of PlyCYU have been characterized using different techniques, and the results revealed that PlyCYU is a promising candidate for further development as a novel antimicrobial alternative for bovine mastitis treatment.

Phyllosticta capitalensis, AN ENDOPHYTIC FUNGUS ISOLATED FROM *Ocimum sanctum* WITH ANTIBACTERIAL ACTIVITY

Pattaranan Ounjai, Khwanruedee Sangjan, Onchapron Jitkumkoon, Urarux Romruen, Eakaphun Bangyeekhun*
Department of Microbiology, Faculty of Science, Silpakorn University, Nakhon Pathom, Thailand
*e-mail: Bangyeekhun_e@su.ac.th

Abstract:
Endophytic fungi are recognized as prolific sources of novel bioactive metabolites. This study aimed to isolate endophytic fungi from *Ocimum sanctum*, *Ocimum basilicum*, and *Mentha cordifolia* (Lamiaceae) and to evaluate their antimicrobial potential. A total of 25 fungal isolates, designated MSSU01–MSSU025, were obtained. Antibacterial screening against *Bacillus subtilis*, *Staphylococcus aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa* revealed that 44% of the isolates exhibited inhibitory activity, with isolate MSSU017 showing the strongest and broad-spectrum effects. Ethyl acetate extraction of MSSU017 culture filtrate yielded 0.93 ± 5.1 mg/mL of a dark green to blackish-viscid crude extract, with a maximum solubility of 3.5 mg/mL in 10% DMSO. Broth microdilution assays demonstrated minimum inhibitory concentrations (MICs) of 437.5–875.0 µg/mL, with bactericidal activity against Gram-positive strains but no detectable MBC values for Gram-negative bacteria. Phytochemical screening indicated the presence of terpenoids, consistent with previous reports of terpenoid-type metabolites in endophytic fungi. Morphological and molecular identification confirmed MSSU017 as *Phyllosticta capitalensis*, representing the first report of this species isolated as an endophyte from *O. sanctum*. These findings highlight the potential of *P. capitalensis* MSSU017 as a source of bioactive compounds for future pharmaceutical and biotechnological applications.

CULTIVATION OF ACTINOMYCETES AND THEIR ANTIMICROBIAL PRODUCTION IN STERILIZED SEMISOLID HUMUS-BASED MEDIUM

Kota Kobayashi,[1] Shinya Kodani,[2] Takeshi Hosaka[1,*]
[1] Graduate School of Science and Technology, Department of Biomedical Engineering, Shinshu University, Japan
[2] College of Agriculture, Academic Institute, Shizuoka University, Japan
*e-mail: thosaka@shinshu-u.ac.jp

Abstract:
Humus is a soil-like substance formed through the decomposition and fermentation of dead leaves by microbes and other organisms. Actinomycetes, well-known antibiotic-producing bacteria, are abundant in humus, which provides favorable conditions for their growth. We, therefore, hypothesized that isolated actinomycetes could be cultivated in humus. This study investigated whether actinomycete strains could be cultured in semisolid media containing sterilized humus and evaluated their production of antimicrobials under this method. Commercially available humus was dried at room temperature for three days, before it was sterilized by dry heat at 180°C for 2 h and by pressurized steam at 125°C for 30 min. Thirty-one actinomycete strains, including 13 rare actinomycetes, were incubated at 30°C in a humus-based medium prepared by mixing 1 g of sterilized humus with 5 mL of sterile water. Their growth and antimicrobial productivity were then assessed; growth was evaluated by measuring viable cells. Antimicrobial assays were performed using Mueller-Hinton agar with *Escherichia coli* and *Staphylococcus aureus* as test bacteria. Most of the tested actinomycete strains grew successfully in a humus-based medium. Interestingly, *Streptomyces* sp. SUIC-MA508 produced an antibacterial compound when grown on humus medium, whereas its production was scarcely detectable on Humic Acid-Vitamin agar medium. These results suggest that the antimicrobial production may be specific to cultivation in humus-based medium. This presentation will report these findings and discuss the potential of humus-based medium for antibiotic discovery.

IMPROVEMENT OF RETINAL PRODUCTION IN *Escherichia coli*

Sae Amemiya[1], Kosuke Goto[2], Yoko Hirono-Hara[3], Fumio Matsuda[4], Yoshihiro Toya[4], Jun Ishii[5], Takashi Gojobori[2,6], Yoshimoto Saito[2], Kiyotaka Hara[1,*]
[1]Grad. Sch. Integr. Pharm. Nutr. Sci. Univ. Shizuoka. Japan
[2]MaOI Inst. Japan
[3]396bio Co., Ltd. Japan
[4]Grad. Sch. IST, Osaka Univ. Japan
[5]EGBRC, Kobe Univ. Japan
[6]National Cheng Kung Univ. Japan
*e-mail: k-hara@u-shizuoka-ken.ac.jp

Abstract:
Retinal (ATR, all-trans-retinal) is a retinoid necessary for vision, bone development, reproduction, and skin health. It is mainly used as a cosmetic material and is expected to be effective for acne and anti-aging. We developed ATR producing *E. coli*, a microorganism mostly used for bioproduction due to its rapid growth rate, expressed genes encoding crtEBIY and β-carotene 15,15'-dioxygenase (Blh) (Fig.1). To improve ATR productivity in *E. coli* and to stabilize ATR produced, we introduced rhodopsin, an ATR-binding protein, and examined optimal culture conditions. Furthermore, to further enhance ATR productivity, random mutations were introduced into Blh obtained from uncultured marine bacterium 66A03 (UMB66A03). We screened Blh mutants and expressed the selected Blh in *E. coli* and compared ATR productivities. As a result, several mutant strains with increased ATR productivity were obtained; those with decreased ATR productivity were found to have mutations introduced in the transmembrane region. For the screening, a phylogenetic analysis was also conducted using the sequences of 18,322 prokaryotic species registered as representative in NCBI Refseq (as of November 6, 2023). The result suggests that Blh genes belonging to the same cluster as the Blh from UMB66A03 in the phylogenetic tree show relatively high levels of ATR production.

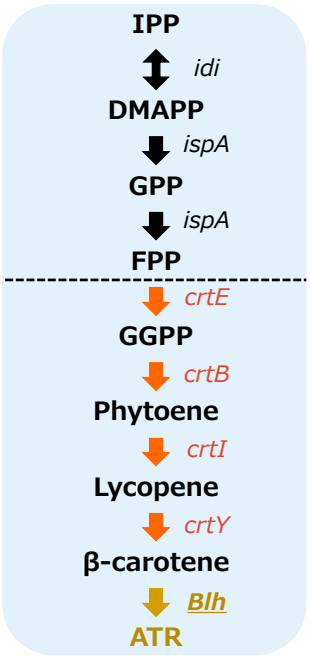


Figure. 1
Metabolic pathway of ATR in engineered *E. coli*

SCREENING OF POTENT FLAVOR COMPOUNDS PRODUCED BY Non-*Saccharomyces* YEAST

Naphattarachon Thammapanyaphong, Thamonwan Tassanaset, Jirasin Koonthongkaew *
Department of Microbiology, Faculty of Science, Chulalongkorn University, Phayathai Rd., Pathumwan, Bangkok 10330, Thailand
*e-mail: Jirasin.K@chula.ac.th

Abstract:
Saccharomyces cerevisiae is widely applied in beverage fermentation for its strong fermentation ability and stress tolerance, but its limited aroma profile can generate undesirable flavors. Non-*Saccharomyces* yeasts provide flavor diversity but often show lower ethanol productivity. This study aimed to identify a non-*Saccharomyces* strain with improved aroma potential. A total of 19 yeast isolates were obtained from 5 isolated from potato peels, 5 isolated from pineapple, and 9 from sugar factory samples, of which four non-*Saccharomyces* strains were identified by colony morphology and biochemical profiling using the API 32C system. Among them, strain JK319, isolated from a sugar factory, was identified as *Kluyveromyces marxianus* and selected for further evaluation. Growth curves in Synthetic Dextrose medium demonstrated its rapid exponential growth compared to the control *S. cerevisiae* strain Lalvin EC-1118. A sensory panel consisting of one certified evaluator and three trained panelists compared the aroma profiles of both yeasts. Fermentation assays in Yeast Nitrogen base medium showed similar CO_2 production, and both yeasts tolerated pH 2–10. Notably, K. marxianus tolerated up to 16% ethanol, a concentration inhibitory to *S. cerevisiae* strain Lalvin EC-1118. Sensory evaluation described *S. cerevisiae* strain Lalvin EC-1118 as producing astringent alcohol and musty notes, whereas *K. marxianus* generated citrus and lime peel aromas. These findings highlight *K. marxianus* JK319 as a promising alternative yeast for industrial fermentation under stressful conditions. Future studies will quantify ethanol and volatile compounds by HPLC and GC–MS and apply transcriptomic analysis to elucidate genes involved in aroma biosynthesis and stress tolerance.

ANTIMICROBIAL ACTIVITY AGAINST *Cutibacterium acnes* OF CORN AGRO-RESIDUES EXTRACT AS WASTE UTILIZATION FOR COSMETIC APPLICATION

Natthawut Thitipramote[1,2*], Ranchana Samaniam[2], Prinyaporn Pradmeeteekul[1], Junniphaphorn Nimkamnerd[1], Thiyapan Noppakoon[1], and Witayapan Nantitanon[2]
[1] Center of Excellence in Natural Products Innovation (CENPi), Mae Fah Luang University, Chiang Rai, 57100, Thailand
[2] School of Cosmetic Science, Mae Fah Luang University, Chiang Rai 57100, Thailand
*e-mail: natthawut.thi@mfu.ac.th

Abstract:
Corn agro-residues (CARs) productions or cultivations (e.g. tassels, leaves, and stalks) have higher amounts and low value. The most of these CARs are either as natural fertilizer or burnt. Agricultural burning is one of the causes of the particulate matter (PM2.5) that reached a hazardous point of human health and environment. Thus, this study aimed to utilize corn agro-residues (CARs) as bioactive in cosmetic application. CARs (tassels-CRT, leaves-CRL, and stalks-CRS) were extracted with two solvents (ethyl acetate-EA and ethanol-ET) using shaking extraction 24 hours. Bioactive compounds (total phenolic; TPC, and total flavonoid; TFC contents) and antibacterial activity against *Cutibacterium acnes* [using agar well diffusion method (AWD), minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC)] as well as the cytotoxicity of these CARs extracts were investigated. The results showed that ethanolic CARs extract tended to exert greater TPC than ethyl acetate extract at the same CARs part. The highest TPC was found in the CRT-ET extract (773.7 ± 17.2 mg GAE/g extract, $p<0.05$). However, the highest TFC was found in the CRT-EA extract (876.3 ± 2.5 mg QE/g extract, $p<0.05$). The results of antimicrobial activity against *C. acnes* showed that the inhibition zone was mostly found at high concentration of CARs extracts (≥ 5 mg/mL). In terms of MIC, corn leaves extracted with ethyl acetate (CRS-EA) showed the lowest MIC value (3.12 mg/mL). The MBC of CARs extracts, all three parts extracted with ethyl acetate (CRS-EA, CRL-EA and CRT-EA) showed highest effectiveness of MBC (12.50 mg/mL). The ethanolic extracts of CARs showed no toxicity at concentrations of 0.5 and 1 mg/mL (85% cell viability). Thus, CARs extracts can be value-added by being used as a natural active ingredient in cosmetic applications and other related products.

