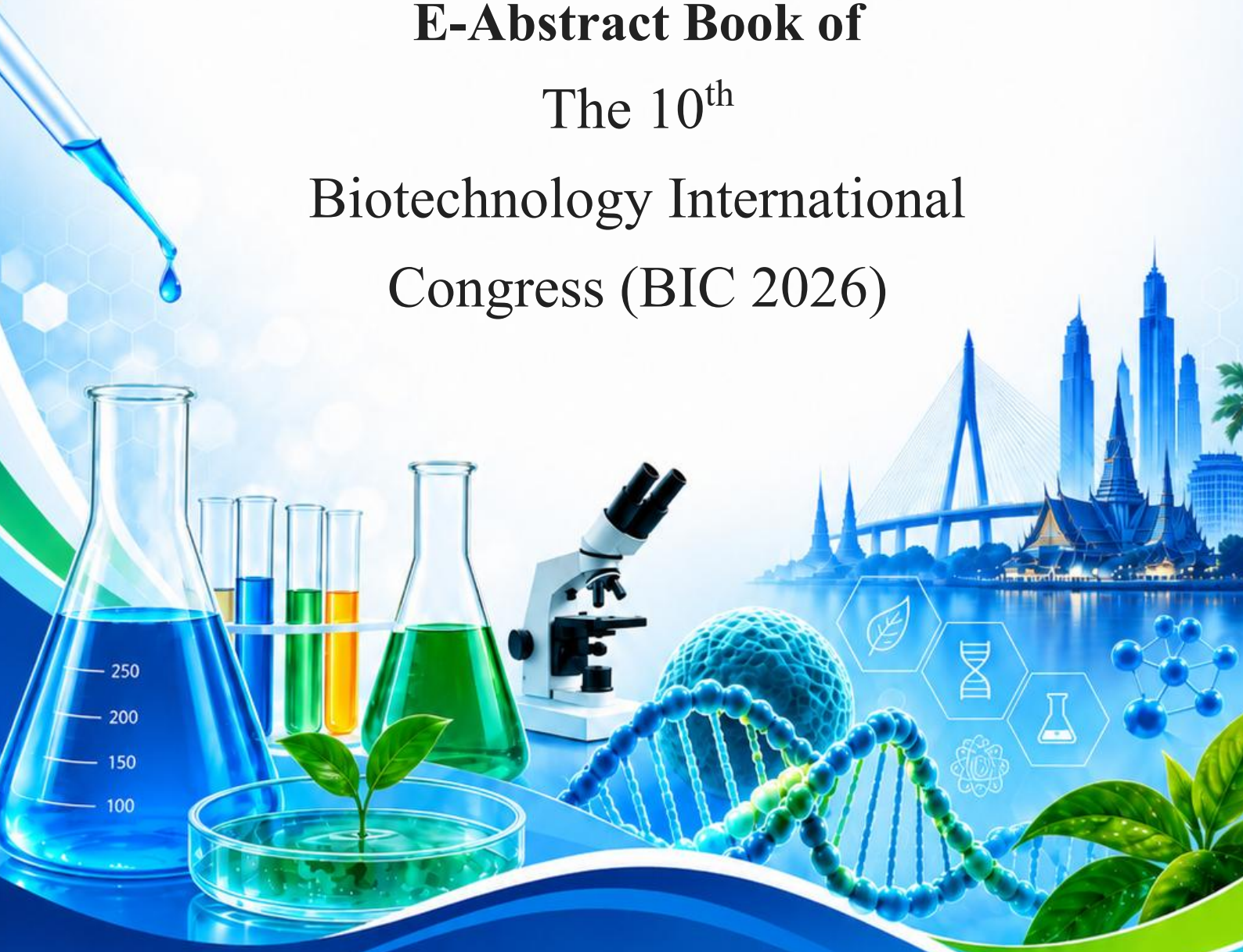
BIC

BIOTECHNOLOGY
INTERNATIONAL CONGRESS
2026

E-Abstract Book of

The 10th Biotechnology International Congress (BIC 2026)



2-3 September 2026

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WELCOME MESSAGE

Dear Esteemed Colleagues and Friends,

On behalf of the Thai Society for Biotechnology (TSB) and the Asian Federation of Biotechnology – Thailand Regional Branch Office (AFOB–Thailand RBO), it is my great pleasure to warmly welcome you to the **10th Biotechnology International Congress (BIC 2026)**, to be held on 2–3 September 2026.

This congress serves as a dynamic platform for knowledge exchange, fostering collaboration, and advancing scientific innovation across the biotechnology community.

The theme of this year's congress, *"Next Generation Biotechnology: from Research to Sustainable Global Impacts,"* underscores the transformative power of next-generation biotechnology in translating cutting-edge research into real-world solutions. It highlights how emerging technologies such as synthetic biology, precision fermentation, genomics, and AI-driven innovations are converging to address pressing global challenges in health, food security, industry, and environmental sustainability.

We are honored to welcome distinguished speakers from Thailand and our valued partner organizations, including Biotechnology and Bioengineering Society of Taiwan (BEST), Korea Society for Biotechnology and Bioengineering (KSBB), Asian Federation of Biotechnology-Malaysian Chapter (AFOB-MC), and Society for Biotechnology Japan (SBJ). Our collaboration with the AFOB Division on Biopharmaceutical and Medical Biotechnology will provide valuable insights into the latest advancements in these rapidly evolving fields.

In addition, we are pleased to encourage the participation of high school students in research project exchanges, fostering early engagement in science and strengthening STEM education at the foundational level.

Let us come together to connect, learn, and be inspired at BIC 2026. I would also like to express our sincere appreciation to VNU Asia Pacific for their invaluable support in co-organizing this event alongside Thailand LAB INTERNATIONAL.

Wishing you a successful congress, fruitful discussions, and a rewarding experience at the **10th Biotechnology International Congress (BIC 2026)** and Thailand LAB INTERNATIONAL, taking place on 2–3 September 2026.

With warm regards,

(Associate Prof. Chuenchit Boonchird)

President Thai Society for Biotechnology
Vice President AFOB-Thailand

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Associate Professor Thanyaporn Wongnate	Vidyasirimedhi Institute of Science and Technology

CONFERENCE SCHEDULE

The 10th Biotechnology International Congress (BIC 2026)

DAY 1 : Wednesday, 2 September 2026

ROOM: MR212 - MR213					
Start Time	End Time	Code	Speaker	Topic	Chair/Co-Chair
8.00 AM	9.30 AM	Registration			
9.30 AM	10.00 AM	Opening Ceremony	Welcome Speech: - Mr. Anucha Parnpichat (Assistant Director Competence Center LAB & Health VNU Asia Pacific) - Prof. Takeshi Omasa (President of The Asian Federation for Biotechnology, AFOB) Opening Speech: Assoc. Prof. Chuenchit Boonchird (Acting President of The Thai Society for Biotechnology)		MC: Assoc. Prof. Rujikan Nasanit
10.00 AM	10.30 AM	Plenary I	Prof. Takeshi Omasa (Osaka University)	Mammalian Cells: A Workhorse Platform for Biologics Production	Chair: Prof. Chi-Wei Lan Co-Chair: Assoc. Prof. Rujikan Nasanit
10.30 AM	11.00 AM	Plenary II	Prof. Jian-Jiang Zhong (Shanghai Jiao University)	Biomanufacturing Technology: Its Evolution and Contribution to the Society	
11.00 AM	11.20 AM	Break			
11.20 AM	11.50 AM	Plenary III	Prof. Vip Viprakasit (Mahidol University)	The Cure is in the Code: The Rise of Gene Therapy	
11.50 AM	1.00 PM	Lunch and Visit Exhibition Hall EH102 – EH104			

CONFERENCE SCHEDULE

DAY 1 : Wednesday, 2 September 2026

ROOM: MR212					
Start Time	End Time	Code	Speaker	Topic	Chair/Co-Chair
Session I					
1.00 PM	1.20 PM	Keynote I	Prof. Penjit Srinophakun (Kasetsart university)	Life Cycle Assessment of Lignin-Derived Biomaterial for Better Environmental Friendliness	Chair: Prof. Mohd Fauzi Mh Busra Co-Chair: Dr. Phattanon Prasithichoke
1.20 PM	1.35 PM	Invited I	Prof. Ir Juferi Idris (UiTM Sarawak Branch)	Optimization of Biochar Derived from Gaharu Waste (*Aquilaria malaccencis*) for the Adsorption of Methylene Blue via the Taguchi Method	
1.35 PM	1.50 PM	Invited II	Prof. Joongoo Lee (POSTECH)	Automated, Molecular Assembly of Reconstituted Cell-Free Systems from in Vitro Produced Components	
1.50 PM	2.02 PM	OP-01	Anuyut Yootoum	Comparative Pretreatment of Coffee Cherry Pulp for Polyhydroxyalkanoate Production by Thermotolerant *Inquilinus* sp. CF22	
2.02 PM	2.14 PM	OP-02	Mary Segbefia	Sustainable Pretreatment of Durian Rind for Cellulose Nanofiber Extraction as a Bio-Based Reinforcement Material	
2.14 PM	2.26 PM	OP-03	Bana Azad Tawfeeq	Plant-Microbe Interactions for Microplastic Removal Using Mangrove-Associated Herbaceous Plants in a Hydroponic System	
2.26 PM	2.38 PM	OP-04	Hamza Ghilzay	Green Extraction and Isolation of Cellulose Nanofibrils from Kiam (*Cotylelobium melanoxylon*) Wood Waste	
2.50 PM	3.50 PM	Break & Poster Session (Foyer between MR213 - MR214)			
		PP-01 PP-02 PP-03 PP-04 PP-05 PP-06 PP-07 PP-08 PP-09 PP-10 PP-11 PP-12 PP-13 PP-14 PP-15 PP-16 PP-17			
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Session III					
3.50 PM	4.10 PM	Keynote III	Prof. Mohd Fauzi Mh Busra (Universiti Kebangsaan Malaysia)	Next-Generation Chronic Wound Therapy: Enhancing ColPatch® with Plasma-Functionalised Bioscaffolds	Chair: Prof. Penjit Srinophakun Co-Chair: Assoc. Prof. Nopphon Weeranoppanant
4.10 PM	4.30 PM	Keynote IV	Assoc. Prof. Datin Ts. Khairani Idah Mokhtar (International Islamic University Malaysia (IIUM)	Harnessing Nature's Potential: *In vitro* Evaluation of Malayan Deer Velvet Antler Extract and Chitosan Scaffolds on Dental Stem Cell-Based Bone Regeneration	
4.30 PM	4.50 PM	Keynote V	Assoc. Prof. Indranil Banerjee (Indian Institute of Technology)	Serum Albumin Supramolecular Complex based NIR-Responsive Multifunctional Phototherapeutic Platform for Chronic Wound Healing	
4.50 PM	5.02 PM	OP-05	Naga Darsshini	Physicochemical Characterization and 2D In Vitro Wound Healing Evaluation of a Novel Tripeptide	
5.02 PM	5.14 PM	OP-06	Fang Lim	Effect of Peptide Sequence Length on the Physicochemical Properties and Biological Performance in Hyperglycaemic Wound Healing	
5.14 PM	5.26 PM	OP-07	Suppanut Sripratum	Cellulase-Assisted Enzymatic Remodeling of Bacterial Cellulose as a Scaffolds for Tissue Engineering Applications	