UTILIZING OF *Spirulina* WASTEWATER AS A BIOFERTILIZER: EFFECTS ON GREEN COS LETTUCE GROWTH AND THE SOIL MICROBIOME

Julalak Mungmart[1], Araya Lublao[1], Sudarat Dulsawat[1], Thanawat Duangfoo[1], Supapon Cheevadhanarak[1,2], Jiraporn Jirakkakul[1], Weerayuth Kittichotirat[1] and Peerada Prommeenate[1,3,*]

[1]Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Bangkok, Thailand, 10150

[2]School of Bioresources and Technology, King Mongkut's University of Technology Thonburi, Bangkok, Thailand, 10150

[3]Biochemical Engineering and Systems Biology Research Group, National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Bangkok, Thailand, 10150

*e-mail: peerada.pro@biotec.or.th

Abstract:

Algal cultivation wastewater, typically discarded, contains residual nutrients with strong potential for reuse as a liquid biofertilizer in sustainable agriculture. This study investigated the effect of a modified *Spirulina* cultivation medium on the growth of green cos lettuce and soil microbiome profile. The experiment was conducted using a complete randomized design (CRD) with four replications. Results showed that applying the modified algal medium, especially SM (Modified *Zarrouk's Medium*), led to a significant increase in the dry weight of the yield. Regarding the enhancement of soil nutrient content, both SM and SAC (modified *Zarrouk's medium* after *Spirulina* cultivation) improved soil nutrient levels in green cos lettuce cultivation. Although SAC exhibited slightly lower effectiveness, a noticeable difference was still observed compared to the control. Furthermore, the soil microbiome was analyzed using next-generation sequencing (NGS) to characterize the microbial profile following wastewater application. In the treated soil, the abundance of bacteria from the phyla *Actinobacteriota* and *Firmicutes* decreased, while those from the phyla *Verrucomicrobiota*, *Myxococcota*, *Chloroflexi*, *Acidobacteriota*, *Planctomycetota*, and *Gemmatimonadota* increased. Although many of these have been previously reported as plant-growth-promoting bacteria (PGPB), they responded differently to the algal medium application. The microbes identified as beneficial for green cos growth under these conditions will be used to develop a microbiome-based technological framework. This research aims to introduce an eco-friendly agricultural practice and create a circular system that transforms waste into a valuable resource.

STUDY OF DIVERSITY AND METALAXYL RESISTANCE IN *Phytophthora* spp. CAUSING BLACK ROT DISEASE IN ORCHIDS

Muthita Singsakulrat,[1] Kultida Pantayak,[2,3] Chanwit Suriyachadkun, [2] Vanicha Vichai, [2] Chatsuda Sakdapetsiri[3,*]
[1]Program in Agricultural Biotechnology, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University Kamphaeng Saen Campus, Nakhon Pathom 73140 Thailand
[2]National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, 113 Paholyothin Road, Klong 1, Klong Luang, Pathumthani 12120 Thailand
[3]Department of Plant Pathology, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University Kamphaeng Saen Campus, Nakhon Pathom 73140 Thailand
*e-mail: chatsuda_sak@ku.th

Abstract:
Orchids are considered economically valuable ornamental plants in Thailand, which serves as one of the major global hubs for orchid cultivation and the largest exporter. Among the various diseases hindering orchid production, black rot disease, caused by *Phytophthora* spp., is one of the most devastating, affecting a wide variety of orchids. Metalaxyl is widely used to control this disease in orchid cultivation. While fungicide resistance among plant pathogens is on the rise worldwide, limited studies have been conducted on metalaxyl resistance in *Phytophthora* affecting orchids in Thailand. This study investigated the diversity of *Phytophthora* species isolated from orchids and their sensitivity to metalaxyl. Diseased orchid samples were collected from orchid farms in Samut Sakhon and Phetchaburi provinces. *Phytophthora* isolation was performed by surface-sterilizing infected tissues and subsequently culturing on carrot agar supplemented with 200 µg/ml penicillin at 20°C for 5–7 days. Seventeen isolates were obtained and evaluated for pathogenicity in orchids. All isolates produced typical symptoms of black rot disease, characterized by water-soaked lesions and progressive tissue blackening in infected plants. The isolates were identified using internal transcribed spacer (ITS) and 5.8S rDNA sequences. Five isolates showed the highest similarity (>99%) to *P. palmivora* CPHST BL 105 and were classified as *P. palmivora*. The remaining isolates showed similarity to *P. haveae* CPHST BL 67 (7 isolates), *P. nemorosa* CPHST BL 27 (2 isolates), *P. pseudosyringae* CPHST BL 51G (1 isolate), *P. lateralis* CBS:168.42 (1 isolate), and *P. foliorum* JKI CBS 121655 (1 isolate), with similarity ranging from 86.89–88.01%. A representative isolate from each of the 6 *Phytophthora* species identified was investigated for metalaxyl resistance, ranging from 0.15% to 1%, using a mycelial growth inhibition assay. Results revealed that all six representative isolates were resistant to metalaxyl at the concentration typically used in orchid farms, 0.15% (w/v). The most highly resistant isolate, *P. palmivora* isolate SSMT5, grew in the presence of 1% (w/v) metalaxyl. These results highlight the diverse nature of *Phytophthora* species associated with orchid black rot disease and suggest that the recommended application dose of metalaxyl may be insufficient for black rot disease control. More comprehensive sampling combined with multi-gene phylogenetic analysis is needed to improve taxonomic accuracy and fully characterize pathogen diversity. Further validation under greenhouse conditions is also necessary to confirm the field relevance of these laboratory observations.

OPTIMIZATION OF PECTIN YIELD FROM *CYCLEA BARBATA* MIERS LEAVES USING RESPONSE SURFACE METHODOLOGY

Witayapan Nantitanon[1]*, Pimpailin Rodpradit[1], and Natthawut Thitipramote [1,2]
[1]School of Cosmetic Science, Mae Fah Luang University, Chiang Rai 57100, Thailand
[2]Center of Excellence in Natural Products Innovation (CENPi), Mae Fah Luang University, Chiang Rai, 57100, Thailand
*e-mail: witayapan.nan@mfu.ac.th

Abstract:
Pectin is a polysaccharide widely used in the food, pharmaceutical, and cosmetic industries as a gelling, stabilizing, emulsifying agent, prebiotic, and an attractive moisturizing agent ingredient in skin care, resulting in a continuously growing global demand. *Cyclea barbata* Miers is a traditional local plant widely distributed in Southeast Asia, including Thailand. It grows rapidly and is abundant in rural areas. Its leaves are rich in pectin, making them a sustainable raw material compared with conventional fruit peels. However, no study has yet optimized the extraction process from this plant. This work employed central composite design (CCD) to determine the optimal conditions for pectin extraction, especially examining the effects of temperature (70–90 °C), extraction time (30–60 min), and solution pH (1.5–3.5). The finding indicated that the quadratic model provided a superior fit ($p<0.001$) with a non-significant lack of fit ($p>0.6418$). Both individual factors and the interaction of temperature with pH and extraction time significantly influenced the obtained pectin yield. The optimal condition to give the experimental pectin (14.23 ± 0.17%) was established at 81.80 °C, pH 2.08, and 59.50 min under a sample-to-solution ratio of 1:20 (w/v) in an ultrasonic bath. The obtained pectin yield at this condition deviated by less than 5% from the predicted value, confirming the reliability of the quadratic model.

Keywords: *Cyclea barbata* Miers; Cosmetics; Optimization; Pectin; RSM

ISOLATION AND CHARACTERIZATION OF INDOLE-3-ACETIC ACID (IAA)-PRODUCING RHIZOBACTERIA FROM WHITE BUTTERFLY PEA (*Clitoria ternatea* L.)

Rattiya Padungpol,[1] Surak Jamjumrus,[1] Porntip Sangsil,[1] Siriphan Sukkhaeng,[1] Chommanat Kerdkhong[1,*]
[1] Central Laboratory and Greenhouse Complex, Research and Academic Service Center, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom, 73140, Thailand
*e-mail: rdicnke@ku.ac.th

Abstract:
Indole-3-acetic acid (IAA) is a key plant hormone in the auxin group that regulates plant growth and development by promoting cell elongation, division, and differentiation. Auxins are essential in plant tissue culture techniques, particularly for root and shoot development. However, synthetic auxins such as NAA, 2,4-D, and IBA may be ineffective in certain plant species. This study aimed to isolate and screen IAA-producing bacteria and determine the optimal L-tryptophan concentration for IAA biosynthesis. We hypothesized that increasing L-tryptophan levels would enhance IAA production. A total of 38 bacterial isolates were obtained from the rhizosphere soil of white butterfly pea (*Clitoria ternatea* L.) and cultured in nutrient broth (NB) supplemented with 0.1% (w/v) L-tryptophan and incubated at 37°C, 200 rpm for 2 days to screen for IAA-producing bacteria. CT33 showed the highest IAA production (175.82 mg/L) and was identified as *Enterobacter chuandensis* (99.72% similarity via 16S rRNA sequencing). To determine the optimal *L*-tryptophan concentration for IAA production, *E. chuandensis* CT33 was cultured in NB containing varying L-tryptophan concentrations (0–1.0% w/v) and incubated at 37°C, 200 rpm. The culture medium was collected daily for 5 days for IAA concentration analysis, with three replicates per treatment. The results showed that increasing the concentration of L-tryptophan led to a corresponding increase in IAA production. *E. chuandensis* CT33 produced the highest IAA concentration (600.6±32.4 mg/L) at 1.0% L-tryptophan after 5 days of incubation. IAA was extracted from the culture medium, confirmed, and quantified using HPLC against a standard. Furthermore, IAA produced by *E. chuandensis* CT33 will be further studied for its potential application in root induction using ornamental plant tissue culture techniques.

Session V.
Agriculture Biotechnology

SSR-BASED MARKER-TRAIT ASSOCIATIONS FOR THE SELECTION OF DROUGHT-TOLERANT MAIZE S1 GENOTYPES

Theerawut Wongwarat,[1,]* Chaiyawat Nantachot,[2] Suriphat Thaitad[3,]
[1]Khon Kaen Field Crops Research Center, 180, Sila, Mueang, Khon Kaen, Thailand
[2]Nakhon Sawan Field Crops Research Center, 146, Suksumran, Takfa, Thailand
[3]Field and Renewable Energy Crops Research Institute, 50, Chatuchak, Bangkok, Thailand
*e-mail: theerawut6949@gmail.com

Abstract:
The aim of this study was to evaluate the effectiveness of SSR markers in selecting drought-tolerant S_1 maize genotypes, with the goal of reducing the number of genotypes advanced to the S_2 generation for further breeding. Climate change has intensified drought condition, lead to reduced yields of field maize (*Zea mays* L.) and negatively affecting the domestic livestock feed production chain. Drought tolerance in maize is a complex quantitative trait influenced by both genetic and environmental factors. Although conventional breeding is effective, it is often time-consuming and resource-intensive. In this study, a total of one hundred and fifty S_1 genotypes derived from a cross between a drought-tolerant parent (Takfa 7) and a drought-susceptible parent (Ki 48) were genotyped using six SSR markers previously associated with drought-adaptive traits. These included umc1069 (glutathione-S-transferase 1), umc1139 (small kernel 501), umc1239 (trihelix transcription factor 43), umc1962 (pollen specific leucine rich repeat extensin 3) bnlg1079 (QTLs for vanillin and syrigaldehyde) and bnlg1526 (QTL for phophorus utilization under deficit condition). Cluster analysis grouped the S_1 genotypes into distinct subpopulations, with two groups showing high frequencies of favorable drought-tolerance alleles. Based on cumulative marker profiles, seventy-three S_1 genotypes were selected as candidates for drought tolerance. The use of SSR-based marker-trait associations enabled the efficient identification of genotypes carrying favorable alleles, thereby reducing the number of genotypes advanced to the next generation. While this molecular approach shows promise, future studies incorporating phenotypic validation under drought condition will be essential to confirm the effectiveness of the selected genotypes. This combined strategy offers a robust pathway to accelerate the development of drought-resilient maize through marker-assisted selection.

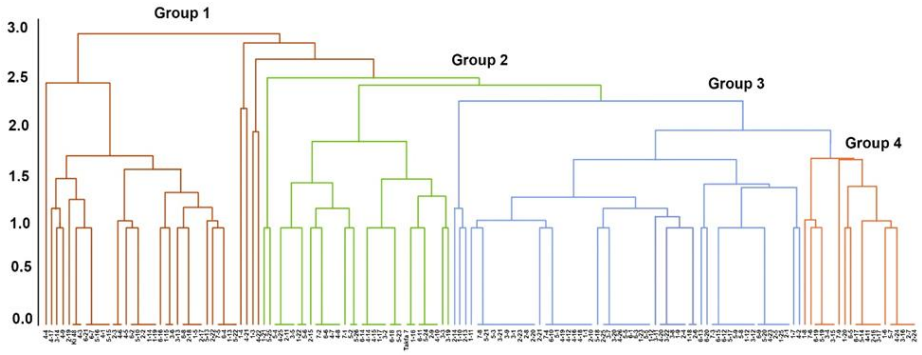


Figure 1.
Dendrogram of the one hundred and fifty S_1 genotypes based on six drought-related molecular markers using Ward's method with squared Euclidean distance. The analysis classified the genotypes into four group; Group 1 (drought sensitive, including the susceptible parent Ki 48), Group 2 (drought tolerance, including the tolerant parent Takfa 7), Group 3 (intermediated drought tolerance) Group 4 (mixed genotypic profile). Candidate genotypes for future selection were primarily found in Groups 2 and 3.