CONFERENCE SCHEDULE

DAY 1 : Wednesday, 2 September 2026

ROOM: MR213					
Start Time	End Time	Code	Speaker	Topic	Chair/Co-Chair
Session II					
1.00 PM	1.20 PM	Keynote II	Prof. Kunal Pal (National Institute of Technology)	Functional Mimicry of Solid Shortenings via Synergistic Polymer–Lipid Emulgels: Engineering Structure–Quality Relationships in Steamed Bread Formulations	Chair: Prof. Takeshi Omasa Co-Chair: Asst. Prof. Nisit Watthanasakphuban
1.20 PM	1.35 PM	Invited III	Assoc. Prof. Paiboon Tunsagool (Kasetsart University)	Genome-Based Analysis and Anti-Oomycete Activity of *Priestia aryabhattai* PTKU-123 Against the Durian Pathogen *Phytophthora palmivora*	
1.35 PM	1.47 PM	OP-08	Mahmood-ur-Rahman Ansari	Investigating the Potential of Transcription Factors in Multiple Stress Tolerance: A Way Forward for Stress-Resilient Crop Plants under Climate Change Conditions	
1.47 PM	1.59 PM	OP-09	Mohibah Musa	Development and Optimization of Sustainable Fish Feed Formulations Using High-Lipid Algae Species for Aquaculture	
1.59 PM	2.11 PM	OP-10	Fina Amreta Laksmi	Single-Site Polarity Modulation Improves the Catalytic Efficiency and Thermostability of D-allulose 3-epimerase through Flexibility–Rigidity Rebalancing	
2.11 PM	2.23 PM	OP-11	Anusada Pattaravipak	Development of Oil-in-Water Emulsion Formulations to Enhance the Efficiency of Vitamin D3 Encapsulation	
2.23 PM	2.35 PM	OP-12	Pornpavit Phewkum	Application of Ohmic Heating Pretreatment to Accelerate the Aging Process and Modulate the Bioactive Profile of Black Shallots	
2.35 PM	2.47 PM	OP-13	Farida Pattanabhumi	Evaluation of the Protective Effects of an Energy- and Electrolyte-Enhanced Mulberry Beverage Against Delayed Onset Muscle Soreness Through Redox Balance Regulation	
2.47 PM	3.50 PM	Break & Poster Session (Foyer between MR213 - MR214)			
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Session IV																		
3.50 PM	4.10 PM	Keynote VI	Prof. Hideki Aoyagi (University of Tsukuba)	Development of an *In Vitro* Co-Culture Platform for Studying Interactions Between Intestinal Epithelial Cells and the Gut Microbe	Chair: Prof. Kunal Pal Co-Chair: Assoc. Prof. Paiboon Tunsagool
4.10 PM	4.25 PM	Invited IV	Dr. Tsung-ju Li (Grape King Bio Co, Ltd.)	Liquid Fermentation Tech for Sustainable Health and Industry Advancement	
4.25 PM	4.40 PM	Invited V	Asst. Prof. Nisa Patikarnmonthon (Mahidol University)	Evolution of Nanoparticle Assembly: Bridging Proven Encapsulation with Reconfigurable Microfluidic Platforms	
4.40 PM	4.55 PM	Invited VI	Assoc. Prof. Jittima Luckanagul (Chulalongkorn University)	Designing Impactful Nanomedicine: Bridging Scientific Discovery and Global Translation	
4.55 PM	5.07 PM	OP-14	Faiz Ahmad Joyia	Recombinant Fibrinolytic Proteins: Production, Isolation, and Application of 'Recombinant Lumbrokinase' against Chemically Induced Thrombosis in Mice	
5.07 PM	5.19 PM	OP-15	Ekaterina Grizanova	Evolution of Bacillus thuringiensis virulence during passage through the resistant and susceptible host	
5.19 PM	5.31 PM	OP-16	Nichapat Wongsaenkham	Encapsulation of Anti-Dengue Virus NS3 Monoclonal Antibody in PEG-PLGA Nanoparticles for Intracellular Delivery	

CONFERENCE SCHEDULE

The 10th Biotechnology International Congress (BIC 2026)

DAY 2 : Thursday, 3 September 2026

ROOM: MR212 - MR213					
Start Time	End Time	Code	Speaker	Topic	Chair/Co-Chair
8.00 AM	9.30 AM	Registration			
9.30 AM	10.00 AM	Plenary IV	Prof. Alissara Reungsang (Khon Kaen University)	Sustainable Utilization of Sugarcane Industry Biomass and Residues for Bioenergy and Biochemical Production	Chair: Prof. Hideki Aoyagi Co-Chair: Assoc. Prof. Tatsaporn Todhanakasem
10.00 AM	10.30 AM	Plenary V	Dr. Uracha Ruktanoncha (NANOTEC)	Next-Generation Nanobiotechnology: Transforming Healthcare, Food Systems, and Sustainability	
10.30 AM	10.50 AM	Break			
10.50 AM	11.05 AM	Industry talk I	Dr. Walaiporn Timbuntam (Amano Enzyme Asia Pacific Co.,Ltd)	Industrial Enzymes for a Circular Future: Global Market Landscape and Amano Specialty Solutions"	
11.05 AM	11.20 AM	Industry talk II	Ms Sawitree Suklour (Gibthai Co. Ltd.)	From Discovery to Biomanufacturing - Integrated Biotechnology Solutions for Sustainable Innovation	
11.20 AM	1.00 PM	Lunch and Visit Exhibition Hall EH102 – EH104			

CONFERENCE SCHEDULE

DAY 2 : Thursday, 3 September 2026

ROOM: MR212					
Start Time	End Time	Code	Speaker	Topic	Chair/Co-Chair
Session V					
1.00 PM	1.20 PM	Keynote VII	Prof. Ivan Dubovskiy (Siberian State University of Engineering and Biotechnology)	Biocontrol of Insects Pests in Russia: from Classic Bioinsecticides to State of Art Technology / or Pest Insects Biocontrol using Microbials and Genetic Biotechnologies	Chair: Prof. Alissara Reungsang Co-Chair: Dr. Phattanon Prasithichoke
1.20 PM	1.35 PM	Invited VII	Assoc. Prof. Thawatchai Chaijarasphong (Mahidol University)	CRISPR Detection Platforms for Diseases in Aquaculture	
1.35 PM	1.47 PM	OP-17	Nantavadee Bootprom	Development and Evaluation of a Pumpkin Seed-Enriched Functional Cream Cheese for Modulating Risk Factors of Polyendocrine Metabolic Ovarian Syndrome	
1.47 PM	1.59 PM	OP-18	Pincha Kwandee	Fecal Microbiota Alterations Induced by Triphala Extract	
1.59 PM	2.11 PM	OP-19	James Konkov	*In Vitro* Activity of a Co-Eluted Amphiphilic Crude Mixture Obtained from *Priestia aryabhattai* PTKU-123 Against *Phytophthora palmivora*	
2.11 PM	2.23 PM	OP-20	Agnibha Banerjee	Co-Solvent-Driven Structural Engineering of Rice Bran Oil-Based Oleogels Through Multidimensional Characterization: Advancing Solid Fat Mimetics in Food Biotechnology	
2.23 PM	2.35 PM	OP-21	Sampurna Ghosh	Multiscale Investigation of Pectin-Mediated Structural Reinforcement and Shelf-Life Enhancement in Whole Wheat Bread	
2.35 PM	3.35 PM	Break & Poster Session (Foyer between MR213 - MR214)			
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Session VI					
3.35 PM	3.55 PM	Keynote VIII	Prof. Chi-Wei Lan (Yuan Ze University)	Nano–Bio Synergy: Biomass-Derived Carbon Quantum Dots for Enhancing Microbial Metabolism and Biochemical Production	Chair: Prof. Ivan Dubovskiy Co-Chair: Assoc. Prof. Thawatchai Chaijarasphong
3.55 PM	4.15 PM	Keynote IX	Dr. Sissades Tongsima (BIOTEC)	Pioneering the Computational Genomic Bedrock of Next-Generation Biotechnology	
4.15 PM	4.30 PM	Invited IX	Assoc. Prof. Thanyaporn Wongnate (VISTEC)	Research and Innovation for Sustainable Waste Management in the Bio-Based Economy	
4.30 PM	4.45 PM	Invited X	Dr. Thapakorn Jaroentomeecha (Mahidol University)	Cell-Free Synthetic Glycobiology: Engineering Glycomolecules for Next-Generation Biotherapeutics and Vaccines	
4.45 PM	4.57 PM	OP-22	Sachidanand Singh	*In-Silico* Evaluation of *Moringa oleifera* and *Solanum americanum* Phytochemicals to Protect Red Blood Cell Membrane in Haemolytic Anemia: A Network Pharmacology Approach	
4.57 PM	5.09 PM	OP-23	Sivatch Imrattanarak	Characterization, Purification and Media optimization of S. cerevisiae BHF5D35-2ΔAde2 for Superoxide dismutase production	
5.09 PM	5.55 PM	Awards and Closing Ceremony			Asst. Prof. Adisak Romsang

CONFERENCE SCHEDULE

DAY 2 : Thursday, 3 September 2026

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<tr><td colspan="11">Youth Science</td></tr>
<tr><td>1.00 PM</td><td>1.15 PM</td><td>Invited VIII</td><td>Asst. Prof. Adisak Romsang (Mahidol University)</td><td>Shaping the Future of Responsible Biotechnology in Thailand through Biosafety Education and Training</td><td rowspan="6">Chair:
Prof. Joongoo Lee

Co-Chair:
Dr. Thapakorn Jaroentomeechai</td></tr>
<tr><td>1.15 PM</td><td>1.30 PM</td><td>OP-24</td><td>Korapak Thaweechaithaworn</td><td>SPIDERS DETECH: An AI Innovation for Classifying Spider Species via a LINE Chatbot</td></tr>
<tr><td>1.30 PM</td><td>1.45 PM</td><td>OP-25</td><td>Noppatsorn Virulbuntheng</td><td>A Deep Learning-Based Smartphone Solution for Thai Jasmine Rice Quality Assessment</td></tr>
<tr><td>1.45 PM</td><td>2.00 PM</td><td>OP-26</td><td>Thanistar Kingnara</td><td>Deep Learning-Based Skin Disease Classification Chatbot</td></tr>
<tr><td>2.00 PM</td><td>2.15 PM</td><td>OP-27</td><td>Jiratchaya Sathitkul</td><td>Evaluation of Antioxidant Activity, Total Phenolic Content, and Total Flavonoid Content of Phyllanthus emblica and Garcinia mangostana Extracts for Potential Biotechnological Applications in Herbal Oral Healthcare</td></tr>
<tr><td>2.15 PM</td><td>2.30 PM</td><td>OP-28</td><td>Kanatpol Sahakanjanakul</td><td>Bid by Bit: A Micro:bit-Based Wearable Device for Lower-Limb Motion Monitoring and Rehabilitation</td></tr>
<tr><td rowspan="4">2.35 PM</td><td rowspan="4">3.35 PM</td><td colspan="9">Break & Poster Session (Foyer between MR213 - 214)</td></tr>
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<tr><td colspan="11">Youth Science</td></tr>
<tr><td>3.35 PM</td><td>3.50 PM</td><td>OP-29</td><td>Aana Singhapong</td><td>A Preliminary Study of Liquid Biopsy-Based Detection of Epidermal Growth Factor Receptor Mutations Using a Surface Acoustic Wave Biosensor</td><td rowspan="5">Chair:
Asst. Prof. Adisak Romsang

Co-Chair:
Asst. Prof. Nisa Patikarnmonthon</td></tr>
<tr><td>3.50 PM</td><td>4.05 PM</td><td>OP-30</td><td>Kantapat Harnborvonkij</td><td>A Low-Carbon Biochar Module for Nitrogen Reduction, Eutrophication Mitigation, and Sustainable Urban Water Resilience</td></tr>
<tr><td>4.05 PM</td><td>4.20 PM</td><td>OP-31</td><td>Alin Kasemtanakul</td><td>KneeHab Pro: A Wearable Motion Tracking System for Post Knee Surgery Rehabilitation</td></tr>
<tr><td>4.20 PM</td><td>4.35 PM</td><td>OP-32</td><td>Punika Prempiyakij</td><td>AI-Engineered Nanoproteins: A De Novo Approach to Rapidly Suppress Human-to-Human Hantavirus Transmission</td></tr>
<tr><td>4.35 PM</td><td>4.50 PM</td><td>OP-33</td><td>Gaweewat Thanasitnaphitkul</td><td>Evaluation of CRISPR/Cas12f-Mediated Genome Editing Targeting the BCL11A Enhancer in HEK293T Cells</td></tr>
<tr><td>5.09 PM</td><td>5.55 PM</td><td colspan="4">Awards and Closing Ceremony (ROOM: MR212)</td><td>Asst. Prof. Adisak Romsang</td></tr>
</table>

CONFERENCE SCHEDULE

Poster Session

Foyer between Room MR213 - 214		
Code	Presenter	Topic
PP-01	Chia-Hung Kuo	Gelatin/agar Film Combined with Psidium cattleianum Leaves Carbon Dots for Food Preservation
PP-02	Panyisa Potibut	Population Dynamics of Ammonia-Oxidizing and Nitrite-Oxidizing Bacteria in Outdoor Shrimp Culture Ponds
PP-03	Mongkhol Phanthura	Development of a SYBR Green Real-Time PCR Assay Targeting the *amoA* and *nxrB* Genes for Monitoring Nitrifying Bacteria in a Recirculating Aquaculture System (RAS)
PP-04	Weera Piyatheerawong	Valorization of Sweet Sorghum Juice for Sustainable Protein Production Through Co-cultivation of Microalgae and Yeast Cells
PP-05	Rattiya Waeonukul	Effect of Maltose Concentration on the Production of Long-Chain Isomaltooligosaccharides by *Bacillus subtilis strain* AP-1
PP-06	Prattana Ketbot	Production of Manno Oligosaccharides from Soybean Residues by *Bacillus tequilensis* PLM1
PP-07	Watchaphon Wuttiyan	Genomic Resequencing Reveals Genetic Diversity and Population Structure of Durian in Uttaradit Province, Thailand
PP-08	Noppakorn Thadasawate	Postbiotic Potential of Cell-Free Supernatants from Khao-mak Microbial Isolates: Antimicrobial Activity and Stability
PP-09	Saharit Palasan	Nested Recombinase Polymerase Amplification Coupled with a CRISPR-Cas12a Assay for Sensitive and Specific Detection of *Streptococcus iniae* in Fish
PP-10	Suparada Suwanlertlum	Rapid CRISPR-Based Detection Platform for Species-Specific Identification of *Edwardsiella* Bacteria
PP-11	Rungnapa Pichaikarn	Whole Genome Characterization of *Streptomyces angustmyceticus* as a Potential Biological Control Agent Against Southern Blight Disease Caused by *Agroathelia rolfsii*
PP-12	David Herawan	Substantial Catalytic Enhancement of D-allulose 3-epimerase from *Arthrobacter psychrolactophilus*: A Sustainable Chitosan Immobilization Strategy for Production of Low-Calorie Sweetener
PP-13	Yeryeong Lee	Preparation and Characterization of Mealworm-Contained Rice Starch Soft Foods for Older Adults with Dysphagia
PP-14	Mamoru Wakayama	Isolation and characterization of α-1,3-glucanase from alkaliphilic bacterium, *Alkalihalobacillus* sp.
PP-15	Paphanpawn Lekboonphet	Optimal Conditions for Mycelial Growth of the Ectomycorrhizal Mushroom Het Ra-ngok Lueang (*Amanita javanica*)
PP-16	Sirilak Baramee	D-Tagatose Production Using Recombinant L-Arabinose Isomerase from *Cellulomonas palmilytica*
PP-17	Jinnawat Nakmuang	Evaluation of Factors Affecting Phase Separation in Pickering Emulsions Stabilized by *Microbacterium esteraromaticum* SBS1-7
PP-18	Yuka Oe	Analysis of the Growth of Lactic Acid Bacteria Producing D-Serine under Controlled pH Conditions and the Expression of Genes Related to Serine Metabolism
PP-19	Nanako Mizuno	Identification and Functional Analysis of Serine Racemase Genes in D-Serine-Producing Lactic Acid Bacteria
PP-20	Otono Tsurudome	Roles of Aspartate β-Decarboxylases in Aspartate Metabolism in *Acetobacter pasteurianus* SKU1108
PP-21	Nang Yee Mon Htoo	Structural Basis for the High Catalytic Efficiency of the Iron-Dependent Xylose Isomerase from *Lactococcus lactis* IO-1
PP-22	Thunyamas Guntawang	Development of a Paper-Based Test Strip for Colorimetric Detection of Cholinesterase Activity in Canine Serum
PP-23	Apinya Singkhala	Valorization of Soybean Processing Residue as an Alternative Nitrogen Source for Enhanced Dark Fermentative Biohydrogen Production

CONFERENCE SCHEDULE

Poster Session

Foyer between Room MR213 - 214		
Code	Speaker	Topic
PP-24	Nurulhuda Madawa	Isolation and Identification of Thermoacidophilic Bacteria for Accelerated Food Waste Degradation
PP-25	Chonticha Janprungton	Evaluation of Culture–Substrate Compatibility and Hydraulic Retention Time for Enhanced Biohydrogen Production
PP-26	Thiyapan Noppakoon	Valorization of Corn Tassel Agro-Residues: Polyphenol Recovery and Cosmetic Potential via Conventional and Ultrasound-Assisted Extractions
PP-27	Thanpitcha Jenkit	Antioxidant and Antimicrobial Activities of Crude Extracts from *Phellinus* sp.
PP-28	Wasupol Phakamas	In Vitro Generation of Multispecific Cytotoxic T Lymphocytes Targeting GD2, PRAME, and PD-L1
PP-29	Thanakorn Tangsereesuk	Cloning, Heterologous Expression, and Purification of Sphingomyelinase of *Staphylococcus epidermidis*
PP-30	Sidra Bibi	Optimizing Mycelium Pellet Morphology and Its Impact on Bioactive Compound Production via a Taguchi Image Analysis Framework
PP-31	Worraanong Leewattanapasuk	Nucleotide Variations in the Middle Region of Melanocortin 4 Receptor Gene and Their Potential Association with Obesity Risk in the Thai Population
PP-32	Nitikul Teankrajang	Expression and Purification of Recombinant *SpCas9-HF1*-Plus Protein in *Escherichia coli* lys*Y*/I^q for High-Precision Gene Editing
PP-33	Tung Anh Hoang	A Multipurpose Antibody Format for Flexible Assay Development Using Cell-Based and Cell-Free Production
PP-34	Yujin Jeong	Thermo-Responsive Morphological Evolution and Rheological Behavior of Wax/Butter-Based Phase Change Microparticles
PP-35	Hwain Lee	Skin-Adhesive Illite-Containing Amphiphilic Hydrogel Composite Patches for Wound Care
PP-36	Jarunluk Keerativoranant	Investigating the Role of *Fusobacterium nucleatum* in Colorectal Cancer and the Inhibitory Effect of *Dendranthema morifolium* as a Natural Antibacterial Agent
PP-37	Thanabodee Worrakul	AI-Based Oral Lesion Detection System with Integrated Online Chatbot
PP-38	Saowaphak Duangram	Deciphering the Tissue-Specific Molecular Imprint of Oral Mesenchymal Stem Cells: A Comparative RNA-Seq Analysis
PP-39	Panisa Ngiampaisal	Transcriptomic Effects of Propylene Glycol on Oral Mucosal Barrier Integrity
PP-40	Siwat Viriyaoydiyiem	PANI Smart Sutures
PP-41	Poonnapa Warunyurattana	Development of a Graphene-Modified Quartz Crystal Microbalance Biosensor for Non-Invasive Prostate Cancer Detection
PP-42	Tiarn Sripongtanakul	*mecA* and *dnaG* Gene Knockout in *Staphylococcus aureus* via CRISPR-Cas9 System as a Model for Methicillin-resistant *Staphylococcus aureus* inhibition
PP-43	Pititada Preechapongmit	An AI-Based System for Facial Expression Classification: A Comparative Study of Model Training Across Various Emotions
PP-44	Punyada Vanitchanont	Development of an AI-Based LINE Chatbot for Preliminary Classification of Common Pediatric Skin Conditions
PP-45	Wasitpol Akkawattananukul	Computational Evaluation of Understudied Second-Shell Residues Surrounding the Catalytic Triad of PETase
PP-46	Panisara Kraichotchai	Deep Learning-Based Classification of Oral Diseases

Mammalian Cells: A Workhorse Platform for Biologics Production

Takeshi Omasa[1,2*], and Noriko Yamano-Adachi[1,2]

[1]Department of Biotechnology, Graduate School of Engineering, The University of Osaka, Suita, Osaka 565-0871, Japan

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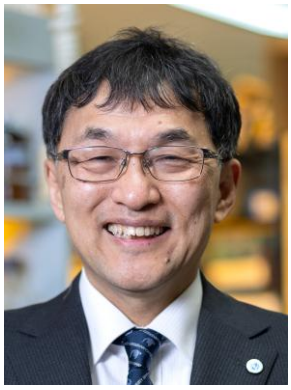
ABSTRACT: Mammalian cell lines are indispensable platforms for the industrial-scale production of pharmaceutical proteins (biologics) because of their ability to perform accurate protein folding, assembly, and post-translational modifications. Among these, Chinese hamster ovary (CHO) cells have become the gold standard for the production of therapeutic proteins, owing to their high reliability and robustness. In our recent work, we established novel cell lines derived from lung and ovary tissues of the Chinese hamster (*Cricetulus griseus*), thereby expanding the repertoire of host cells available for recombinant protein manufacturing. These cell pools were gradually adapted to serum-free conditions through stepwise reduction of serum concentrations. The resulting serum-free cell pools were designated Chinese hamster lung (CHL)-YN (Riken BioResource Bank: RCB5004) and Chinese hamster ovary (CHO)-MK, respectively. Both CHL-YN and CHO-MK cell lines exhibit rapid proliferation, with doubling times of less than 10 hours. In this presentation, we introduce the characteristics of these two cell lines and discuss their potential impact on recombinant protein manufacturing[1,2)].

Keyword: Antibody drug, Chinese hamster ovary (CHO) cells, Cell engineering, Cell culture engineering.



Ph.D. (Engineering), Fermentation Technology, Graduate School of Engineering, Osaka University, 1992
Dean of Graduate School/School of Engineering, The University of Osaka (Osaka University) (2024-)
Senior Vice President of the University of Osaka (2026-)
Professor, The University of Osaka (2015-)
Project Leader of Manufacturing Technology Association of Biologics (2013-) (therapeutic antibody and gene-therapy vector project)
President of AFOB (Asian Federation of Biotechnology) (2022-)

Biomanufacturing Technology: Its Evolution and Contribution to the Society

Jian-Jiang Zhong[1*]

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ABSTRACT: Biomanufacturing technology originates from the penicillin fermentation in the 1940s under the intimate collaboration of microbiologists and chemical engineers. It has evolved rapidly with the fast development of biology, engineering and interdisciplinary boundaries, including synthetic biology in recent years. In this presentation, recent work in biomanufacturing technology including the strain breeding and fermentation production of ethanol, antibiotics and enzymes will be briefly introduced. Considering the significance of the natural and health-enhancing functional foods in preventing diseases and promoting human health, studies on the edible medicinal mushroom *Ganoderma lucidum* (Lingzhi) and the medicinal plant ginseng, both of which have been used for over 2000 years as oral administration medicines in East Asia to treat various diseases and improve human health, are to be presented in detail, which produces bioactive triterpenoids ganoderic acids (GAs) and ginsenosides, respectively. An example of synthetic biology-based biomanufacturing of GAs by engineering baker's yeast is further shown. We design an GA biosynthetic pathway, and have identified key P450 enzymes catalyzing the triterpenoid structure modification and reprogrammed the GA biosynthetic network in the yeast *Saccharomyces cerevisiae*. For example, the P450 enzymes CYP512W2 (oxidization), CYP512W6 (hydroxylation) and CYP512A13 (catalyzing the conversion of carbon-carbon conjugated double bonds on lanostane skeleton) were identified and analyzed. By engineering the key enzymes, a higher titer of GAs was achieved in the yeast fermentation. In addition, we reveal the catalytic mechanism of related CYPs. Our work provides new insights into the post-modification of triterpenoids. In addition, we investigated bioactivities of GAs, e.g., the inhibition of GA-T on hepatocellular carcinoma both *in vitro* and *in vivo* was revealed. Our work creates an efficient biomanufacturing platform for functional food key components - GAs, and it is of great impact on the development of GAs-producing yeast based dietary nutrition for human health.

Keyword: Biomanufacturing technology, human health, synthetic biology, bioactive compounds, catalytic mechanism of enzymes

Dr. JJ Zhong is a distinguished professor at Shanghai Jiao Tong University, China. He has published over 270 papers in peer-reviewed international journals. He was awarded the Cheung Kong Scholar Professorship from the Ministry of Education (MOE), National Science Fund for Distinguished Young Scholars by National Natural Science Foundation of China, the inaugural award of "Young Asian Biotechnologist Prize" by the Society for Biotechnology (Japan), the 1st-class Prize for Advancement of Science & Technology by MOE for twice (in 2004 & 2014), and the "Research Exchange Award" from the Korean Society for Biotechnology and Bioengineering. He is on the editorial board of 10 SCI-cited international journals and was an invited speaker in about 90 international conferences.

The Cure is in The Code: The Rise of Gene Therapy

Vip Viprakasit[1,2*], Warut Tulalamba[3], Thidarat Suksangpleng[3] and Supachai Ekwattanakit[2]

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ABSTRACT: Cell and gene therapy have transitioned from conceptual innovation to transformative clinical reality, redefining the therapeutic landscape for both inherited and acquired diseases. This presentation provides a comprehensive overview of the evolution of gene-based interventions, from early viral vector strategies to current precision genome editing platforms, including CRISPR/Cas systems and next-generation delivery technologies. Emphasis is placed on the translation of these advances into real-world clinical applications, particularly in monogenic disorders such as thalassemia, where gene addition and gene editing approaches have demonstrated curative potential by restoring effective erythropoiesis and eliminating transfusion dependence. Beyond hematologic diseases, the field has expanded rapidly into immunotherapy, where genetic modification of immune cells—most notably chimeric antigen receptor (CAR) T cells and emerging CAR-NK platforms—has revolutionized cancer treatment. These strategies are now being extended to autoimmune diseases, offering the possibility of durable immune reprogramming. As the burden of cancer and immune-mediated disorders continues to rise globally, including in Thailand, such approaches represent a paradigm shift toward highly personalized and potentially curative therapies. Critical challenges remain, including scalability, cost, long-term safety, and equitable access, particularly in low- and middle-income settings. The integration of regulatory innovation, such as adaptive frameworks and "sandbox" models, alongside regional manufacturing capabilities, will be essential to bridge the gap between discovery and accessibility.