REEMERGENCE AND CHARACTERIZATION OF SNAKEHEAD RHABDOVIRUS IN THAI AQUACULTURE

Kitipong Angsujinda,[1] Nabhasbhichayabha Daewang,[2] Nopadon Pirarat[3], Timothy J. Mahony[4], Wanchai Assavalapsakul[2,*]
[1]Aquatic Resources Research Institute, Chulalongkorn University, Bangkok 10330, Thailand
[2]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand
[3]Department of Pathology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok 10330, Thailand
[4]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD 4072, Australia
*e-mail: wanchai.a@chula.ac.th

Abstract:
In mid-2024, a severe outbreak of snakehead fish (*Channa striata*) resulted in 100% cumulative mortality across commercial farms in Suphan Buri Province, Thailand. Clinical signs and histopathological analysis suggested a viral etiology, consistent with Snakehead Rhabdovirus (SHRV) infection. This study aimed to characterize the causative agent using virological and molecular techniques. SHRV was successfully isolated from affected fish using E11 cells, with confirmation by semi-quantitative RT-PCR, transmission electron microscopy, and sequencing. Infectious virions were purified by sucrose gradient ultracentrifugation, with peak infectivity observed in the 40% sucrose fraction. SDS-PAGE analysis of the purified virus revealed four prominent structural proteins—glycoprotein (G), nucleoprotein (N), phosphoprotein (P), and matrix protein (M)—consistent with known SHRV profiles. Sequence analysis of the RNA-dependent RNA polymerase (L gene) indicated 5.51% amino acid divergence from the original Thai strain (GenBank accession: AF147498.1), suggesting genetic evolution. These findings indicate the re-emergence of a highly virulent SHRV lineage in central Thailand and support the need for immediate updates to SHRV molecular diagnostics to capture sequence drift, a re-evaluation of antigen match, and the protective efficacy of existing inactivated or autogenous vaccines, as well as rapid farm-side testing with strengthened biosecurity measures to limit the spread.

A NOVEL *Azospirillum vistecanum* STRAIN ISOLATED FROM METHANE DIGESTATE ENHANCES PLANT GROWTH THROUGH HIGH-EFFICIENCY INDOLE-3-ACETIC ACID (IAA) BIOSYNTHESIS

Surat Moomthong,[1] Thamonwan Woraruthai,[1] Charndanai Tirapanampai,[1] Sasithon Rungjroenchaiwat,[1] Worarat Kruasuwan,[2] Pichahpuk Uthaipaisanwong,[3] Kanthida Kusonmano,[3,4] Piroon Jenjaroenpun,[2] Thidathip Wongsurawat,[2] Thanyaporn Wongnate,*
[1]School of Biomolecular Science & Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC), Wangchan Valley, Rayong, 21210, Thailand
[2]Oxford Nanopore Centre of Excellence, Division of Medical Bioinformatics, Department of Research, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, 10700, Thailand
[3]Systems Biology and Bioinformatics Research Laboratory, Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Bangkok, 10150, Thailand
[4]Bioinformatics and Systems Biology Program, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi, Bangkok, 10150, Thailand
* Corresponding author. E-mail address: thanyaporn.w@vistec.ac.th (T. Wongnate).

Abstract:
The urgent need for sustainable agricultural inputs has accelerated the search for microbial alternatives to synthetic agrochemicals. In this study, we report the isolation and comprehensive characterization of a novel strain, *Azospirillum vistecanum* VT-I1, obtained from a methane-enriched digestate system. This strain demonstrated exceptional plant growth-promoting potential through the biosynthesis of indole-3-acetic acid (IAA), a key phytohormone. Genome sequencing and annotation revealed the presence of genes associated with the indole-3-pyruvate (IPyA) pathway, *aro*9, *ipd*C, and *ald*A, with no detectable IAA-degrading gene clusters, supporting a high net auxin yield. Under optimized culture conditions, VT-I1 produced up to 1.206 mM of IAA, significantly surpassing the levels observed in *A. brasilense*. Functional assays confirmed the bioactivity of this microbial IAA, which enhanced root development in *Exacum affine* and improved seed germination in *Andrographis paniculata*. Collectively, these results establish *A. vistecanum* VT-I1 as a promising candidate for next-generation biofertilizers, offering a scalable, eco-friendly alternative to chemically synthesized auxins. This work expands our understanding of auxin biosynthesis in rhizobacteria and provides a strong foundation for future field applications and microbiome-based crop enhancement strategies.

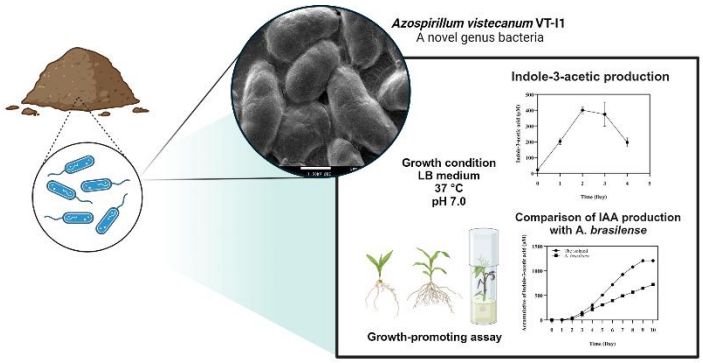


Figure 1.

NOVEL ANTISEPTIC CONSISTING OF AN IODINE-POLYSORBATE 80 COMPLEX WITH LONG-TERM RETENTION AND A BROAD ANTIMICROBIAL SPECTRUM

Shingo Shimada,[1] Shigekazu Yano,[1,*] Wasana Suyotha,[2] Satoshi Asakura,[3] Takahiro Sato[3]
[1]Graduate School of Science and Engineering, Yamagata University, Japan
[2] International Program of Biotechnology, Center of Excellence in Innovative Biotechnology for Sustainable Utilization of Bioresources, Faculty of Agro-Industry, Prince of Songkla University, Thailand
[3]Ise Chemicals Corporation, Japan
*e-mail: shige-y@yz.yamagata-u.ac.jp

Abstract:
Iodine exhibits antimicrobial activity against various bacteria, fungi, and viruses, but it is highly volatile and has low solubility in water. Hence, iodine is used as an antiseptic in its complex form with a carrier material. Iodine-polyvinylpyrrolidone complex (PVP-I) is widely used, and PVP-I, containing high concentrations of iodine (about 7%), slowly releases iodine and reduces its volatilization. However, PVP-I does not exhibit antimicrobial activity unless it is diluted to an iodine concentration of about 200 ppm. The amount of free iodine, acting as an antimicrobial agent, does not increase without dilution.

In this study, we prepared a complex of iodine and a nonionic surfactant, polysorbate 80 (PS80), and investigated properties of the complex (PS80-I). Figure 1 shows that the growth of *Pseudomonas putida* was inhibited at iodine concentrations of 100, 75, 50, and 25 ppm in the presence of 0%, 0.01%, 0.1%, and 1% PS80, respectively. We evaluated the long-term retentivity and found that PS80 retained iodine for about 4 months and prevented its volatilization (Fig. 2). Furthermore, PS80-I retained its growth inhibitory activity upon storage for about 4 months. Here, we also report on the antibacterial activity of PS80-I against various bacteria and fungi.

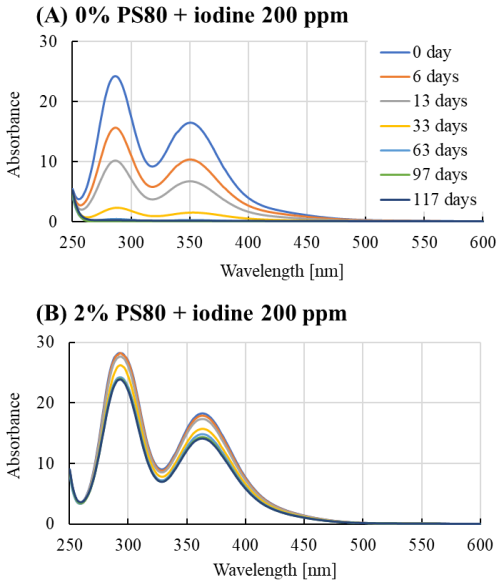


Figure 1
Growth inhibition assay against *P. putida* with various concentrations of PS80 and I_2-KI solutions. I_2 conc. refers to I_2 concentration; the solution contained eight times the amount of KI as I_2.

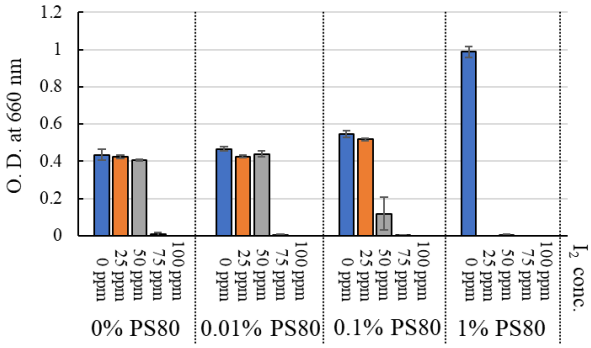


Figure 2

Absorption spectra for the I_2-KI solution (A) and the complex of PS80 and iodine (B).

ENCAPSULATED FREEZE-DRIED LACTIC ACID BACTERIA MODULATE GUT MICROBIOTA, HEALTH, AND GROWTH OF *Penaeus monodon*

Narongchai Chupoon[1]*, Nomchit Kaewthai Andrei[1], Sirinat Srionnual[1], and Thanikan Thorasin[1]

[1]*Department of Food Innovation and Management, Faculty of Agro-Industry, Rajamangala University of Technology Srivijaya, Thung Yai District, Nakhon Si Thammarat 80240, Thailand*

Abstract:

Black tiger shrimp (*Penaeus monodon*) is a high-value aquaculture species, yet its production is limited by recurrent disease outbreaks and growth constraints. This study evaluated dietary supplementation with freeze-dried encapsulated lactic acid bacteria (FEL) on growth, immunity, survival, and gut microbiota of *P. monodon* under hatchery and pond conditions. In the hatchery trial, shrimp fed 0.2–0.6% FEL showed significantly higher specific growth rate and enhanced immune responses, including total hemocyte count, phenoloxidase activity, and bacterial clearance, compared with the control. Survival after *Vibrio parahaemolyticus* (non-AHPND) challenge reached 100% in all FEL groups, versus 82.2 ± 8.0% in the control. In the pond validation trial, shrimp receiving 0.2% FEL attained significantly greater body weight after 40 days than the control. High-throughput 16S rRNA sequencing further revealed that FEL reduced the relative abundance of pathogenic *Photobacterium damselae* while enriching beneficial Roseobacter-group taxa such as *Phaeobacter inhibens* and *Ruegeria lacuscaerulensis*. Overall, FEL acted as both an immunostimulant and microbiota modulator, highlighting its potential as a functional feed additive for sustainable and biosecure *P. monodon* aquaculture.

Keywords: *Penaeus monodon, lactic acid bacteria, microencapsulation, immunity, growth performance, gut microbiota*

EFFECT OF SALINITY ON POLY-γ-GLUTAMIC ACID PRODUCTION IN *Bacillus subtilis* FSO3

Thanaporn Wichai[1], Emmanuel O. Opadokun[2], Panaya Kotchaplai[1,3,4]*
[1]Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, Thailand
[2]Program in Biotechnology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
[3]Center of Excellence in Bioconversion and Bioseparation for Platform Chemical Production, Institute of Biotechnology and Genetic Engineering, Chulalongkorn University, Bangkok, Thailand
[4]Water Science and Technology for Sustainable Environment Research Unit, Chulalongkorn University, Bangkok, Thailand
*Corresponding author: E-mail: panaya.k@chula.ac.th

Abstract:
Poly-γ-glutamic acid (γ-PGA), a bacterial biopolymer of glutamic acid, demonstrates significant promise for promoting plant growth, even under stress conditions. This study evaluated the impact of salt stress on the γ-PGA-producing *Bacillus subtilis* FSO3 using PGA medium supplemented with 0-5% (w/v) NaCl. Bacterial growth was adversely affected by 5% NaCl, as shown by the formation of markedly small colonies on PGA agar, particularly during the initial 12 hours of cultivation. After 48 hours of cultivation in PGA medium, γ-PGA content in the precipitated extracellular polymeric substances (EPS) was quantified using the cetyltrimethylammonium bromide (CTAB) assay. γ-PGA production was explored under both static and shaking (150 rpm) conditions. Under static conditions, overall γ-PGA yields remained comparable (approximately 4 g/L) across salt concentrations up to 1% NaCl. Notably, the proportion of γ-PGA within the total EPS was approximately 1.6 to 2-fold higher under these saline conditions compared to the non-stress control (31% of total EPS). At 5% NaCl, yields decreased to approximately 1 g/L (14.91% of total EPS). Under shaking conditions, the γ-PGA yield at 0% NaCl was approximately 4.4 g/L (64% of total EPS). Addition of low NaCl concentration (0.25%) resulted in a comparable γ-PGA yield but a substantially 2-fold lower proportion of γ-PGA in the EPS. Higher NaCl concentrations (1.25-5%) resulted in an approximate 1.7- to 2-fold decrease in γ-PGA yield. These findings demonstrate *B. subtilis* FSO3's potential for producing γ-PGA under salt stress, even when cultivated statically. Further research is required to explore its efficacy in promoting plant growth in saline soils, contributing to sustainable agriculture in challenging environments.

EXPRESSION OF CHITINASE ENCODING GENE FROM *Serratia marcescens* MC_G07 AND TERMITICIDAL ACTIVITY AGAINST THE WOOD-FEEDING TERMITE *Microcerotermes* sp.

Kittipong Chanworawit,[1] Torphan Vitoonpanyakij,[1] Pinsurang Deevong[1,*]
[1]Department of Microbiology, Faculty of Science, Kasetsart University, 10900, Bangkok, Thailand
*e-mail: fsciprd@ku.ac.th

Abstract:
Termites (Isoptera) are insects that have the capacity to cause significant damage to wooden structures and materials. Chitinase, a chitinolytic enzyme that breaks down chitin, a major component of insect exoskeletons, is considered a promising tool for alternative biological control of pests including termites. The objectives of this study were to characterize the chitinase-encoding gene (*chi*) from the bacteria *Serratia marcescens* Mc_G07 obtained from termite guts and evaluate the ability of recombinant chitinase to enhance the mortality of wood-feeding termite *Microcerotermes* sp. The *chi* gene (~ 1,500-bp length) of *S. marcescens* Mc_G07 was amplified using polymerase chain reaction (PCR) and then cloned into the pGEM-T Easy vector. The positive clone was selected based on restriction analysis using the restriction enzyme *Eco*RI. The target gene was verified by DNA sequencing and subcloned into the expression vector pET-28a(+). The recombinant pET-28a(+)-*chi* was transformed into *Escherichia coli* BL21 (DE3) for protein expression and the expressed protein was purified using Ni-NTA affinity chromatography of His-tagged proteins. The purified recombinant chitinase had a specific activity of 234.52 mU/mg protein with a 15.52-fold purification and recovery yield of 70.02%. The 52-kDa recombinant chitinase exhibited strong termiticidal activity against *Microcerotermes* sp. with a lethal concentration 50 (LC_{50}) value of 440.10 ± 7.75 mU/treatment within 24 h. The results of this study provide insights for molecular biotechnological research and serve as a model for the development of bioinsecticides in the future.

PROOF OF CONCEPT FOR EXTERNAL PROTEIN IMMOBILIZATION ON LACTIC ACID BACTERIA: A NON-GMO APPROACH

Pinpunya Riangrungroj[1,*]
[1]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 113 Thailand Science Park, Phahonyothin Road, Klong Nueng, Klong Luang, Pathum Thani 12120, Thailand
*e-mail: pinpunya.ria@biotec.or.th

Abstract:
Surface display of proteins on lactic acid bacteria (LAB) holds great promise for broad biotechnological applications. Conventional strategies for LAB surface display typically rely on genetic modification, which can raise regulatory concerns and limit industrial implementation. To address this, we present a non-genetically modified (non-GMO) approach for surface immobilization of proteins on LAB, using green fluorescent protein (GFP) as a model. A recombinant GFP fused with a cell wall-binding domain (CBD) was expressed in *Escherichia coli* and purified via nickel affinity chromatography. The fusion protein was externally applied to various LAB strains, such as *Lactobacillus plantarum*, *Lactococcus lactis*, and *Pediococcus pentosaceus*. Binding to the bacterial surfaces was confirmed by immunofluorescence microscopy and flow cytometry. This proof-of-concept demonstrates the feasibility of anchoring functional proteins without genetic engineering and could be adapted for proteins of different sizes. Although steric hindrance, peptide stability, and the non-covalent nature of CBD–cell wall interactions may affect binding efficiency and durability, these challenges can be addressed through further optimization, and the approach remains practical. Overall, this strategy offers a safe, regulatory-friendly platform with diverse potential in oral vaccine delivery, whole-cell biocatalysis, and biosensing for food and feed industries.

COMPARATIVE ANALYSIS OF GLUTATHIONE S-TRANSFERASE GENE FAMILY IN EXTREMOPHILIC CYANOBACTERIA

Thanawat Leknawin[1], Chananwat Kortheerakul[1], Sasiprapa Samsri[1], Hakuto Kageyama[2,3] and Rungaroon Waditee-Sirisattha[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Pathum Wan, Bangkok, Thailand
[2]Graduate School of Environmental and Human Sciences, Meijo University, Nagoya, Aichi 468-8502, Japan
[3]Department of Chemistry, Faculty of Science and Technology, Meijo University, Nagoya, Aichi 468-8502, Japan
*e-mail: rungaroon.w@chula.ac.th

Abstract:
The glutathione S-transferase (GST) family comprises a set of enzymes that play crucial roles in cellular detoxification. GSTs participate in various physiological aspects of cells, such as stress tolerance, cellular apoptosis, secondary metabolite transport and antibiotic resistance. In this study, we comprehensively analyzed GST gene family in extremophilic cyanobacteria**.** Based on the availability of entire genome sequencing, thermophilic cyanobacteria consist of a great number of GST-encoding genes, followed by halophilic and xerophilic cyanobacteria. Phylogenetic analysis was performed with 184 cyanobacterial GSTs, and subfamilies of thermophilic GSTs were identified. Furthermore, the physicochemical properties of thermophilic and halophilic GSTs are distinct. These results provide global patterns of cyanobacterial GST evolution and lead to an understanding of fundamental functions of the GST gene family across taxa.

GENOME-BASED DISCOVERY OF NOVEL CYANOBACTERIAL NATURAL PRODUCTS DERIVED FROM *Gloeocapsa* sp. Strain BRSZ

Hari Winanda[1], Sasiprapa Samsri[1], Stephen B. Pointing[2], Hakuto Kageyama[3,4], and Rungaroon Waditee-Sirisattha[1*]
[1]Microbiology Department, Faculty of Science, Chulalongkorn University, Thailand
[2]Department of Biological Sciences, National University of Singapore, Singapore
[3]Graduate School of Environmental and Human Sciences, Meijo University, Japan
[4]Department of Chemistry, Faculty of Science and Technology, Meijo University, Japan
*****e-mail: rungaroon.w@chula.ac.th

Abstract:
Extremophilic cyanobacteria are important microorganisms that having a great capacity for producing bioactive compounds (BACs). These BACs are produced through a set of enzymes that encoded by biosynthetic gene clusters (BGCs), either nonribosomal peptide synthetases (NRPS), polyketide synthases (PKS) or hybrids thereof, and ribosomally-synthesized and post translationally modified peptides (RiPPs). These BACs and BGCs can be predicted through genome mining approach to get putative BGCs and its BACs by using its genome sequencing data. *Gloeocapsa* sp. strain BRSZ, a thermophilic cyanobacterium, isolated from the Bo Khlueng hot spring (55 °C) comprised a total of 6,084,403 bp with a GC content 43.5%. Putative BGCs were divided into 6 categories with total 13 main putative BACs. These BACs may functionate as antibiotics, novel inhibitors, and bioactive compounds. Thus, this study revealed that *Gloeocapsa* sp. strain BRSZ is a potential source for biosynthesis of BACs.

EXPLORING CYANOBACTERIAL DIVERSITY FROM A NEUTRAL-ALKALINE HOT SPRING IN THAILAND AND THEIR PHOTOPROTECTIVE COMPOUND PRODUCTIONS

Chatchadarat Anantasophon,[1] Pawat Wangthaphan,[1] Tanawat Leknawin,[1] Sasiprapa Samsri,[1] Stephen B. Pointing,[2] Hakuto Kageyama[3,4] and Rungaroon Waditee-Sirisattha[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand
[2]Department of Biological Sciences, National University of Singapore, Singapore 117557, Singapore
[3]Department of Chemistry, Faculty of Science and Technology, Meijo University, 1-501 Shiogamaguchi, Tenpaku-ku, Nagoya, Aichi 468-8502, Japan
[4]Graduate School of Environmental and Human Sciences, Meijo University, 1-501 Shiogamaguchi, Tenpaku-ku, Nagoya, Aichi 468-8502, Japan
*e-mail: Rungaroon.W@Chula.ac.th

Abstract:
Thermophilic cyanobacteria are prokaryotic photoautotrophic microorganisms that can grow at high temperatures. This study, the diversity of thermophilic cyanobacteria was explored in a neutral-alkaline Bo Khlueng hot spring, Ratchaburi Province in central Thailand. To classify the taxonomy of the isolated strains, we used combination methods, including phenotypic, genotypic, and chemotaxonomic data. We discovered an interesting cyanobacterial strain with a morphological match to the genus *Stanieria*. Based on morphological features, this thermophilic cyanobacterium is a baeocyte producer. Moreover, its cell typically appeared to produce a dark blue-green pigment, implicating that the composition of chromophores is distinct. Molecular phylogenetic analysis of the 16S rRNA gene placed this strain with the closest similarity to *Stanieria cyanosphaera* (96% nucleotide identity). We therefore named this thermophilic cyanobacterium as *Stanieria* sp. strain Black (BL). HPLC and LC/MS analyses identified a UV-absorbing compound as porphyra-334, produced by *Stanieria* sp. strain BL. Our results suggest that a thermally hot spring is a good bioresource for exploring novel extremophilic cyanobacteria.

PHENOTYPIC VARIATION AND PLASTICITY OF ROOT HAIR TRAITS IN AUSTRALIAN DURUM WHEAT (*Triticum turgidum* subsp. *Durum*) UNDER PHOSPHORUS DEFICIENCY

Sukrita Majak,[1] Samir Alahmad,[2] Lee Thomas Hickey, [2] Alexander Bucksch,[3,4] Patompong Johns Saengwilai [1],*
[1] Department of Biology, Faculty of Science, Mahidol University, 10400 Thailand
[2] Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Brisbane, QLD 4072, Australia
[3] School of Plant Sciences, The University of Arizona, AZ, 85721 USA
[4] Bio5 Institute, The University of Arizona, AZ, 85721 USA
*e-mail: patompong.sae@mahidol.edu

Abstract:
Durum wheat (Triticum durum L.) is an important cereal crop in arid and semi-arid regions. However, its yields can be greatly reduced under phosphorus (P) deficiency. Root hairs play an important role in the uptake of water and nutrients by expanding root surface areas, which could mitigate stresses. The phenotypic diversity and plasticity of root hair traits in durum wheat, despite their importance for nutrient uptake, are still largely unexplored. This study evaluated root hair length (RHL), root hair density (RHD), and root hair diameter in twelve parental genotypes, including two Australian cultivars and ten ICARDA founder lines, under P-sufficient (0.2 mM) and P-deficient (0 mM) hydroponic conditions. Significant genotypic variation was observed for RHL and RHD responses to P availability, while RH diameter remained stable. Under P deficiency, DBA Aurora showed a 16.34% reduction in RHL. Among ICARDA lines, Fastoz03B had the largest decrease in RHL by 65.73%, while Outrob4 increased RHL by 44.41%. Plasticity analysis revealed diverse patterns, such as Fastoz07 had high plasticity, while DBA Aurora had low plasticity in RHL. These findings demonstrate diversity in root hair phenotypes and plasticity, providing potential targets for breeding durum wheat with improved P-use efficiency in P-deficient environments.