Keyword: Gene therapy; Genome editing; Thalassemia; CAR-T cells; Precision medicine

Prof. Vip Viprakasit, MD, DPhil (Oxon) is a Professor of Pediatrics at Mahidol University and a leading hematologist at Siriraj Hospital, Bangkok. He directs one of Southeast Asia's largest thalassemia centers, with expertise in red cell disorders, genomics, and gene therapy. His work spans clinical care, translational research, and precision medicine. He has received numerous national and international awards for clinical excellence and research innovation including the Outstanding Scientist Award and Outstanding Researcher Award of the year and is widely recognized for advancing curative therapies and fostering global collaborations in hematology and gene therapy.

Sustainable Utilization of Sugarcane Industry Biomass and Residues for Bioenergy and Biochemical Production

Alissara Reungsang[1,2,*], Prawit Kongjan[3,4], Sureewan Sittijunda[5], and Rattana Jariyaboon[3,4]

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[2]Academy of Science, Royal Society of Thailand, Bangkok, 10300, Thailand
[3]Department of Science, Faculty of Science and Technology, Prince of Songkla University, Mueng, Pattani 94000, Thailand
[4]Bio-Mass Conversion to Energy and Chemicals (Bio-MEC) Research Unit, Prince of Songkla University, Mueng, Pattani 94000, Thailand
[5]Faculty of Environment and Resource Studies, Mahidol University, Nakhon Pathom, 73170, Thailand

***Correspondence to:** Department of Biotechnology, Faculty of Technology, Khon Kaen University, Khon Kaen, 40002, Thailand. E-mail: alissara@kku.ac.th*

ABSTRACT: Thailand is among the world's largest sugarcane and sugar producers and generates enormous volumes of residues — bagasse, sugarcane leaves, filter cake, filter press, and bagasse ash — together with downstream by-products such as molasses and hydrogenic effluent. Much of this material is still disposed of by open-field burning or landfilling, contributing to PM2.5, greenhouse-gas emissions, and the loss of valuable carbon and nutrients. This keynote presents an integrated biorefinery strategy, executed under Thailand's Bio-Circular-Green (BCG) Economy framework, that converts these residues into bioenergy, biochemicals, and biomaterials. Hydrothermal carbonization (HTC) of bagasse and sugarcane leaves under dual-optimized conditions produced hydrochar with HHV of 23.4–23.6 MJ/kg, an 18–23% upgrade over raw biomass. Its quality was comparable to lignite, but with sulfur below 0.05%. The hydrochar also exhibited ammonium adsorption of 23.76 mg/g. Integration with solar drying reduced energy cost by 83% and CO_2 emissions by approximately 80%. Metal-modified (Fe, Ni) biochar from the same residues enhanced dark fermentative biohydrogen yield to 108.77 mL-H_2/g-glucose, a 58.77% increase over the control. Fermentation of sugarcane leaf hydrolysate by Actinobacillus succinogenes TISTR 1994 yielded 18.87 g/L succinic acid (yield 0.59 g/g, sugar utilization 95.3%), with transcriptomic analysis revealing an inverse relationship between Reductive-TCA gene expression and product output. Sugarcane-waste-derived pellets enabled simultaneous CO_2 and H_2S removal from real biogas, with an IRR of 51% and a 2-year payback. Downstream, freshwater microalgae Coelastrella sp. KKU-P1 and Acutodesmus sp. KKU-P2 valorized hydrogenic effluent into polyhydroxybutyrate (up to 6.35% of dry cell weight) while removing 38–53% COD, 14–20% nitrogen, and 56–69% phosphorus. Together, these results demonstrate a cascading biorefinery that transforms every fraction of the sugarcane industry residue stream into bioenergy, biochemicals, and biomaterials — supporting Thailand's transition toward carbon neutrality and the UN Sustainable Development Goals.

Keyword: Sugarcane residues; Biorefinery; Biohydrogen; Hydrothermal carbonization; Bio-Circular-Green economy

EDUCATION

Ph.D. Water Resources, Iowa State University, USA (2000)
M.Sc. Pharmaceutical Sciences (Microbiology), Mahidol University, Thailand (1991)
B.Sc. Biotechnology, Khon Kaen University, Thailand (1989)

RESEARCH INTERESTS

Biohydrogen, biomethane, and biohythane production from lignocellulosic biomass; bioremediation and phytoremediation; waste treatment and utilization; biorefinery technologies for circular bioeconomy

KEY ACHIEVEMENTS

245+ publications (Scopus) 300+ (Google Scholar) | 7,300+ citations (Scopus) 9,000+ citations (Google Scholar) | h-index 49 (Scopus) h-index 53 (Google Scholar) | Stanford Top 2% World Scientist (2020–2025)
16 petty patents | 70+ funded research projects as PI | 8 book chapters
TRF/TSRI Senior Research Scholar (2016–2022)

SELECTED HONORS & AWARDS

National Distinguished Researcher Award (NRCT, 2020) | NRCT Research Awards (2016, 2023, 2026)
Toray Science & Technology Prize (2022) | ASAIHL Research Excellence Award (2023)
AAAE Researcher/Innovator of the Year (2024) | Associate Fellow, Royal Institute of Thailand (2020–present) | High-Caliber Researcher (NRCT, 2024)

Next-Generation Nanobiotechnology: Transforming Healthcare, Food Systems, and Sustainability

Uracha Ruktanonchai[1]*

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ABSTRACT: In the era of rapid global transitions, next-generation nanobiotechnology drives paradigm shifts across healthcare, food systems, and environmental sustainability. As a key engine for deep-tech development, we pioneer the translation of bio-based nano-delivery platforms into high-impact socioeconomic solutions. Our research focuses on utilizing sophisticated nanocarriers such as nanostructured lipid carriers (NLCs), liposomes, and transfersomes to amplify the bioavailability, controlled release, and targeted efficacy of natural bioactive compounds. In advanced nanomedicine, NANOTEC has successfully developed cannabidiol (CBD)-loaded lipid nanoparticles that stabilize the gut-brain-bone axis and enhance neuroplasticity, alongside oral and nasal andrographolide-loaded nanocarriers designed to mitigate systemic neuroinflammation and acute lung injury. In oncology, dual-folate/biotin-decorated liposomes deliver methylnaphthazarin (MNZ) with enhanced specificity against receptor-overexpressing cancer cells. Bridging nanotechnology with dermatological care, CBD-loaded hydrogel scaffolds, transfersomal *Centella asiatica* extracts, and novel dihydrooxyresveratrol (DHO)-loaded NLCs offer highly permeable, safe topical solutions that accelerate wound healing and treat hyperpigmentation. Beyond therapeutics, NANOTEC reshapes precision nutrition by valorizing regional agricultural assets to combat metabolic syndromes. The encapsulation of *Kaempferia parviflora* (Black Ginger) methoxyflavones within tailored NLCs dramatically upgrades oral bioavailability to manage obesity and dyslipidemia, while the standardized extraction of gymnemic acid derivatives from *Gymnema inodorum* (Chiang Da) provides scientifically validated anti-diabetic activities for functional food ingredients. Crucially, we strictly adhere to green chemistry principles by utilizing biodegradable matrices and ultrasound-assisted technologies, ensuring that the full lifecycle of these advanced materials minimizes environmental footprints and directly supports the Bio-Circular-Green (BCG) economy model. In conclusion, the integration of next-generation nanobiotechnology into healthcare and food systems represents a monumental step toward achieving sustainable global impact. By transforming volatile, poorly soluble natural molecules into highly stable, targeted nano-formulations, we successfully translate lab-scale innovations into tangible real-world applications that unlock the commercial potential of biodiversity and address global challenges.

Keyword: Nanobiotechnology, Nano-delivery Systems, Thai Herbal Valorization, Healthcare Innovation, Sustainable Food Systems.

EDUCATION

2002: Ph.D. Advanced Drug Delivery, University of Nottingham, England
1998: B.Sc. Pharmaceutical Sciences, Khon Kaen University, Thailand

Research Areas

Lipid and polymeric nanoparticles, Nano-encapsulation, Advance drug delivery system

KEY ACHIEVEMENTS

AWARDS/ACHIEVEMENTS

1. 2025: The Alumni of Honor Award for Research and Innovation for Society from Khon Kaen University.
2. 2025: World's Top 2% Scientistes 2025 in the field of Pharmacology & Pharmacy, baesed on citation impact in 2024, (Standford University & Elsevier database).
3. 2020-2024: being listed as top 2% of the mosted cited scientist in the field of Pharmacy & Pharmacology, Elsevier database.
4. 2018: UK alumni Award Professional Acheivement from the British council and UK Embassy
5. 2017 – present: selected to be Fellow of the Royal Society of Chemistry, UK (FRSC)
6. 2017 – present: appointed to be Honorary Professor by University of Queensland, Australia
7. 2015 – present: appointed to be Adjunct Professor of Asian Institute of Technology, Thailand
8. 2011: For Women in Science fellowship Award from UNESCO-L'Oreal Foundation.
9. The Young Scientist Award of 2010 from the Foundation for the Promotion of Science and Technology under the Patronage of His Majesty the King, Thailand
10. Selected to be 1 of "66 Young Leaders Shaping Thailand's Future of 2012" by the Bangkok Post newspaper which celebrated its 66 years in operation
11. Selected as one of ten prestigious Top careers for 2020 "This's My Future" in 2009 organized by Thaikom foundation
12. Selected to be 1 of 10 "prestige Women of the Year 2006" by Prestige magazine, The nation, and Bangkok Business.
13. Selected to be one of Thai Young leader representatives to join STS forum, Japan 2014

Life Cycle Assessment of Lignin-Derived Biomaterial for Better Environmental Friendliness

Penjit Srinophakun*, Anusith Thanapimmetha, Maythee Saisriyoot, Nutchapon Chiarasamran, and Khemmathin Lueangwattanapong

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ABSTRACT: Lignin is an important component in biomass, alongside cellulose and hemicellulose. In ligno-cellulosic ethanol and nanocrystalline cellulose production, lignin is removed and disposed of in wastewater. The black color of lignin is difficult to remove, but it is biodegradable and antimicrobial. Therefore, in this study, lignin was recovered from the wastewater system through precipitation and used to produce lignin-derived biomaterials, which were combined with polyvinyl alcohol (PVA) for mulch films and with polylactic acid (PLA) and polybutylene adipate-co-terephthalate (PBAT) for packaging plastics. It was found that incorporating lignin improved the mechanical properties and biodegradability of the biomaterials. The biomaterials' characteristics were analyzed using SEM, FTIR, XRD, and TGA. Mechanical properties such as tensile strength, elongation at break, and Young's modulus were measured, and biodegradation tests were conducted. A life cycle assessment using SimaPro software and the ReCiPe 2016 Midpoint method indicated both biomaterials had a positive environmental impact and improved biodegradability. The main environmental concerns were global warming, terrestrial ecotoxicity, and marine and freshwater ecotoxicity related to solvent and chemical use. Results showed that adding small amounts of lignin enhanced biodegradability and reduced the environmental footprint of the biomaterials, highlighting their potential for sustainable UV protection material in agriculture and biomedical packaging.

Keyword: Lignin, Antimicrobial activity, Biomaterials, Mulch film, Life Cycle Assessment

Professor Dr. Penjit Srinophakun graduated in Chemical Engineering from the University of Queensland, Australia, in 1996. Then, she returned to work at the Chemical Engineering Department, Faculty of Engineering, Kasetsart University, Thailand. In 2005, 2010, and 2011, she was appointed as the director of the KU-biodiesel Project, director of the Center of Excellence for Jatropha, and the Vice President of the Asian Federation of Biotechnology (AFOB). During 2011-2016 and 2020-2022, she was elected President of the Thai Society for Biotechnology (TSB). Currently, she is more active in research focusing on bioenergy and biorefinery, ligno-cellulosic ethanol, biomaterial, techno-economic feasibility, and Life Cycle Assessment.

Functional Mimicry of Solid Shortenings via Synergistic Polymer–Lipid Emulgels: Engineering Structure–Quality Relationships in Steamed Bread Formulations

Anannya Sahoo[1#], Debmalya Banerjee[1#], Agnibha Banerjee[1#], Bala Chakravarthy Neelapu[1], Sivaraman Jayaraman[1], Maciej Jarzębski[2], Prakit Sukyai[3*], and Kunal Pal[1*]

[1] *Department of Biotechnology and Medical Engineering, National Institute of Technology Rourkela, Rourkela, 769008, Odisha, India*

[2] *Department of Physics and Biophysics, Poznan University of Life Sciences, Poznań, 60-637, Poland*

[3] *Cellulose for Future Materials and Technologies Special Research Unit, Department of Biotechnology, Faculty of Agro-Industry, Kasetsart University, Bangkok 10900, Thailand*

[#] *Authors contributed equally*

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ABSTRACT: The role of traditional shortenings is vital in modulating the stability of gas cells, water retention, and crumb structure in bakery products. Thus, replacing them with alternative structuring agents becomes significantly challenging. In the present study, novel synergistic polymer-lipid emulgels based on cassia gum powder (CGP), psyllium husk polysaccharide (PHP), and rice bran oil (RBO) were prepared to serve as functional shortening mimics and were further utilized in the formulation of a steamed bread (SB) system. Structural features and quality attributes of formulated SBs were evaluated using various techniques, such as surface microscopy, electrochemical impedance spectroscopy (EIS), moisture analysis, and colorimetric analysis. It was found that substituting the SB formulations with polymer-lipid emulgels induced physicochemical alterations, especially in terms of structural and quality parameters, largely dictated by the emulgel composition. Specifically, both too low and too high amounts of oil in the emulgel formulations drastically affected the crumb architecture. In this context, among the formulations, SB-CI2 (SB formulation prepared with 20% RBO) exhibited an optimal structure-quality equilibrium, as evidenced by a consistent porous crumb structure, high moisture content, and desirable impedance profiles and color attributes. The balanced polymer-lipid network of SB-CI2 promoted gas retention, trapping of the water molecules, and the formation of a coherent matrix, thereby facilitating the development of an organized crumb structure and improved quality characteristics. Notably, SB-CI2 could mimic the functionality of conventional shortenings while incorporating only a lower amount of actual oil, translating to 80% less oil incorporated into the SB matrix. These results revealed that these synergistic polymer-lipid emulgels could serve as tools for structuring the quality attributes of SB formulations and as an alternative for developing healthier bakery products with lower oil content while preserving the structural attributes.

Keyword: Polymer-lipid emulgels; Steamed bread; Solid shortening mimics; Structure–quality relationships; Reduced-oil bakery products.

Next-Generation Chronic Wound Therapy: Enhancing ColPatch® with Plasma-Functionalised Bioscaffolds

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ABSTRACT: Chronic diabetic and full-thickness skin wounds remain significant clinical challenges, characterised by impaired cell migration, persistent inflammation, and heightened susceptibility to infection. This presentation integrates two complementary research streams that advance collagen-based biomaterials from mechanistic preclinical investigation to early clinical translation. The first study centres on a three-dimensional acellular ovine tendon collagen type I (OTC-I) bioscaffold, crosslinked with genipin and functionalised via post-carvone plasma polymerisation (GNPppCar). In a streptozotocin-induced diabetic murine model, GNPppCar markedly accelerated wound closure, promoted re-epithelialisation and granulation tissue formation, and reduced inflammatory cell infiltration relative to controls. In vitro assays using human dermal fibroblasts and keratinocytes further demonstrated enhanced cell viability, migration, and proliferation. Mechanistic analyses revealed activation of focal adhesion kinase and PI3K/Akt signalling pathways, underpinning improved cellular attachment and survival. The second study translates this biofunctional scaffold strategy into clinical application through the dermal regeneration template, ColPatch®. In a prospective pilot study of patients with full-thickness skin defects, ColPatch® was well tolerated, with no adverse events reported over a six-month follow-up period. Consistent wound progression and improved scar quality were observed, supporting its safety, feasibility, and therapeutic potential in human use. Collectively, these findings establish a translational continuum from advanced scaffold biofunctionalisation to clinical implementation, underscoring the promise of plasma-enhanced collagen biomaterials as next-generation therapies for chronic wound regeneration.

Keyword: Full thickness wound, collagen type I, Plasma polymerization, plastic surgery, reconstruction, skin substitutes

Prof. Dr. Mohd Fauzi Mh Busra (Fauzi MB) is a Full Professor of Advanced Regenerative Medicine (Advanced Biomaterials & Tissue Engineering) at Universiti Kebangsaan Malaysia (UKM) and a leading researcher in advanced biomaterials, tissue engineering, and regenerative medicine, with a focus on collagen-based biomatrices and other natural-based resources for wound healing and tissue repair. He is affiliated with the Department of Tissue Engineering and Regenerative Medicine at Faculty of Medicine, UKM and has contributed extensively to high-impact publications on biomaterial scaffolds and regenerative therapies. He is also actively involved in translational research and commercialization, notably leading the development of ColPatch®, a collagen-based implantable biomaterial for wound management that has demonstrated strong biocompatibility and potential as a therapeutic medical device. The product has progressed from laboratory research toward clinical application and commercialization pathways, reflecting his role in bridging fundamental science with clinical innovation. In addition to teaching and supervising postgraduate students, he has led million dollar research grants and multidisciplinary collaborations, contributing significantly to advancements in biomedical science and regenerative medicine in Malaysia.

Harnessing Nature's Potential: In vitro Evaluation of Malayan Deer Velvet Antler Extract and Chitosan Scaffolds on Dental Stem Cell-Based Bone Regeneration

Khairani Idah Mokhtar[1*], Azalea Nur-Qistina Azami[2], Basma Ezzat Mustafa[1], Norzaity Mohd. Kenali[3], Munirah Sha'ban[2], Azlina Ahmad[4], Ismail Zainol[5]

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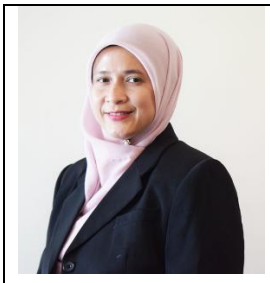
ABSTRACT: In the pursuit of sustainable healthcare, next-generation biotechnology is increasingly exploring natural bio-resources as viable alternatives to synthetic drugs for tissue repair. Deer velvet antler (DVA), or *tanduk rusa,* is traditionally used for its health benefits, yet fundamental research on its effects on dental stem cells remains essential for scientific validation. This presentation explores the scientific translation via fundamental approach of DVA; a traditional Asian remedy, into a potential biological stimulus for regenerative medicine. This study aimed to evaluate the scientific merit of water-extracted DVA from the Malayan deer *(Rusa timorensis)* as a natural stimulus for bone development. Specifically, it investigated the impact of DVA on the biological activity of stem cells from human exfoliated deciduous teeth (SHED) and the combined influence of DVA and chitosan scaffolds in driving osteogenic differentiation. The research employed multidisciplinary approach: cell viability and proliferation were assessed via MTT and alamarBlue assays, while osteogenic potential was quantified through alkaline phosphatase (ALP) activity, calcium mineralization (Alizarin Red-S), and scanning electron microscopy (SEM). Molecular modulation was determined using RT-qPCR for key markers including *RUNX2, OSX,* and *OCN.* DVA water extract was non-cytotoxic across all tested concentrations, with 3.125 ug/ml identified as the optimal concentration for cell proliferation. At the functional level, DVA significantly enhanced ALP activity and mineral deposition in SHED. While chitosan scaffolds effectively supported cell proliferation, they were found to inhibit early-stage differentiation. Crucially, the addition of DVA "rescued" this effect, promoting functional osteogenesis and the upregulation of osteogenic gene *RUNX2*. These findings establish DVA as a potent natural osteoinductive factor capable of driving osteoblast differentiation even within suboptimal scaffold environments. By integrating bio-resources with biocompatible materials, this research highlights a sustainable biotechnological framework for bone tissue engineering, bridging the gap between traditional research and future medical impact.

Keyword: DVA-water extract; SHED; Chitosan scaffold; Osteoblast differentiation

	Assoc. Prof. Ts. Dr Khairani Idah Mokhtar is a researcher at the Kulliyyah of Dentistry, International Islamic University Malaysia (IIUM), specializing in Developmental Biology with interest in craniofacial genetics, dental stem cells and natural products Her research work focuses on the fundamental developmental processes of craniofacial structures, particularly secondary palate development and craniofacial abnormalities, and the application of dental stem cells and natural product extracts for tissue regeneration. On top pf craniofacial abnormality research, a key pillar of her research is the exploration of bioactive natural products, such as flaxseed extract and Malayan deer antler velvet to modulate the osteogenic differentiation of stem cells from human exfoliated deciduous teeth (SHED). She has secured multiple high-impact projects under the National Fundamental Research Grant Scheme (FRGS) and collaborating on transdisciplinary studies involving natural products, tissue regeneration and craniofacial abnormalities. Her scholarly output includes over 50 publications, and publications of seminal books such as Dental Stem Cells: Culturing for the Future. Her research excellence is recognized through her appointment as a National Panel Assessor for FRGS and her status as a Professional Technologist (Ts.). She has successfully translated her research expertise into academic leadership by assisting in the establishment of research-based Master of Dental Sciences and PhD programs in Kulliyyah of Dentistry, while supervising numerous postgraduate students; both PhD and Master students, to completion.

Serum Albumin Supramolecular Complex based NIR-Responsive Multifunctional Phototherapeutic Platform for Chronic Wound Healing

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ABSTRACT: Chronic wounds such as diabetic foot ulcers and infected lesions exhibit delayed healing driven by antibiotic-resistant infection, ischemia, tissue degradation, and fibroblast senescence. Traditional therapies often fail because they lack a comprehensive mechanism of action. To address this, we developed a near-infrared (NIR)-responsive phototherapeutic supramolecular complex composed of bovine serum albumin (BSA), indocyanine green (ICG), and Cu (II) to provide a multifunctional treatment for chronic infected wounds. This platform was designed to simultaneously eradicate bacteria via photothermal and photodynamic effects under 808 nm laser exposure, stimulate angiogenesis through copper-mediated signaling, and activate fibroblasts to accelerate tissue regeneration. Three BSA variants (A7030, A3059, A3294) based on different fatty acid, globulin and protease content were screened to identify an optimal carrier for ICG and Cu (II). The biophysical characterization of 1:1 BSA–ICG complexes showed a pronounced red shift and broadening of ICG absorption and fluorescence for BSA-A7030, indicating improved excitation flexibility and emission properties. The BSA-ICG-Cu(II) complex was then synthesised via a green chemistry approach with BSA-A7030. SEM analysis revealed bead-and-fibril microstructures, and spectroscopy (UV–vis–NIR, fluorescence, circular dichroism) confirmed stable complexation. Under 808 nm NIR irradiation, the complex produced mild hyperthermia and strong photodynamic antibacterial effects in vitro against *Staphylococcus aureus*, *Escherichia coli*, and *methicillin-resistant S. aureus* (MRSA). The complex was further treated with human dermal fibroblasts, which showed enhanced migration and increased VEGF expression, and HUVEC angiogenesis assays displayed improved tube formation. In a S. aureus–infected diabetic mouse wound model, NIR-irradiated treatment accelerated wound closure and achieved >90% bacterial burden reduction by day 7 in comparison to control. These findings indicate that the BSA-ICG-Cu(II) complex is a promising NIR-responsive platform combining antibacterial, proangiogenic, and fibroblast-activating activities for chronic wound healing.

Keywords: Diabetic foot ulcer, Phototherapy, Indocyanine Green, Angiogenesis, Serum albumin

Dr. Indranil Banerjee is an associate professor in the Department of Bioscience and Bioengineering, Indian Institute of Technology Jodhpur and a Fellow of the Royal Society of Chemistry. He has been working in the domain of tissue engineering, regenerative medicine, biomaterials, and therapeutic delivery systems for the last 15 years. He has so far published 90 papers, edited 4 books, and having h-index of 44. He received Institute Research Excellence Award in 2022 from IIT Jodhpur. Beyond academia, Dr. Banerjee is an active entrepreneur.

Development of an *In Vitro* Co-Culture Platform for Studying Interactions Between Intestinal Epithelial Cells and the Gut Microbe

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ABSTRACT: Conventional co-culture systems are often complex, lack versatility, and fail to adequately reproduce the intestinal lumen environment. In this study, we developed a novel co-culture system that enables intermittent sampling of culture media, growth monitoring, aerobic–anaerobic co-culture, simple operation, and high-throughput evaluation. By separating the growth spaces of aerobic cells and anaerobic bacteria using liquid paraffin and sealing the anaerobic compartment with mineral oil, co-culture of microbe and MDCK epithelial cells was successfully achieved. The barrier function and viability of MDCK cells, as well as bacterial growth, were comparable to those in monocultures. Enhanced metabolic activity under sealed anaerobic conditions was also confirmed. This versatile system provides a practical platform for studying host–microbe interactions. I will also introduce the activities of the Society for Biotechnology, Japan.