UNVEILING THE QUANTITATIVE LANDSCAPE OF GINGEROL AND ITS DERIVATIVES IN THAI GINGER (*Zingiber officinale* Roscoe)

Kronsirinut Rothjanawan[1], Nattakanwadee Khumpirapang[2], Alisa Kongthong[3], Pimprapa Chaijak[3,*]

[1] Department of Computer Engineering, Faculty of Engineering, Princess of Naradhiwas University, Naradhiwat 96000, Thailand
[2] Department of Pharmaceutical Chemistry and Pharmacognosy, Faculty of Pharmaceutical Science, Naresuan University, Phitsanulok 65000, Thailand
[3] Department of Biological Science, Faculty of Science and Digital Innovation, Thaksin University, Phatthalung 93210, Thailand
*e-mail: pimprapa.c@tsu.ac.th

Abstract:
The ginger rhizome is consumed worldwide as a spice and medicine owing to its sensory and bioactive compounds, which are mainly phenolic compounds known as gingerols. Among these, 6-gingerol is a major pharmaceutical component in the ginger rhizome. This study aimed to profile six major gingerol-related metabolites (6-gingerol, 8-gingerol, 10-gingerol, 6-shogaol, 8-shogaol, and 10-shogaol) in ginger samples collected from various regions across Thailand using HPLC. The analysis of total gingerols and total shogaols revealed significant variation in metabolite concentrations among the samples, largely influenced by regional growth conditions. Notably, the Narathiwat extract contained the highest level of total gingerols (6-gingerol, 8-gingerol, and 10-gingerol), followed by the Phitsanulok extract. In contrast, the concentration of 8 -shogaol displayed minimal variation across regions, suggesting limited sensitivity to environmental factors compared to other analogues. These findings contribute to a better understanding of the chemical diversity of Thai ginger and provide a basis for its potential applications in nutraceutical and pharmaceutical industries.

IDENTIFICATION OF POTENTIAL GENES INVOLVED IN SWARMING ACTIVITIES-RELATED VIRULENCE OF *Vibrio parahaemolyticus* AHPND

Theerisara Klahan[1], Wanilada Rungrassamee[2], Ponsit Sathapondecha[1,*]

[1]Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla 90110
[2] Biosensing and Bioprospecting Technology Research Group, National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, 111 Thailand Science Park, Phahonyothin Road, Khlong Luang, Pathum Thani 12120
*e-mail: ponsit.s@psu.ac.th, ponsit.sat@gmail.com

Abstract:
Shrimp aquaculture is confronted with problematic diseases that lead to economic losses. One of the most serious shrimp diseases is acute hepatopancreatic necrosis disease caused by *Vibrio parahaemolyticus* (VpAHPND). In recent years, a variety of VpAHPND have been isolated from shrimp and water, and they have shown varying levels of virulence for shrimp. One of several factors involved in the virulence of *Vibrio* is the ability to motility, especially swarming activity. However, the genetic relationship between swarming activity and virulence levels has not yet been elucidated. Therefore, in this study, the genetic association of swarming activities was investigated using whole genome sequencing and bioinformatics. Thirty-one VpAHPND isolated from various individual shrimp and from the water of shrimp ponds obtained from the Songkhla Aquatic Animal Health Research and Development Center were used in this study. First, the virulence level of these VpAHPND isolates in shrimp and the swarming activity on agar were investigated. To investigate the genetic relationship, whole genomes of 31 bacterial isolates were sequenced with the DNBSeq platform, and Roary and Scoary programs were used to analyze the genomic comparison and association to swarming activity, respectively. The result showed a wide range of virulence (lethal time 50; LT50 from 24-116 hours) and swarm length (2.5-45 mm) among these VpAHPND. Although LT50 and swarming activity were not significantly correlated, a negative trend with a correlation coefficient of –0.14 was observed suggesting that a lower LT50 leads to faster swarming activity. After comparative analysis with Roary, the absence and presence of genes were identified among the bacterial isolates. The result of association of genes with swarming behavior result showed that a total of 27 genes were significantly associated with swarming activity in these examined VpAHPND, including tyrosine–type recombinase, contractile injection system protein, and ProQ/FINO family. These genes will be further validated for association in additional VpAHPND isolates. This study provides comprehensive genetic information related to swarming activity that can be used as biomarkers and drug targets.

EVALUATION OF ANTIFUNGAL ACTIVITIES OF *Streptomyces* sp. AGAINST *Agroathelia rolfsii*

Rungnapa Pichaikarn,[1] Khemmikar Khompatara,[2] Warapond wanna[1,*]
[1]Program in Molecular Biotechnology and Bioinformatics, Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla 90110, Thailand
[2]Office of Agricultural Research and Development Region 8, Department of Agriculture, Ministry of Agriculture and Cooperatives, Hat-Yai, Songkhla 90110, Thailand
*e-mail: w.warapond@gmail.com

Abstract:
Streptomyces is recognized as a biocontrol agent due to its antifungal activity against various fungal phytopathogens. *Agroathelia rolfsii* (syn. *Sclerotium rolfsii*) is the pathogen responsible for southern blight, significantly impacting crop production. However, information on the interaction between *Streptomyces* and *A. rolfsii* remains limited. This study aimed to investigate the antifungal potential of *a Streptomyces* sp. isolated from agricultural soil in southern Thailand. The strain was identified by 16S rRNA gene sequencing, and BLAST analysis confirmed its classification within the genus *Streptomyces* with 100% identity. Antifungal activity was evaluated using dual culture and culture filtrate (toxic medium) assays, both of which demonstrated the suppression of *A. rolfsii* growth. Metabolites in the culture filtrate were analyzed using Gas Chromatography–Mass Spectrometry (GC–MS) and identified through comparison the Wiley 275 library. After one week of incubation, compounds such as hexadecanoic acid, octadecanoic acid, and 9-octadecenamide were detected, while longer incubation (four weeks) revealed 2,5-piperazinedione, 3,6-bis(2-methylpropyl)-, and pyrrolo [1,2-a] pyrazine-1,4-dione, hexahydro-3-(2-methylpropyl)-. These compounds are documented as having antimicrobial activities by mechanisms including membrane disruption, modification of cell permeability, and interference with vital cellular processes. Taken together, our findings indicate that this *Streptomyces* strain and its bioactive metabolites possess significant promise as biocontrol agents for the management of southern blight, consequently supporting the development of sustainable agricultural disease management systems.

CHARACTERIZATION OF MULTI-STRESS TOLERANT PGPR FROM ORCHARD SOILS IN CHANTHABURI PROVINCE, THAILAND

Jirapat Chanthamalee[1],* Winyou Puckdee[1], Chewa Thassana[2]
[1]Department of Biology, Faculty of Science and Technology, Rambhai Barni Rajabhat University, Muang, Chanthaburi, 22000, Thailand
[2]Department of Physics and General Science, Faculty of Science and Technology, Rambhai Barni Rajabhat University, Muang, Chanthaburi, 22000, Thailand
*e-mail: jirapat.c@rbru.ac.th

Abstract:
Abiotic stresses are considered major factors in the reduction of plant yield and quality worldwide. Plant growth-promoting rhizobacteria (PGPR) have emerged as a sustainable alternative due to enhancing plant stress resilience. However, only a few studies have evaluated abiotic stress of PGPR strains from orchard soils which represent unique reservoirs of stress-adapted microbes. This study aimed to characterize nineteen PGPR isolates from orchard soils in Chanthaburi for their tolerance to various abiotic stresses and to identify elite candidates for bioinoculant development. They were screened for tolerance to salinity (7% NaCl), alkalinity (pH 12), acidity (pH 4), high temperature (45–50 °C), and drought stress simulated with PEG 6000. Collectively, sixteen isolates were found to withstand drought conditions, while eight PGPR isolates exhibited tolerance to alkaline pH levels, suggesting a high degree of adaptability. Among them, the MuD01-2 isolate exhibited multi-stress tolerance by showing robust growth at high NaCl concentrations, drought, and temperatures up to 50 °C. While NaD01-2 and ThD02-2 isolates demonstrated significant tolerance to acidic and alkaline environments, respectively. This research successfully identified PGPR with distinct and complementary stress-tolerant profiles. MuD01-2 stands out as a prime candidate for developing bioinoculants to promote sustainability and resilience in orchard management under changing climatic conditions.

EFFECT OF SKIM MILK SUPPLEMENTATION ON THE PRODUCTION OF AIR-DRIED LACTIC ACID BACTERIAL STARTER CULTURE IMMOBILIZED ON CORN HUSK AND ITS ANTAGONISTIC ACTIVITY AGAINST *Aspergillus flavus*

Possawee Boonyong,[1] Cheewanun Dachoupakan Sirisomboon,[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand
*e-mail: cheewanun.d@chula.ac.th

Abstract:
The present study aimed to investigate the effects of skim milk supplementation on immobilized lactic acid bacterial starter cultures on corn husk, to evaluate their antagonistic activity against fungal growth, and to establish optimal rehydration conditions. The immobilized *Lactobacillus paracasei* AN3 on ground corn husk, with and without skim milk addition, was subjected to air drying at 45°C for 6 h. The effect of adding skim milk at different concentrations (0, 0.5, 1, and 2% w/v) to the cultured medium before air drying on the production of air-dried *L. paracasei* AN3 starter culture was evaluated. Skim milk supplementation increased the surface tension of the cultured media, and the SEM image showed the formation of a rough surface on the corn husk due to matrix deposition. The addition of 2% skim milk resulted in the highest survival rate of air-dried *L. paracasei* AN3 (66.02%) on ground corn husk after air drying. Skim milk supplementation did not affect the antagonistic activity of *L. paracasei* AN3 against *Aspergillus flavus* M3T8R4G3. Rehydration conditions for air-dried *L. paracasei* AN3 with 2% skim milk were investigated. Tap water without sucrose supplementation at ambient temperature and 30°C yielded the highest bacterial viability (8.53 and 8.57 log CFU/mL, respectively) and recovery rates (100.93% and 94.09%, respectively). The findings indicate that air drying represents a promising alternative for producing lactic acid bacterial starter cultures. Future studies should focus on evaluating the long-term stability of the starter culture during storage and its application.

BIOELECTRICITY FROM PALM OIL MILL EFFLUENT: THE ROLE OF THE PENTOSE PHOSPHATE PATHWAY IN *Choricystis parasitica* SW-03

Alisa Kongthong, Thanopon Yooyen, Pimprapa Chaijak*
Department of Biological Science, Faculty of Science and Digital Innovation, Thaksin University, Phatthalung 93210, Thailand
*e-mail: pimprapa.c@tsu.ac.th, chaijak.pimprapa@gmail.com

Abstract:
Palm oil mill effluent (POME) is a major environmental concern in Thailand due to its large volume and high organic load, which pose serious risks to ecosystems and human health if discharged untreated. This study investigates the potential of the heterotrophic microalga *Choricystis parasitica* SW-03 for simultaneous POME bioremediation and bioelectricity generation using microbial fuel cell (MFC) technology. The system achieved a maximum open-circuit voltage (OCV) of 0.863 ± 0.032 V, with corresponding volumetric current and power densities of 137.17 ± 3.69 mA/m^3 and 18.82 ± 1.00 mW/m^3, respectively. Although the maximal biomass concentration (0.03 ± 0.00 g/L) and yield (0.002 ± 0.000 g/L/day) were relatively low, the cells exhibited chlorophyll a (0.38 ± 0.01 µg/mL) and chlorophyll b (0.28 ± 0.01 µg/mL), indicating active photosynthetic and heterotrophic metabolism. These findings suggest that the pentose phosphate pathway in *C. parasitica* SW-03 plays a key role in channeling POME-derived organic matter toward both energy metabolism and electron transfer. This work highlights the dual role of heterotrophic microalgae in bioelectricity generation and wastewater valorization, offering a sustainable strategy for POME management.

ISOLATION AND CHARACTERIZATION OF FUNGI FROM ORGANIC RICE CULTIVATION SOIL FOR ENHANCING RICE SEED GERMINATION

Anuruk Seeka,[1] Gregorius Nico Adi Setiawan,[2] Manato Nishikawa,[3] Nuttapon Pombubpa[1,*]
[1]Department of Microbiology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
[2]Plant Pathology/Phytopathology, Wageningen University & Research, Wageningen, Gelderland, Netherlands
[3]Department of Biotechnology, Graduate School of Engineering, The University of Osaka, Osaka, Japan
*Corresponding author: E-mail: Nuttapon.Po@chula.ac.th

Abstract:
Rice (*Oryza sativa* L.) seed germination is a critical determinant of yield stability under variable environmental conditions. Seed biopriming with beneficial fungi offers a sustainable approach to enhance seed vigor and early seedling establishment. This study isolated and screened fungal strains from rice rhizosphere soils under three fertilizers: pure fermented chitin waste (FCW), FCW combined with organic fertilizer (OFC), and FCW combined with chemical fertilizer (CFC), to evaluate their potential for promoting germination and gibberellic acid production, as GA_3 leads to breaking seed dormancy and stimulating germination. A total fungal isolate of 37 sporogenous isolates were recovered using soil dilution plating on PDA medium. Seven isolates (FCW201, FCW205, OFC202, OFC305, OFC405, OFC408, and CFC212) have significantly higher germination percentage (90–95%) compared with the control (88.33%) by using one-way ANOVA and Tukey's post hoc test ($p = 0.025$, 0.011, 0.011, 0.001, 0.018, 0.018, and 0.0005, respectively, ($p < 0.05$)). Among these, CFC212 showed the highest germination rate (95%) while six isolates (CFC401, OFC405, OFC305, OFC202, OFC408, and CFC212) produced potentially 3.7–23.7 times higher gibberellic acid compounds absorbance values at 254 nm than the reference strains *Fusarium oxysporum* and the control. These results demonstrate that organic-chitin amendments enrich the functional potential of beneficial fungal communities for seed biopriming to improve germination in sustainable rice production.

IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF SMALL HEAT SHOCK PROTEINS IN SHRIMP IMMUNE RESPONSES TO *Ecytonucleospora hepatopenaei* (EHP) INFECTION

Pithiwat Maiket,[1] Nutthapon Sangklai,[1] Anchalee Tassanakajon[1,*]
[1]Center of Excellence for Molecular Biology and Genomics of Shrimp, Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
*e-mail: Anchalee.K@chula.ac.th

Abstract:

Small heat shock proteins (sHSPs) are ATP-independent chaperones synthesized by cells in response to various stresses, including pathogen infection, to maintain cellular and protein homeostasis. sHSPs range in size from 10 to 40 kDa, yet their biological functions in shrimp immunity remain poorly understood. In this study, we identified *sHSP* genes in the *Litopenaeus vannamei* genome, including *LvHSP10*, *LvHSP21*, and *LvHSP22*. These *sHSPs* were expressed in all examined tissues and were strongly induced by microsporidian *Ecytonucleospora hepatopenaei* (EHP) infection. Notably, *LvHSP10* expression increased more than 20-fold upon EHP challenge. Silencing *LvHSP10* led to a dramatic rise in EHP load, approximately 100-fold higher than the *dsGFP* control at 9- and 11 days post-cohabitation, and was accompanied by up-regulation of antimicrobial peptides (*LvALF1*, *LvPEN3*, *LvLyz-c*). Conversely, suppression of *LvHSP10* down-regulated several immune-related genes, including *Toll*, *JAK/STAT*, and components of the prophenoloxidase cascade. Collectively, these findings indicate that *LvHSP10* may play a crucial role in the shrimp immune response to EHP by modulating the expression of both antimicrobial peptides and components of immune signaling pathways.

PROBIOTIC POTENTIAL OF GUT-DERIVED LACTIC ACID BACTERIA FROM *Heterotrigona itama*: TOWARDS FUNCTIONAL STARTER CULTURES FOR POLLEN FERMENTATION

Wankuson Chanasit[1,*], Naratip Kongsamret[1], Petcharat Ponpichai[1], and Jakkrawut Maitip[2]
[1] Faculty of Science and Digital Innovation, Thaksin University, Phatthalung 93210, Thailand
[2] Faculty of Science, Energy and Environment, King Mongkut's University of Technology North Bangkok, Rayong 21120, Thailand
*e-mail: wankuson.c@tsu.ac.th

Abstract:
Heterotrigona itama, a stingless bee species valued for its high honey productivity, is widely distributed across southern Thailand, where favorable geographic and climatic conditions support colony development. However, seasonal food shortages threaten colony health and productivity. This study aimed to isolate and characterize lactic acid bacteria (LAB) from the gut of *H. itama*, evaluate their probiotic properties, and apply selected strains as starter cultures for stingless bee pollen fermentation. Three potential probiotic LAB isolates such as BP-2, BP-3, and BPW-B1 were identified through 16S rRNA sequencing, API 50 CHL, and API ZYM analyses. Results indicated that BP-2 and BP-3 were most closely related to *Lactobacillus delbrueckii* ssp. *delbrueckii*, whereas BPW-B1 showed the closest match to *Lactobacillus acidophilus*. Enzymatic profiling revealed consistent production of leucine arylamidase, acid phosphatase, and naphthol-AS-BI-phosphohydrolase. Safety assessments confirmed that all three isolates were γ-hemolytic and broadly susceptible to antibiotics. Specifically, BP-2 and BP-3 exhibited intermediate resistance to gentamicin and streptomycin, with BP-2 also showing intermediate resistance to vancomycin, whereas BPW-B1 was fully susceptible to all antibiotics tested. Compatibility assays demonstrated their ability to co-exist without antagonistic effects, supporting their suitability for mixed-strain formulations. The antibiotic resistance profiles of these LAB strains were unchanged in mixed-strain combinations, confirming that coexistence did not alter resistance and supporting their biosafety as starter cultures. During pollen fermentation, treatments supplemented with mixed LAB strains reduced pH to approximately 4.0, achieved the highest titratable acidity (49.42%), primarily due to acetic and lactic acid production, and significantly enhanced protein digestibility (74.33%) compared with the control (58.67%), contained only the yeasts *Starmerella* sp. TSU and *Zygosaccharomyces* sp. TSU, which are recognized as nutritional symbionts that promote brood development and colony health. These findings highlight the potential of LAB starter cultures to enhance the nutritional and functional quality of stingless bee pollen, providing a promising strategy to support *H. itama* colony health and resilience under changing environmental conditions.

Keywords: *Heterotrigona itama*; stingless bee; lactic acid bacteria; starter culture; bee bread

IDENTIFICATION OF SIGNALING PATHWAYS CONTROLLING ANTIMICROBIAL PEPTIDE GENE EXPRESSION IN BLACK TIGER SHRIMP *Penaeus monodon*

Chayanit Khunrit [1,2,3], Thapanan Jatuyosporn [2,3], AnchaleeTassanakajon [3] and Kuakarun Krusong [2,*]

[1] Program in Biotechnology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

[2] Center of Excellence in Structural and Computational Biology, Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

[3] Center of Excellence for Molecular Biology and Genomics of Shrimp, Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

*e-mail: Kuakarun.k@chula.ac.th

Abstract:

Black tiger shrimp (*Penaeus monodon*) farming in Thailand has faced increasing impacts from infectious diseases over the past few decades, causing significant economic losses. Improving disease resistance requires a deeper understanding of the shrimp's innate immune system. A key part of this defense involves antimicrobial peptides (AMPs), such as penaeidins and anti-lipopolysaccharide factors (ALFs), which help protect against bacteria, fungi, and viruses. However, the regulatory mechanisms that link immune signaling pathways to AMP expression remain unclear. This study focuses on two AMP genes, ALF*Pm*3 and Pen*Pm*5, the latter of which includes two isoforms (Pen*Pm*5.1 and Pen*Pm*5.2). Using a luciferase reporter assay, we examined whether these genes are transcriptionally regulated through the Toll signaling pathway via the transcription factor *Pm*Dorsal. The results showed a significant increase in luciferase activity when *Pm*Dorsal was co-expressed, suggesting that *Pm*Dorsal binds to the promoter regions of both genes. These findings indicate that Pen*Pm*5 and ALF*Pm*3 are transcriptionally regulated via the Toll pathway, providing new insights into the immune response mechanisms of *P. monodon*. This knowledge may contribute to the development of strategies to enhance shrimp immunity and reduce disease-related losses in aquaculture.

THE EFFICACY OF IN STRAW DILUTION METHOD ON SURVIVAL RATES OF VITRIFIED BOVINE EMBRYOS.

Chanyada Angchuan[1], Traimat Boonthai[2], Rangsun Parnpai[1]*

[1]Embryo Technology and Stem Cell Research Center, School of Biotechnology Institute of Agricultural Technology, Suranaree University of Technology, Nakorn Ratchasima 30000, Thailand

[2]Department of Aquatic Science, Faculty of Science, Burapha University, Chon Buri 20130, Thailand

*Corresponding author: rangsun@g.sut.ac.th

Abstract:

Cryopreservation of bovine embryos is a key technology for facilitating genetic improvement and reproductive efficiency in cattle. Vitrification has largely replaced conventional slow freezing because of its higher survival and developmental rates; however, its practical use in the field is limited by the need for laboratory-based warming procedures. To address this challenge, in-straw warming methods have been developed to simplify embryo handling and reduce reliance on laboratory infrastructure. This study aimed to evaluate the efficiency of an in-straw warming protocol using different sucrose concentrations for vitrified in vitro–produced (IVP) bovine blastocysts under field conditions. A total of 500 blastocysts were randomly allocated into five groups (n = 100 each): fresh control, conventional warming, and vitrification followed by in-straw dilution with 0.2 M, 0.3 M, or 0.4 M sucrose. Embryo survival and development were assessed based on re-expansion at 2 h and 24 h, and full expansion and hatching at 48 h post-warming. The fresh control group exhibited the highest survival and developmental rates, with 100.00% re-expansion at 2 h, 93.33% at 24 h, 82.61% full expansion, and 72.87% hatching. Among vitrified groups, in-straw warming with 0.2 M sucrose achieved the most favorable outcomes, with 89.88% re-expansion at 2 h, 78.99% at 24 h, 65.96% full expansion, and 44.91% hatching at 48 h. These results were significantly higher than those of conventional warming (79.29%, 55.09%, 46.75%, and 32.70%, respectively) and closer to the fresh control group. In contrast, embryos treated with 0.3 M or 0.4 M sucrose displayed reduced survival, particularly the 0.4 M group, which showed only 3.42% hatching at 48 h. In conclusion, in-straw warming with 0.2 M sucrose provides an effective, practical, and field-adaptable alternative to conventional warming methods. This protocol minimizes the need for specialized laboratory equipment while maintaining embryo viability and developmental potential. The adoption of this approach may enhance the efficiency and accessibility of bovine embryo transfer programs, particularly in settings with limited infrastructure.

Session VI.
Food Biotechnology & Food Security

IMPACT OF CONTROLLED POSTHARVEST CONDITIONS ON ENHANCEMENT OF AROMA-ACTIVE PROFILES AND SENSORY PREFERENCE IN THAI COCOA NIBS

Pakavit Mathatheeranan,[1,3] Tansiphorn Na-Nan,[2] Ting-Jang Lu,[3,*] Inthawoot Suppavorasatit[1,*]
[1] Department of Food Technology, Faculty of Science, Chulalongkorn University, Phayatai Road, Wangmai, Pathumwan, Bangkok 10330, Thailand
[2] School of Agricultural Resources, Chulalongkorn University, Phayatai Road, Wangmai, Pathumwan, Bangkok, 10330, Thailand
[3] Institute of Food Science and Technology, National Taiwan University, No. 1, Sec. 4, Roosevelt Road, Taipei 10617, Taiwan
*e-mail: tjlu@ntu.edu.tw, inthawoot.S@chula.ac.th

Abstract:
Aroma volatile compounds in roasted cocoa products significantly influence consumer preference. However, limited information is available on the volatile profiles of cocoa products produced in Thailand. Cocoa products exhibit diverse aroma profiles that define their unique characteristics, primarily influenced by the fermentation and roasting processes. In this study, cocoa samples were collected from local farmers across various regions of Thailand. These farmers received technology transfer training from the Innovation Center for Research and Development of Sustainable Thai Cocoa (ISTC), Chulalongkorn University. Despite this, local cocoa products are fermented by the activity of indigenous microflora under uncontrolled temperatures, followed by natural sun-drying for 5–7 days. Both fermentation and drying processes are highly dependent on climatic conditions. The aim of this research was to improve the aroma characteristics of cocoa products through controlled postharvest conditions, involving standardized fermentation and drying processes. Cocoa samples prepared under controlled postharvest conditions were compared with those prepared under uncontrolled conditions to study the differences in aroma volatile compound profiles. All samples were roasted at 120°C for 20 min to generate desirable aroma volatile compounds. Volatile aroma compounds in roasted cocoa samples were analyzed using solid-phase microextraction (SPME) coupled with gas chromatography–mass spectrometry (GC–MS), and the odor activity value (OAV) technique was applied to identify aroma-active compounds. Classification of roasted cocoa samples was assessed using heatmaps and principal component analysis (PCA). Results revealed that cocoa prepared under controlled postharvest conditions achieved the highest hedonic sensory preference scores from forty consumer panelists (recruited from Department of Food Technology, Chulalongkorn University). These samples contained a wide range of aroma-active compounds associated with chocolate, malty, cocoa, roasted, nutty, floral, fruity, citrus, smoky, woody, fermented, sour, buttery, and creamy attributes. This research highlights the importance of controlled postharvest practices for local manufacturers and provides a foundation for improving aroma quality, ensuring product consistency, and developing an aroma wheel as a practical tool for characterizing Thai cocoa products.