Keyword: Aerobic-anaerobic culture, co-culture device, epithelial cell, host–microbe interaction.

Prof. Hideki Aoyagi received his M.S. degree in Environmental Science in 1990 and his Ph.D. in Agricultural Sciences in 1993, both from the University of Tsukuba, Japan. He is currently a Professor at the Institute of Life and Environmental Sciences, University of Tsukuba. Now, he is vice president of the Society for Biotechnology, Japan. He specializes in cell cultivation engineering, biochemical engineering, and plant tissue culture. His research key words are useful metabolites production, bioreactors, microbes, unculturable microbe, plant cells, protoplasts, insect, animal cells, and various cell culture techniques.

Pest Insect Biocontrol using Microbial and Genetic Biotechnology Approaches

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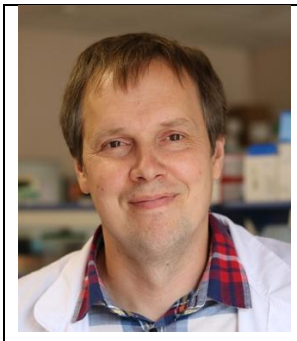
ABSTRACT: Entomopathogenic bacteria *Bacillus thuringiensis* and fungi of the genus Metarhizium are actively used to create insecticidal preparations for plant protection. They account for the majority of the market of biological plant protection products in Russia. In addition to the basis of bioinsecticides, *B. thuringiensis* bacteria are the main source of genes for the transgenesis of agricultural plants, and entomopathogenic fungi of the genus Metarhizium are beginning to be actively used as biofertilizers. The talk will present the mechanism of action and ways to increase the effectiveness of biological preparations based on bacteria and fungi. Modern developments in the genetic transformation of entomopathogens and the use of RNA interference, botanicals, nanoparticles will be considered as strategies to increase the activity of biological products. In addition, the ways of formation of insect pest resistance to *B. thuringiensis* bacteria and promising approaches to delay the formation and overcoming of resistance will be shown. The possibility of using entomopathogenic microorganisms and their consortia as multifunctional and growth-stimulating drugs in agriculture will be discussed. The study was supported by the Russian Science Foundation (grant № 26-16-00228).

Keyword: Biological preparations, RNA interference, pest control, biofertilizers.



Ivan M. Dubovskiy, D. Sc.
Head of Research Center of Biological Plant Protection,
Siberian State University of Engineering and Biotechnology
H-index (WoS): 24
WoS ResearcherID: B-8252-2008

Research Interests:
Insect immunity, experimental evolution, resistance, insect infections, Bacillus thuringiensis, Metarhizium, microevolution, antioxidant systems, genes expressions, biological control

Scientific societies:
Russian Microbiological Society (since 1997), Russian Entomology Society (since 2000), Russian Biotechnology Society (since 2006), Russian Parasitology Society (since 2008), Society for Invertebrate Pathology (since 2018)

Scientific awards:
Dubovsky I.M. awarded the prize of the governor of the Novosibirsk region (for outstanding scientific achievements, 2012) and the city administration of Novosibirsk (Best young researcher, 2018). President of Russian Foundation award grants for young scientists 2011, 2013, 2017 years. Certificate of Honor from the Ministry of Science and Education of the Russian Federation 2023 year. Gratitude from the Governor of the Novosibirsk region 2026 year.

	Editorial board member: Journal of Fungi (WoS, Q1); All Life (WoS, Q2); Bulletin of NSAU (Novosibirsk State Agrarian University) (RSCI); Frontiers in Fungal Biology (WoS) **Science popularization:** Tiktok's "Clear Science" channel is a finalist for the Fidelity to Science Award in 2022. Diploma YouTube channel "Ivan Dubovsky" for 100,000 subscribers. Participants (2021, 2022) and the winner (2025) of the Film Science contest. YouTube (@DubovskiyLab) and Tiktok (@labbio_nsau) "Harm the pest". Total number of subscribers in social media (TikTok, YouTube, VK) more than 1,000,000 people. **Key publications** − Butt T.M., Coates C.J., Dubovskiy I.M., Ratcliffe N.A. Entomopathogenic fungi: new insights into host-pathogen interactions. Advances in Genetics. 2016, 94:307-364. − Dubovskiy I.M., Grizanova E.V., Whitten M.M.A., Mukherjee K., Greig C., Alikina T., Kabilov, M., Vilcinskas, A., Glupov, V.V., Butt, T.M. Immuno-physiological adaptations confer wax moth *Galleria mellonella* resistance to *Bacillus thuringiensis.* Virulence. 2016, 30:1-11. − Grizanova EV, Coates CJ, Butt TM, Dubovskiy IM. RNAi-mediated suppression of insect metalloprotease inhibitor (IMPI) enhances *Galleria mellonella* susceptibility to fungal infection. Dev Comp Immunol. 2021, Sep;122:104126. − Dubovskiy, I.M., Grizanova, E.V., Gerasimova, S.V. Plant Recombinant Gene Technology for Pest Control in the Twenty-First Century: From Simple Transgenesis to CRISPR/Cas. In: Kumar, A., Arora, S., Ogita, S., Yau, YY., Mukherjee, K. (eds) Gene Editing in Plants. 2024. Springer, Singapore. − Dubovskiy I., Grizanova E., Wang C. Chapter 2 - Physiological and Behavioral Responses of Insects to Entomopathogenic Fungi, Editor(s): Arash Zibaee, Davide Malagoli, Ivan Dubovskiy, Entomopathogenic Fungi in Insects, Academic Press, 2026, Pages 21-58, ISBN 9780443214530

Nano–Bio Synergy: Biomass-Derived Carbon Quantum Dots for Enhancing Microbial Metabolism and Biochemical Production

John Chi-Wei Lan[1*], Morgan Meng-Chien Wu[1], Kyle Kai-Yu Han[1], Sandy En-Chi Yeg[1], Annie Yi-Zhen Chiang[1], and Penny Pei-Yin Lin

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ABSTRACT: This study presents a novel nano–bio synergistic platform utilising biomass-derived carbon quantum dots (CQDs) as sustainable functional agents to enhance microbial bioprocesses. CQDs were synthesised from complex biomass feedstocks, including microalgal residues and spent brewer's grains, via facile carbonisation, enabling the valorisation of waste into high-value nanomaterials. Functioning as nanoscale electron mediators within bioelectrochemical systems, CQDs effectively stimulate microbial metabolism and cellular bioenergetics. Experimental results demonstrate that CQD supplementation significantly increases intracellular ATP levels, promotes cell growth, and enhances polyhydroxybutyrate (PHB) accumulation, achieving up to 68.13% PHB content without genetic modification. Furthermore, the study elucidates the critical role of CQD surface chemistry, where hydroxyl and carboxyl functional groups contribute to redox activity and antioxidant behaviour, thereby influencing microbial physiology. Nitrogen doping via urea improves CQD yield, dispersion, and structural uniformity, although with altered bioactivity. Overall, this work highlights the integration of nanotechnology and microbial biotechnology, supported by emerging AI-driven biorefinery frameworks, as a promising and eco-friendly strategy for sustainable waste valorisation and efficient biochemical production within a circular bioeconomy.

Keyword: Carbon Quantum Dots; Nano–Bio Synergy; Microbial Bioprocessing; Bioelectrochemical Systems; Circular Bioeconomy.

Professor John Chi-Wei Lan is a leading scholar in biochemical engineering and sustainable biotechnology, currently serving as Professor and Chair of the Department of Chemical Engineering and Materials Science and Chair of the Graduate School of Biotechnology at Yuan Ze University, Taiwan. He also serves as the President of the Biotechnology and Biochemical Engineering Society of Taiwan (BEST), where he promotes international collaboration and academic exchange in biochemical engineering and industrial biotechnology. Professor Lan received his Ph.D. in Biochemical Engineering from the University of Birmingham, United Kingdom, in 2000. He subsequently conducted postdoctoral research at Academia Sinica, Taiwan, and later held research positions at Yamaguchi University in Japan and the Industrial Technology Research Institute (ITRI) in Taiwan. Since joining Yuan Ze University in 2007, he has played an important role in advancing research and education in biochemical engineering and sustainable bioprocess technologies. His research focuses on biorefinery technologies, circular bioeconomy systems, electro-fermentation, and the development of bio-based materials. His work aims to integrate microbial biotechnology, biomass valorization, and advanced bioprocess engineering to develop

	sustainable platforms for converting renewable resources and industrial residues into high-value biochemical products. Through international collaborations across Asia and beyond, his research contributes to the advancement of low-carbon biotechnology and net-zero bioeconomy strategies. Professor Lan has published extensively in leading international SCI journals, including Bioresource Technology, Renewable and Sustainable Energy Reviews, and Biochemical Engineering Journal. His work has achieved an h-index of 33 and reflects sustained impact in the field of sustainable biotechnology. He is the recipient of several prestigious honors, including the Young Asian Biotechnologist Prize from the Society of Biotechnology Japan and the Y. S. Hsu Foundation Chair Professor Award in 2025. In addition to his academic contributions, he is also an inventor holding multiple patents and the co-founder of Lans Brewing Cooperation, demonstrating his commitment to translating biotechnology innovation into real-world industrial applications.

Next-Generation Genomic Infrastructure: Translating Population Research into Sustainable Global Impact

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ABSTRACT: Implementing equitable precision medicine requires overcoming the global bottleneck of analyzing population-scale genomic data. The Genomics Thailand (GeTH) initiative addresses this challenge through a centralized computational ecosystem. The GeTH framework manages 50,000 whole-genome sequences targeting rare diseases, hereditary cancers, and infectious diseases. These data establish the Thailand Genomic Reference (ThaiGeR). Functioning similarly to gnomAD, ThaiGeR captures the local genomic variant landscape to correct the diagnostic blind spots inherent in global reference databases. Translating this population-scale data into clinical utility relies on v@pp, a domestically engineered clinical decision support system. Functioning as a sovereign alternative to commercial platforms, v@pp integrates the post-processing of sequencing data directly with local diagnostic guidelines and the ThaiGeR allele frequency database. This integration streamlines the prioritization of etiologic mutations. Applying this system to carefully phenotyped clinical cohorts allows regional hospitals to achieve diagnostic yields of 38.9% for singletons and 52% for trios across targeted rare disease classifications. Sustaining this ecosystem requires a secure high-performance computing architecture. Centralizing these computational resources eliminates redundant institutional investments and provides equitable access to advanced bioinformatic pipelines across the healthcare system. Building upon this established foundation, the infrastructure now scales to support the Thai PanGenome (T2T) project. This next phase utilizes long-read sequencing to resolve complex structural variants and address a 5% genomic divergence from standard references like GRCh38. This comprehensive model demonstrates that rigorous computational engineering provides a concrete blueprint for precision health capacity. The resulting framework positions Southeast Asia to leverage next-generation biotechnology for sustainable global impact.

Keyword: Computational genomics, Sustainable infrastructure, Next-generation biotechnology, Precision medicine, Genomics Thailand

Dr. Sissades Tongsima is the Research Group Director of Medical Molecular Biotechnology at the National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand. He received his Ph.D. in Computer Science and Engineering from the University of Notre Dame, specializing in parallel and distributed computing. Dr. Sissades is the principal architect of Thailand's national genomic infrastructure and spearheaded the Genomics Thailand (GeTH) computational ecosystem. His research group developed v@pp, the nation's first domestic Clinical Decision Support System for genomic diagnostics. In recognition of his contributions to national health security and technological sovereignty, he received the 2025 Ajinomoto Award for Outstanding Biotechnology Research and Innovation. He also serves as an Associate Editor for the *Journal of Human Genetics*.

Effect of Carbonization Time on the Physicochemical Properties and Methylene Blue Adsorption of Biochar from Gaharu Waste (*Aquilaria malaccensis*)

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ABSTRACT: Growing concerns over pollution, resource depletion, and waste management have increased interest in biochar as an environmentally friendly adsorbent. However, the production of biochar from gaharu waste (*Aquilaria malaccensis*) remains largely unexplored, despite its availability in Malaysia. This study investigated the effect of carbonization time on the yield, physicochemical properties, and adsorption capacity of biochar derived from gaharu waste. Gaharu wood chips were oven dried and subjected to slow pyrolysis in a nitrogen atmosphere at 800 °C with carbonization times ranging from 30 to 150 min. The resulting biochar was characterized using proximate analysis, Brunauer–Emmett–Teller surface area analysis, and scanning electron microscopy (SEM). The adsorption performance was evaluated using methylene blue as a model pollutant. The results showed that increasing the carbonization time reduced the biochar yield but enhanced the fixed carbon content and pore development. The highest adsorption capacity was achieved at a carbonization time of 150 min, with a surface area of 153.11 m^2/g and methylene blue adsorption capacity of 73 mg/g. These findings demonstrate that gaharu waste is a promising biomass source for biochar production and highlight the importance of optimizing pyrolysis conditions to balance the adsorption performance and energy efficiency.