Keywords: cacao bean, fermentation, thermal treatment, GC-MS

COMPARATIVE EFFECTS OF PETROLEUM-BASED AND BIODEGRADABLE MICROPLASTICS ON THE GROWTH AND STRESS RESPONSES OF *Capsicum annuum* L.

Pariyapath Eiamtrakul, Kulaporn Boonyaves, and Prinpida Sonthiphand*
Department of Biology, Faculty of Science, Mahidol University, Ratchathewi, Bangkok 10400, Thailand
*e-mail: prinpida.son@mahidol.ac.th

Abstract:
The increasing use of plastics has raised global concerns, with microplastic accumulation posing risks to agricultural systems. Biodegradable plastics are considered more sustainable alternative to petroleum-based plastics; however, both types produce microplastic debris (<5 mm). This study investigated the effects of petroleum-based and biodegradable microplastics on chilli peppers (*Capsicum annuum* L.), an economically important crop. Polyethylene (PE) and polyethylene terephthalate (PET) represented petroleum-based microplastics, while polylactic acid (PLA), from commercial cups (bPLA) and raw material (nPLA), represented biodegradable microplastics. *Capsicum annuum* L. was cultivated hydroponically with 1% microplastics (50, 75, and 400 µm), and samples were collected at the seedling stage after 24 days. Growth parameters (shoot height, root length, and total leaf area), biochemical contents (chlorophyll a, chlorophyll b, total chlorophyll, β-carotene, and flavonoids), and stress responses (via 3,3′-diaminobenzidine (DAB) staining) were evaluated. Microplastics did not significantly affect growth, but chlorophyll a and total chlorophyll increased with 400 µm PE and 75 µm bPLA. Chlorophyll b, β-carotene, and flavonoids were unaffected. Stress was induced by 50 µm PE. Microplastics can alter plant physiology and stress responses, posing risk to crop yield and food security. Future studies will quantify microplastics in plants to assess their potential transfer through the food chain.

STRUCTURAL INSIGHTS INTO THE EXO-MODE OF ACTION OF *Bc*Xyn26A, A NOVEL EXO-β-1,3-XYLANASE FROM A HUMAN GUT BACTERIUM

Kotone Yamamoto, Sanae Hori, Fumiyoshi Okazaki*
Graduate School of Bioresources, Mie University, Japan
*e-mail: okazaki@bio.mie-u.ac.jp

Abstract:
β-1,3-xylan is a polysaccharide found exclusively in the cell walls of red and green algae. Our previous study revealed that *Bacteroides cellulosilyticus*, a human gut bacterium, harbors a polysaccharide utilization locus encoding β-1,3-xylan-degrading enzymes. This bacterium produces two key enzymes, *Bc*Xyn26B, an endo-β-1,3-xylanase (EC 3.2.1.32), and *Bc*Xyn26A, a novel exo-β-1,3-xylanase (EC 3.2.1.-), which act synergistically in β-1,3-xylan degradation. To the best of our knowledge, *Bc*Xyn26A is the first enzyme reported to act in an exo-mode specifically releasing β-1,3-xylobiose. Despite their high sequence similarity, these enzymes exhibit different degradation modes. This study aimed to elucidate the structural determinants underlying the exo-mode of action of *Bc*Xyn26A. We employed AlphaFold to predict the three-dimensional structures of both enzymes. A distinct β-turn was identified near the minus subsites of the substrate-binding cleft of *Bc*Xyn26A, forming a closed substrate-binding pocket (Fig. 1). In addition, the E120 residue blocks the −3 subsite. To evaluate their roles, we constructed *Bc*Xyn26B (Ins β-turn + A127E) and *Bc*Xyn26A (Del β-turn + E120A) mutants and expressed them in *Escherichia coli*. The former exhibited exo-acting activity, producing β-1,3-xylobiose, whereas the latter produced β-1,3-xylotriose. These results demonstrate that the β-turn and E120 residue are critical structural determinants of the exo-mode of action of *Bc*Xyn26A in β-1,3-xylan degradation. These structural insights enable us to highlight the functional and biotechnological implications of β-1,3-xylan and its hydrolysis products. β-1,3-xylan may selectively promote the growth of beneficial *Bacteroides* species in the human gut, highlighting its potential as a novel prebiotic. Among its products, β-1,3-xylobiose is the minimal unit of β-1,3-linked xylosyl residues, with high solubility and ease of handling. Furthermore, this work contributes to the development of a microbial production system for β-1,3-xylobiose, thereby offering new opportunities for the sustainable utilization of algal biomass and contributing to innovations in prebiotic development and Future Food strategies.

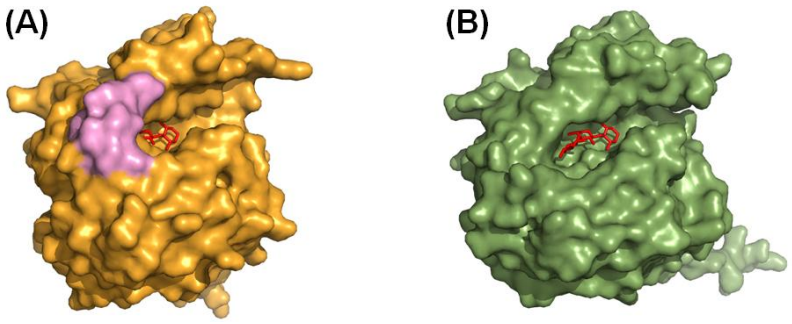


Figure 1.
Predicted three-dimensional structures of *Bc*Xyn26A (A) and *Bc*Xyn26B (B) in surface representation. The *Bc*Xyn26A-specific β-turn is highlighted in pink.

HUMAN GUT BACTERIA POSSESS A POLYSACCHARIDE UTILIZATION LOCUS THAT INCLUDES A NOVEL EXO-β-1,3-XYLANASE FOR METABOLIZING β-1,3-XYLAN, A MACROALGAL POLYSACCHARIDE

Sanae Hori, Kotone Yamamoto, Fumiyoshi Okazaki*
Graduate School of Bioresources, Mie University, Japan
*e-mail: okazaki@bio.mie-u.ac.jp

Abstract:
β-1,3-Xylanase (1,3-β-D-xylan xylanohydrolase; EC 3.2.1.32) is an endo-type enzyme that randomly hydrolyzes β-1,3-xylan, a characteristic polysaccharide found exclusively in the cell walls of red and green algae. To date, enzymes that degrade macroalgal polysaccharides have been reported primarily from marine bacteria, and β-1,3-xylanases are also almost exclusively of marine bacterial origin. However, recent studies have revealed that human gut bacteria are capable of metabolizing macroalgal polysaccharides, highlighting a link between seaweed intake and human health. In our previous study, we identified the β-1,3-xylanase gene *xyn26B* in the human gut bacterium *Bacteroides cellulosilyticus*. In this study, we aimed to elucidate the enzymatic mechanisms underlying β-1,3-xylan utilization in *B. cellulosilyticus*. Genome sequence analysis of *B. cellulosilyticus* identified two β-1,3-xylanase genes, *xyn26A* and *xyn26B*, located together within a putative β-1,3-xylan-specific polysaccharide utilization locus (PUL). This locus also includes a *susC–susD* gene pair, a putative β-1,3-xylosidase gene, and a sugar transporter gene. The genes encoding *Bc*Xyn26A and *Bc*Xyn26B were codon-optimized, synthesized, and expressed in *Escherichia coli*, yielding the recombinant enzymes. Both enzymes exhibited substrate specificity for β-1,3-xylan. *Bc*Xyn26B exhibited the activity of an endo-type enzyme, producing β-1,3-oligosaccharides with varying degrees of polymerization and showing higher activity than previously reported enzymes. In contrast, *Bc*Xyn26A exhibited the activity of an exo-type enzyme, releasing only β-1,3-xylobiose. This distinct activity suggests that *Bc*Xyn26A represents a novel exo-β-1,3-xylanase, which should be classified as a β-1,3-xylobiosidase (1,3-β-D-xylan xylobiohydrolase; EC 3.2.1.-). This study provides new insights into the enzymatic degradation and utilization of β-1,3-xylan in human gut bacteria.

ISOLATION AND CHARACTERIZATION OF *Chlorella* sp. AARLG049N MUTANTS WITH HIGH PROTEIN AND LOW CHLOROPHYLL CONTENT

Kitkarn Veeraphisitt,[1] and Niyom Kamlangdee[2*]
[1]Department of Microbiology, Faculty of Science, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
*e-mail: niyom.kam@kmutt.ac.th

Abstract:
In the current food and pharmaceutical industries, there is interest in microalgae due to the rising demand from health-conscious consumers for supplements. These consumers want products with increased protein and antioxidant properties. Microalgae possess these desired qualities and low-cost resources. Microalgae biomass can be utilized as a coloring in food. However, Limitation is consumer non-acceptance, primarily to green color. The objective of this research was to develop *Chlorella* sp. strain with higher protein and low chlorophyll content. The random mutagenesis with Ethyl methane sulfonate (EMS) was used to induce mutations. EMS affects the targeted cells specifically converting (GC) pairs to (AT). Treated with 300 mM EMS, colonies were analyzed after 168 hours on BG-11 agar under 4400 lumen (LM) of fluorescent light. Colonies with a light green color were identified as Mutant 01. The protein content in wildtype and mutant 01 isolates was 38.83±0.86% and 41.44±1.20% DW. The chlorophyll in the Mutant01 strain was reduced by 4.33 µg/ml compared to the original strain. These results indicated that the successful genetic modification of *Chlorella* sp. has the potential to increase protein content and reduce chlorophyll, which will be useful as an ingredient in the future development of new healthy food.

Keywords: Ethyl methane sulfonate, *Chlorella* sp, Phenotype, Mutant, chlorophyll

ISOLATION, MORPHOLOGICAL IDENTIFICATION AND GROWTH OF THRAUSTOCHYTRID ISOLATED FROM MANGROVE HABITATS IN THE GULF OF THAILAND

Sasiwimol Duangvichai,[1] Niyom Kamlangdee,[2,*] Kaliyamoorthy Kalidasan[3]
[1,2]Department of Microbiology, Faculty of Science, King Mongkut's University of Technology Thonburi, Bangkok, Thailand
[3]Department of Marine Science, Faculty of Science, Chulalongkorn University, Bangkok, Thailand
*e-mail: niyom.kam@kmutt.ac.th

Abstract:
Thraustochytrids are microorganisms used for industrial purposes, particularly in pharmaceuticals and supplements, due to their ability to produce high levels of fatty acids. It can also be cultivated and purified more easily than extracted from marine fish or other microorganisms. This study aimed to isolate thraustochytrids from fallen leaves in mangrove habitats in the Gulf of Thailand to study their growth and biomass accumulation. Six strains of thraustochytrid were isolated from Wat Khun Samut Chin Temple, Samut Prakan Province, Thailand. Morphological observation showed that the characteristics of the isolated strains were exactly like those in previous research. After 120 hours of cultivation, the dry weight of the six isolates ranged from 0.81 to 1.36 g/L, with WK3 producing the highest biomass yield and reaching an OD of 3.863. Based on these results, WK1 and WK3, which had the highest growth rate, were selected to culture with different glucose concentrations (0.3-8% w/v) to observe their ability to grow. The WK3 isolate achieved the highest growth at 4% glucose, reaching an OD of 8.0. This study suggests that thraustochytrid strains, particularly WK3, have the potential to develop increased biomass production or essential fatty acids in the future.