Keyword: Pyrolysis, Biochar, Gaharu waste, Methylene Blue, Adsorption capacity

Professor Ir. Dr. Juferi Idris currently serves as the Deputy Rector of Research and Industrial Linkages at Universiti Teknologi MARA (UiTM) Sarawak Branch, Campus Samarahan, Malaysia. He is a Professor in the field of bioprocess and has been actively involved in advancing research, innovation, and academic collaboration in these areas. Throughout his career, he has contributed to postgraduate supervision, research development, and international scientific engagement, as well as fostering partnerships with regional and global institutions. His work focuses on translating research into impactful and sustainable applications in line with current global needs. In recognition of his academic standing and contributions to the field, he was invited to serve as a Distinguished Speaker at the 10th Biotechnology International Congress (BIC 2026) in Bangkok, Thailand, an international platform that highlights leading experts driving next-generation biotechnology towards sustainable global impact.

Expanded Ribosomal Synthesis of Non-Standard Cyclic Backbones In Vitro

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ABSTRACT: The ribosome polymerizes L-α-amino acids into polypeptides, catalyzing peptide bond formation through aminolysis. This process is facilitated by entropy trapping within its peptidyl transferase center (PTC). In this research, we harness this capability to synthesize polymers containing cyclic motifs in the backbone. We design 26 non-canonical monomers (ncMs) with two distinct substrates: dicarboxylic esters and hydrazinoesters, each containing bifunctional moieties that undergo ring-closing reactions through multiple aminolysis reactions. Using a cell-free system that enables the consecutive incorporation of these ncMs into a growing peptide, we discover that the ribosome can produce 5- and 6-membered cyclic backbones, which have never been reported. We also demonstrate that the formation of such cyclic backbones within the ribosome is tunable by altering the substituents of dicarboxylic esters. This discovery expands the range of non-standard backbones that can be synthesized by the ribosome and motivates future research towards expanding ribosome-mediated chemistries for biopolymer synthesis.

Keyword: ribosome, cell-free systems, cyclic backbones, non-canonical amino acids.

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Selected journal publications
1. *Trend in Biotech*, accepted.
2. *Nat. Commun.* 2025, 16, 495.
3. *Nat. Commun.* 2022, 13, 6322.
4. *Adv. Mater.* 2022.
5. *Cell Systems*, 2021, 12, 593-607
6. *Nat. Commun*. 2020, 11, 4304
7. *Nat. Commun*. 2019, 10, 5097
8. *ACS Nano* 2016, 10, 8843
9. *Proc. Natl. Acad. Sci. U.S.A.* 2015, 112, 13768
10. *Nat. Commun.* 2015, 6, 8351
11. *Adv. Mater.* 2008, 20, 1523

Genome-Based Analysis and Anti-Oomycete Activity of *Priestia aryabhattai* PTKU-123 Against the Durian Pathogen *Phytophthora palmivora*

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ABSTRACT: *Phytophthora palmivora* is a major oomycete pathogen causing destructive root and stem rot in durian, highlighting the need for sustainable disease management. This study investigated the genomic characteristics and anti-oomycete potential of *Priestia aryabhattai* PTKU-123, isolated from durian orchard soil in Thailand. Among 159 bacterial isolates, PTKU-123 showed the strongest inhibition of *Ph. palmivora*, achieving 80.00% inhibition in dual culture and 78.22% using cell-free supernatant. Whole-genome sequencing revealed a 5.15-Mb circular chromosome with 5,086 coding sequences and 237 carbohydrate-active enzymes. Genome mining identified biosynthetic gene clusters associated with paeninodin, surfactin, schizokinen, carotenoids, and type III polyketide synthase, suggesting diverse bioactive potential. Crude extracts strongly suppressed *Ph. palmivora*, with 2 mg/mL achieving 82.18% inhibition, and retained activity during storage at 4 and 28 °C for 14 days. These findings demonstrate the anti-oomycete activity and genomic potential of PTKU-123, supporting its further development as a microbial resource for sustainable management of *Ph. palmivora* in durian production.

Keyword: Biological control; Durian; Genome mining; *Phytophthora palmivora*; *Priestia aryabhattai*

Assoc. Prof. Paiboon Tunsagool, Ph.D. is an associate professor at the Department of Biotechnology, Faculty of Agro-Industry, Kasetsart University, Thailand. He received his Ph.D. in Biochemistry from Prince of Songkla University. His expertise includes metabolomics, proteomics, metagenomics, microbial biotechnology, and multi-omics, with applications in agriculture, food, and biotechnology.

Liquid Fermentation Tech for Sustainable Health and Industry Advancement

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ABSTRACT: As climate pressure reshapes global food and health industries, next-generation biotechnology must convert environmental constraints into platforms for both human well-being and economic resilience. AI-assisted liquid fermentation has emerged as a cornerstone of this transition, enabling precise, low-footprint bioproduction at industrial scale. Grape King Bio Ltd. presents an integrated model in which this technology simultaneously advances functional health products, reduces resource intensity, and aligns operations with TCFD and SBTi climate frameworks. The strategy is built on a closed-loop system that pairs AI-driven precision fermentation with waste valorization and digital process management. Submerged fungal and probiotic cultivation supports functional supplements and meat alternatives that lower greenhouse gas emissions and land use compared with livestock-based production. Residues from high-value supplement fermentation are repurposed into nutrient-dense animal feed for local farmers, while real-time digital monitoring reduces batch deviation and energy consumption, contributing to a total reduction of 227,371 tonnes CO_2e in 2024. To further compress the environmental footprint, academic partnerships have introduced seawater into selected fermentation processes and coupled wastewater treatment with microbial fuel cells, removing organic pollutants while recovering electricity. By linking microbial science, digital engineering, and circular resource design, liquid fermentation offers a replicable bridge from laboratory research to sustainable global impact, delivering health-promoting products, decarbonized industrial growth, and a practical blueprint for next-generation biotechnology coupled with AI.

Keyword: AI-assisted fermentation; liquid fermentation; functional foods; circular bioeconomy; net-zero biomanufacturing

Dr. Tsung-Ju Li is a scientist working across microbe-derived nutraceuticals, AI-driven R&D, and FDA regulatory strategy, with a track record of 20+ SCIE papers, 8 patents, and 2 FDA clearances which including a New Dietary Ingredient notification and a Phase II trial approval for a MASH botanical drug. He recently developed Agentome5, an agentic pipeline that traces a strain's fermentation metabolites from secretome through to predicted clinical outcomes. Recent recognition includes the 2024 BEST Industrial Elite Award and the 2024 Nutra-Ingredients Asia Ingredient of the Year for *Hericium erinaceus*. He is Assistant Department Manager at Grape King Bio Ltd.

Evolution of Nanoparticle Assembly: Bridging Proven Encapsulation with Reconfigurable Microfluidic Platforms

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ABSTRACT: The utility of therapeutic agents—ranging from small-molecule antibiotics to monoclonal antibodies—is frequently compromised by rapid degradation and restricted intracellular access. This talk highlights the progression of our research in poly(ethylene glycol)-*block*-poly(lactide-co-glycolide) (PEG-PLGA) nanocarriers designed to overcome these barriers. Initially, we established a modified ion-pairing method to encapsulate the antibiotic ciprofloxacin, achieving sustained bactericidal activity against *Enterococcus faecalis* while maintaining high cellular viability. This platform was subsequently adapted for the intracellular delivery of anti-dengue monoclonal antibodies, where the resulting nanoparticles facilitated efficient uptake in hepatocytes and significantly suppressed viral replication by inhibiting apoptotic pathways. To transition these laboratory-scale successes toward broader translation, we conclude by introducing a reconfigurable polydimethylsiloxane (PDMS) microfluidic system. By utilizing 3D-printed modular components as a framework, this platform allows for the rapid assembly of diverse channel geometries to optimize nanoparticle formation. This modular approach provides a reproducible and scalable solution that enhances nanoparticle monodispersity and ensures controllable particle size, offering a high-fidelity, customizable pathway for the next generation of topical and intracellular drug delivery systems.

Keyword: PEG-PLGA, Nanoparticles, Microfluidics, Encapsulation, 3D-Printing, PDMS.

Nisa Patikarnmonthon, Ph.D., is a Faculty Member at the Department of Biotechnology, Faculty of Science, Mahidol University, Thailand. Her research lies at the intersection of molecular nanotechnology and biomaterial engineering. Dr. Patikarnmonthon's laboratory has established validated strategies for the nanoencapsulation of biotherapeutics, ranging from small-molecule antibiotics to monoclonal antibodies. Beyond drug delivery, her work extends to the development of advanced scaffolds for 3D cell culture and the engineering of alginate beads as microcarriers. Her current innovation involves integrating these biomaterial strategies with microfluidic systems to enhance precision, scalability, and therapeutic efficacy in nanomedicine.

Designing Impactful Nanomedicine: Bridging Scientific Discovery and Global Translation

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ABSTRACT: Biopolymer-based nanomaterials are emerging as transformative platforms to address critical challenges in the stability, delivery, and efficacy of bioactive compounds. Building upon our work on functionalized hyaluronic acid (f-HA) systems, this presentation highlights the rational design of novel biopolymers and their combinatorial nano-assemblies as enabling technologies for impactful nanomedicine. Through molecular engineering and modular assembly strategies, these biopolymers can be tailored into versatile architectures—including nanogels, and hybrid supramolecular systems—capable of encapsulating diverse bioactives such as growth factors, cannabinoids, curcumin, and plant-derived antioxidants. These nano-assemblies demonstrate high encapsulation efficiency (>80%), enhanced molecular stability, and improved biological performance through controlled release, targeted delivery, and increased cellular uptake. Importantly, this work advances design principles that bridge scientific discovery with global translation, emphasizing biocompatibility, scalability, manufacturability, and regulatory readiness. Case studies of combinatorial systems illustrate synergistic functionalities, including enhanced tissue penetration, prolonged activity, and responsive behavior under physiological conditions. Collectively, these innovations represent a paradigm shift from passive delivery systems to active, intelligent nanomaterials, accelerating next-generation nanomedicine toward global healthcare impact.

Keyword: Biopolymers; Nanomedicine; Nano-assemblies; Drug delivery; Translational biotechnology

Jittima Amie Luckanagul is an academic researcher and innovation leader in biomaterials and nanomedicine. Her research focuses on the design of advanced biopolymer-based nanomaterials for drug delivery, gene delivery, and biomedical applications. She has extensive experience in translating research into real-world impact, including founding a biotech startup and leading strategic initiatives to advance university research toward global competitiveness. Her work integrates scientific excellence with innovation ecosystem development, aiming to bridge deep-tech research with industrial and clinical applications.

CRISPR Detection for Major Diseases in Aquaculture

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ABSTRACT: CRISPR-Cas systems have revolutionized the biology by providing a highly programmable and precise platform for finding and manipulating nucleic acids. Since 2017, this technology has been increasingly adapted for nucleic acid detection, resulting in diagnostic tools that are rapid, accurate, and uniquely suited for onsite applications in resource-limited settings. This capability is crucial for the aquaculture industry, where early and proactive detection remains the most robust strategy for preventing economic losses due to infectious diseases. This presentation details the development of CRISPR-based diagnostic assays designed for the detection of critical pathogens in economic shrimp and fish, including *Enterocytozoon hepatopenaei* (EHP), infectious hypodermal and hematopoietic necrosis virus (IHHNV), yellow head virus (YHV) genotype 1, and tilapia lake virus (TiLV), among others. Furthermore, we explore innovative strategies for enhancing these platforms, including the integration of DNAzymes for colorimetric visualization, the use of photocontrolled protocols for reaction regulation, and the use of smartphone-based readouts. By combining precision with portability, CRISPR tools offer a sustainable solution for disease management in global aquaculture.