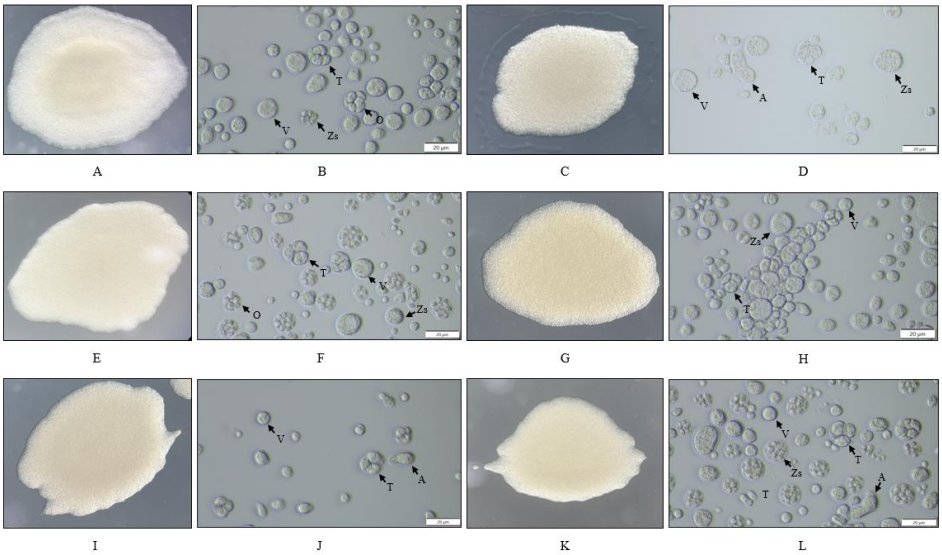


Figure 1.
Thraustochytrid colonies and cells, WK1 (A-B), WK2 (C-D), WK3 (E-F), WK4 (G-H), WK5 (I-J) and WK6 (K-L). (scale bar = 20 μm), (A) Amoeboid cell (O) Octad (T) Tetrad (V) Vegetative cell (Zs) Zoosporangium that contains zoospores.

ULTRASOUND-ASSISTED EXTRACTION, EVALUATION OF INTERFACIAL PROPERTIES AND *IN VITRO* DIGESTIBILITY OF TAMARIND SEED PROTEIN

Pitchayapak Wipakul,[1] Kamolwan Isarakarn,[2] Teerarat Likitwattanasade[1,*]
[1]Department of Biotechnology, Faculty of Science, Mahidol University, Bangkok, Thailand
[2]Advanced Polymer Technology Research Group, National Metal and Materials Technology Center (MTEC), Pathum Thani, Thailand
*e-mail: teerarat.lik@mahidol.edu

Abstract:
Thailand produces approximately 150,000 tons of tamarind annually, with seeds comprising about 34% of pod weight and contributing to considerable agricultural waste. Tamarind seed kernels contain approximately 18.1% protein, indicating their potential as an alternative plant-based protein source. This study optimized extraction conditions for tamarind seed protein and examined the effects of ultrasound treatment on interfacial properties and *in vitro* digestibility. Tamarind kernel powder was pretreated with carbohydrase (5–50%, w/w) at 50°C for 1–2 hours to remove polysaccharides, followed by protein extraction using distilled water or sodium chloride solution at pH 10 or 12 for 15–60 minutes. The optimal polysaccharide removal was achieved with 5% enzyme treatment for 1 hour, while the highest protein recovery (73.73 ± 1.74%) was obtained using distilled water at pH 12 for 15 min. This condition was further applied to ultrasound-assisted extraction (0–200 W). Ultrasound significantly increased foaming capacity in a power-dependent manner but reduced emulsifying properties. *In vitro* digestibility and PDCAAS scores improved with ultrasound treatment, whereas protein molecular weight profiles remained unaffected. These findings demonstrate that ultrasound enhances the functional and nutritional properties of tamarind seed protein, supporting its potential as a sustainable plant-based protein ingredient.

ASSESSMENT OF ANTIMICROBIAL CONSTITUENTS IN FEST™ FOOD SERVICE PAPER PACKAGING USING SPORES OF *Bacillus subtilis* ATCC 6633 AND *Aspergillus niger* ATCC 6275

Charanyarut Sukphattanaudomchoke,[1] Kanittika Samneingjam, [1] Maysinee Kanathananun, [1] Wannaluck Khamwan, [1] Preeyaporn Thongchawee, [1] and Somchoke Limwongsaree [1]*
[1] Innovation and Product Development Center (IPDC), SCG Packaging PLC, Ratchaburi 70110, Thailand
*e-mail: somchokl@scg.com

Abstract:
The safety of food-contact paper products is a critical aspect of food packaging, particularly regarding the potential migration of chemical substances. With the increasing use of paper plates as a sustainable alternative to plastic, ensuring their chemical safety has become essential for consumer protection. This study aims to evaluate the antimicrobial constituent transfer from Food service paper packaging in accordance with ISO EN 1104:2018, which specifies methods for detecting such migration from paper packaging. For each sample, nine pieces were tested for antimicrobial activity against *B. subtilis* ATCC 6633 and *A. niger* ATCC 6275 spores. According to the standard, the presence of 2 mm clear zones in two or more out of nine pieces indicates migration of antimicrobial substances. In this study, none of the nine pieces from the Food service paper packaging samples exhibited clear zones which confirming the absence of antimicrobial constituent transfer. These results demonstrate full compliance with EN 1104 and support the safe use of Fest™ paper plates in food-contact applications whereby ensuring they do not pose a risk of chemical contamination and are suitable for widespread consumer use.

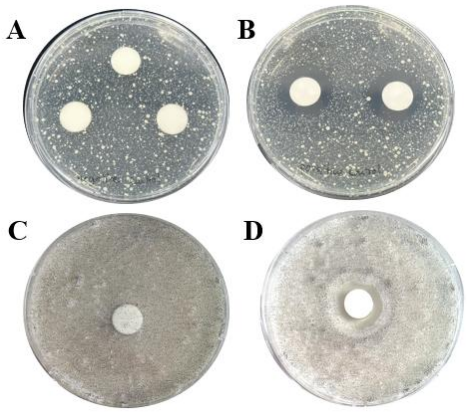


Figure 1.
(A) Negative control of *B. subtilis* ATCC6633, (B) Positive control comprising of 0.03 Unit Penicillin G against *B. subtilis* ATCC6633, (C) Negative control of *A. niger* ATCC 6275 and (D) 20 µg of Amphotericin B for positive control of *A. niger* ATCC 6275

STABILIZATION OF FRESH COFFEE PULP AND EFFECT ON BIOACTIVE COMPOUNDS

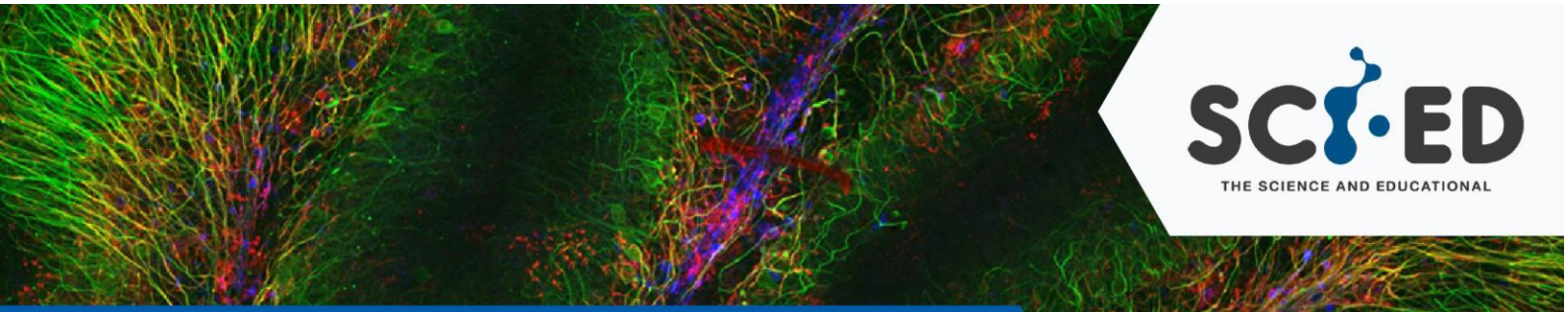
Thean Y Horng[1,2], Solida long[2], Suttiporn Pinijsuwan[1], Sirirung Wongsakul[1,3]*
[1]Food Science and Technology Program, School of Agro-Industry, Mae Fah Luang University, Chiang Rai 57100, Thailand
[2]Bio-Engineering Program, Faculty of Engineering, Royal University of Phnom Penh University, Phnom Penh, Cambodia
[3]Coffee Quality Research Group, Mae Fah Luang University, Chiang Rai 57100, Thailand
*e-mail: sirirung@mfu.ac.th

Abstract:
Coffee pulp, a by-product of the coffee green bean processing, is the outer layer of the coffee berry and is rich in polyphenols and antioxidants. Nevertheless, it is extremely perishable owing to its high sugar and moisture levels, which cause microbial deterioration shortly after pulping, thus resulting in the degradation of bioactive and functional components. To stabilize the fresh pulp for subsequent use, it is necessary to minimize the initial microbial load and inhibit microbial growth during collection and transport from the coffee producing facilities to the processing area. Therefore, this study focuses on the effects of Alkaline Electrolyzed Water (BEW) and Acidic Electrolyzed Water (AEW) in comparison to the common antimicrobial agents the food industry, i.e. Sodium Hypochlorite ($NaClO_2$) and Potassium Metabisulfite (KMS), on preserving the fresh Arabica coffee pulp. The microbial kinetic were monitored, using the total plate count method, immediately after treatment (soaking for 5 minutes before draining) and during 48 hours storage at room temperature. The treated pulps were subsequently dried and checked for the remaining bioactive compounds and compared to the untreated and the water-treated pulp (control). The results showed that AEW (50 ppm) was the most effective board-spectrum treatment that can significantly ($p \leq 0.05$) reduce the microbial load and inhibit bacteria (4.75 to 8.28 log CFU/mL), yeast (4.66 to 7.49 log CFU/mL), and mold (2.15 to 6.10 log CFU/mL) in fresh coffee pulp after 24 hours storage. Proximate analysis revealed AEW-treated coffee pulp retained a composition close to the untreated coffee pulp, both fresh and dried form. In wet form, it contained 84.32 ± 0.14% moisture, 1.12 ± 0.10% ash, and 3.31 ± 0.37% crude fiber. After storage for 48 hours, the pulps were dried and analyzed for chemical composition. In dry form, it had 6.11 ± 0.05% moisture, 8.36 ± 0.12% ash, and 16.25 ± 0.28% crude fiber. Interestingly, AEW treatment ensured the highest total polyphenol retention ($p \leq 0.05$) after 48-h storage with negligible degradation from drying process. Total polyphenol contents of the control and AEW-treated samples were 673.61 ± 4.16 and 567.76 ± 2.35 mg GAE/100g dry weight for the wet samples, and 681.62 ± 3.20 and 576.97 ± 1.85 mg GAE/100g dry weight for the dried samples, respectively. Antioxidant capacity of dried AEW-treated sample was 501.11 ± 1.54 µmol TE/100g dry weight, while the control was 524.10 ± 3.09 µmol TE/100g dry weight. The findings demonstrate AEW as a superior treatment for extending shelf life and ensuring the nutritional and functional quality of coffee pulp, thereby facilitating further valorization and utilization in various applications.

INFLUENCE OF ETHANOL DESOLVATION RATIO ON LUTEIN ENCAPSULATION IN WHEY PROTEIN ISOLATE PARTICLES

Peerapong Wongthahan, Araya Chaoruangrit, Panadda Nonthanum*
Faculty of Technology, Khon Kaen University, Khon Kaen, 40002, Thailand
*e-mail: panano@kku.ac.th

Abstract:
This study examined the influence of ethanol as a desolvating agent on the characteristics of lutein-loaded whey protein isolate (WPI) particles prepared via desolvation. Particles were synthesized with different ethanol to WPI dispersion ratios (0.25x, 0.50x, and 0.75x). Morphological and size analyses (SEM, DLS) revealed a direct correlation between increased ethanol ratios and larger particle sizes, ranging from 246.3 nm to 852.4 nm. Encapsulation efficiency (EE) reached its maximum at 88.51% when an ethanol ratio of 0.50x was employed. In-vitro digestion assays demonstrated that formulations prepared with lower ethanol ratios facilitated more substantial lutein release. Notably, the 0.50x ethanol formulation, exhibiting the highest EE, also provided enhanced storage stability, effectively mitigating lutein degradation across various storage temperatures. These results highlight the significance of precisely modulating the ethanol desolvation ratio for optimizing WPI-based encapsulation systems.



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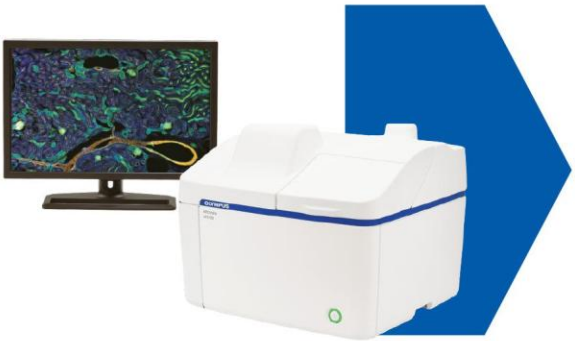

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