Keyword: CRISPR-Cas, Molecular Detection, Aquaculture, Diseases

Thawatchai Chaijarasphong, Ph.D., is an Associate Professor in the Department of Biotechnology at Faculty of Science, Mahidol University. He holds a B.Sc. from Stanford University and a Ph.D. in Chemistry (Chemical Biology) from University of California at Berkeley. Currently, he leads the CRISPR Technology Research Group at the Center of Excellence for Shrimp Molecular Biology and Biotechnology (Centex Shrimp). His research specializes in developing CRISPR-based tools to detect and combat major aquaculture pathogens, including YHV genotype 1, EHP, and TiLV, among others. His work on CRISPR applications in aquaculture appears in journals such as *Aquaculture* and the *Journal of Fish Diseases.*

Shaping the Future of Responsible Biotechnology in Thailand through Biosafety Education and Training

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ABSTRACT: Biosafety and biosecurity have become critical foundations for ensuring that rapidly advancing biotechnology is developed and applied responsibly. Modern recent biotechnology raises concerns related to laboratory risk management, environmental protection, and the potential misuse of biological materials associated with dual use research. International biosafety governance is guided by global frameworks developed by organizations such as World Health Organization. This presentation highlights the role of biosafety education and training in supporting responsible biotechnology development in Thailand. As biotechnology activities expand across universities, research institutes, and industry, developing a workforce with strong awareness of biosafety principles, biosecurity considerations, and responsible research practices becomes increasingly important. Particular attention will be given to biosafety challenges associated with emerging technologies such as engineered microorganisms, synthetic biology, and advanced genetic modification, as well as the integration of biosafety and biosecurity principles into biotechnology curricula and professional training aligned with international standards, national regulations, and institutional policies. Examples of biosafety capacity building initiatives from Faculty of Science at Mahidol University will be presented, including hybrid and onsite training workshops covering laboratory practices in Biosafety Level 1 and 2 laboratories, together with specialized programs for Biosafety Level 3 containment facilities. These initiatives have strengthened biosafety awareness, improved laboratory safety practices, and enabled trained participants to establish or enhance biosafety management systems within their institutions. Collectively, these efforts demonstrate how strategic biosafety education and capacity building can support responsible research practices, strengthen national biosafety infrastructure, and help shape a sustainable and globally competitive biotechnology ecosystem in Thailand.

Keyword: Biosafety and Biosecurity, Responsible Biotechnology, Biotechnology Education and Training, Laboratory Biosafety, Capacity Building

Dr. Adisak Romsang is an assistant professor in Department of Biotechnology, Faculty of Science, Mahidol University, Thailand. He is actively involved in biosafety leadership and education as Chairman of MUSC-IBC. He has served as a key trainer in numerous biosafety workshops, supporting biosafety capacity building across Thailand. His research focuses on microbial virulence and antimicrobial resistance in pathogenic bacteria, integrating biosafety principles with responsible research. He has been recognized with the Mahidol University Outstanding Teacher Award (2024).

Research and Innovation for Sustainable Waste Management in the Bio-based Economy

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ABSTRACT: Sustainable waste management is a critical challenge in advancing circular and bio-based economies, particularly in regions with abundant agricultural, food, and industrial organic residues. This work presents integrated research and innovation strategies that transform organic waste streams into renewable energy, value-added biochemicals, and bio-based resources through advanced anaerobic microbial technologies. Our research combines biocatalysis, enzyme engineering, metabolic engineering, and synthetic microbiology to develop efficient and scalable systems for waste valorization. Key efforts include microbial strain discovery, enzyme optimization, and the design of synthetic and mixed microbial consortia for enhanced organic waste degradation. These platforms enable the production of biohydrogen, methane, volatile fatty acids, and medium-chain fatty acids, as well as the bioconversion of methane and carbon dioxide into chemical precursors. A notable achievement is the isolation of *Enterococcus faecalis* VT-H1 from palm oil mill effluent, which exhibits exceptional hydrogen-producing capacity and supports the development of immobilized-cell systems successfully implemented from laboratory to pilot-scale food waste treatment. To support circular bioeconomy applications, digestates are further utilized as biofertilizers and plant biostimulants. 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 agricultural inputs, with demonstrated applications in households, schools, and municipalities across Thailand. Industrial translation is further achieved through collaborations in wastewater treatment and resource recovery, alongside commercialization via GreenGen Biotechnology. Overall, this work highlights how interdisciplinary integration of microbiology, bioprocess engineering, and circular bioeconomy concepts can deliver scalable, low-carbon solutions for sustainable waste management and real-world impact.

Keyword: Sustainable waste management; Bio-based economy; Circular bioeconomy; Waste valorization; Bioprocess innovation

Assoc. Prof. Dr. Thanyaporn Wongnate is a faculty member at the School of Biomolecular Science and Engineering, Vidyasirimedhi Institute of Science and Technology (VISTEC), Thailand. She obtained her Ph.D. in Biochemistry from Mahidol University, Thailand, and pursued postdoctoral research at the University of Michigan, Ann Arbor, USA. Her research lies at the interface of biocatalysis, mechanistic enzymology, microbial biotechnology, and circular bioeconomy. She develops microbial and enzymatic platforms for the sustainable conversion of organic waste and industrial by-products into renewable energy, biofuels, and value-added biochemicals. Her work spans enzyme engineering, anaerobic fermentation, synthetic and mixed microbial systems, and translational waste valorization technologies. She has led several interdisciplinary projects in biohydrogen production, biogas systems, green biotransformation, and sustainable waste management, with strong emphasis on real-world implementation and industrial relevance. She is the recipient of notable honors including the Taguchi Award for Outstanding Researcher (2025) and the L'Oréal-UNESCO For Women in Science Award (2019).

Synthetic Glycobiology Decoding Context-Driven O-Glycan Interactions on Mucins

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ABSTRACT: Mucins are large O-glycoproteins that form the protective mucus barrier at all wet body surfaces, where their dense and patterned O-glycans mediate critical interactions with the microbiota and the immune system. Yet how the presentation of O-glycans on mucins – their structures, clustering, and protein backbone context – encodes biological specificity remains poorly understood. Here, we present a synthetic glycobiology framework that addresses this challenge by combining precision genetic glycoengineering of mammalian cells with rationally designed glycoprotein reporters called Glycocarrier to systematically dissect context-driven interactions on mucins. Using Glycocarrier platform in glycoengineered HEK293 and CHO cells, we produce libraries of mucin-like O-glycodomain reporters bearing defined, near-homogeneous O-glycan structures for interrogation of glycan-binding interactions. Applying these reagents, we discovered that a small microbial mucin-binding module, designated X409, employs a novel recognition mechanism based on clustered saccharide patches (CSPs) – composite epitopes formed by rows of inner core monosaccharides across adjacent O-glycans. X-ray crystallography and NMR analyses revealed that X409 engages the GalNAc and galactose residues of neighboring core 1 O-glycans simultaneously, and this multivalent binding mode is unique to the clustered O-glycan context found on mucins but rarely on other glycoproteins. Importantly, this binding mode is inherently resistant to trimming of outer glycan residues by microbial glycosidases, providing a potential mechanism for sustained mucin recognition in the glycan-scavenging environment of the gut. We further show that this CSP-recognition principle extends to host immune receptors and bacterial toxins, some of which exploit repeated O-glycan cluster motifs for selective ligand engagement. Together, these findings establish that mucin O-glycans encode biological specificity through higher-order contextual arrangements, and the synthetic glycobiology toolkits provide new avenues for decoding glycan functions and engineering glycan-based biotechnologies.

Keywords: synthetic glycobiology, mucin O-glycosylation, cell-based glycan array, glycoengineering, Glycocarriers

Thapakorn Jaroentomeechai currently leads the SynGlyco Lab at the Department of Biotechnology, Faculty of Science, Mahidol University, Thailand. His research integrates synthetic biology with glycobiology to develop programmable platforms for glycoprotein engineering, focusing on cell-free protein synthesis, mammalian cell glycoengineering, and mucin O-glycobiology. He was an EMBO Postdoctoral Fellow at the Copenhagen Center for Glycomics with Prof. Henrik Clausen at the Copenhagen Center of Glycomics, and previously trained with Prof. Matthew DeLisa and Prof. Michael Jewett, where he co-pioneered cell-free glycoprotein synthesis (CFGpS) platform. He also has industry experience at Biogen in the Antibody Discovery group and has authored over 25 peer-reviewed publications.

Comparative Pretreatment of Coffee Cherry Pulp for Polyhydroxyalkanoate Production by Thermotolerant *Inquilinus* sp. CF22

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ABSTRACT: Polyhydroxyalkanoates (PHAs) are biodegradable biopolymers recognized as sustainable alternatives to petroleum-based plastics within the framework of a circular bioeconomy. This study investigated the valorization of coffee cherry pulp (CCP), a major agro-industrial residue generated during wet coffee processing, as a low-cost carbon source for PHA production by the thermotolerant bacterium *Inquilinus* sp. CF22. To enhance sugar recovery from lignocellulosic biomass, two alkaline pretreatment methods were comparatively evaluated: 5% KOH at 90 °C for 1 h in a water bath and 4% NaOH at 121 °C for 25 min under autoclave conditions. Pretreatment with 4% NaOH resulted in a higher total sugar concentration and was therefore selected for subsequent experiments. Enzymatic hydrolysis of the pretreated CCP generated a sugar-rich hydrolysate containing 68.00 g/L total sugars, predominantly glucose (59.69 g/L), along with smaller amounts of arabinose, xylose, and sucrose. Fermentation conditions were optimized using a one-factor-at-a-time (OFAT) approach by evaluating the effects of hydrolysate concentration, nitrogen source, nitrogen concentration, initial pH, and shaking speed on cell growth and PHA accumulation. The optimal conditions consisted of 10 g/L CCP hydrolysate (containing 9.74 g/L total reducing sugars) supplemented with 0.5 g/L $(NH_4)_2HPO_4$ at an initial pH of 7.2, a cultivation temperature of 45 °C, and a shaking speed of 200 rpm. Under these conditions, the maximum dry cell weight and PHA concentration reached 1.64 ± 0.07 g/L and 0.93 ± 0.02 g/L, respectively, corresponding to a PHA content of 56.7 ± 1.20 wt%. These findings highlight the potential of CCP as a renewable substrate for sustainable PHA production and support its application in agro-industrial waste valorization and bioplastic production within a circular bioeconomy strategy.

Keywords: Biorefinery; Coffee Cherry Pulp; Optimization; Polyhydroxyalkanoate; Thermotolerant bacterium

Sustainable Pretreatment of Durian Rind for Cellulose Nanofiber Extraction as a Bio-Based Reinforcement Material

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ABSTRACT: Conventional physicochemical pretreatment processes of biomass rely on high temperatures (exceeding 150 °C), which lead to high operational costs and energy demand. In this study, sustainable pretreatment strategies comparing accessible, low-energy hydrothermal autoclaving (121 °C, 0.1 MPa, 30 min) with energy-intensive steam explosion (190 °C, 1.3 MPa, 15 min) were investigated to evaluate their effects on cellulose extraction from durian rind. The pretreatments were followed by bleaching using 5 wt% peracetic acid (PAA), autoclave-assisted 5 wt% oxalic acid hydrolysis, and mechanical hand homogenization (MHH) to isolate cellulose nanofibers (CNFs). Following pretreatment and PAA bleaching, cellulose content increased to 64.88% for autoclave-derived fibers and 78.14% for steam-exploded fibers, compared with 37.58% of raw, untreated durian rind. The fibers showed high thermal stability with T_{max} of 355 °C and 360 °C, respectively, while FTIR confirmed successful removal of non-cellulosic components. Oxalic acid hydrolysis followed by MHH yielded CNFs with high crystallinity indices of 70.58% and 71.44% for autoclave-derived and steam-exploded CNFs, respectively. Morphological analysis via transmission electron microscopy (TEM) showed average fiber diameters of 36.07 nm for autoclave-derived CNFs and 37.46 nm for steam-exploded CNFs. Furthermore, the suspensions exhibited strong colloidal stability, with zeta potential values of −38.70 mV for autoclave-derived and −36.10 mV for steam-exploded CNFs. Remarkably, hydrothermal autoclaving yielded cellulose fibers and CNFs with properties comparable to those produced via steam explosion, establishing a low-energy, cost-effective strategy aligned with circular economy principles for valorizing biomass waste into high-value functional materials for bio-based reinforced composites.

Keywords: Bio-based material; Cellulose nanofibers; Durian rind; Green defibrillation; Sustainable pretreatment

Plant-Microbe Interactions for Microplastic Removal Using Mangrove-Associated Herbaceous Plants in a Hydroponic System

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ABSTRACT: Microplastic (MP) pollution in mangrove ecosystems has become a growing environmental concern, yet effective and sustainable removal strategies remain limited. This study investigated the potential of mangrove-associated herbaceous plants and rhizobacteria to remove polypropylene (PP) MPs. Five herbaceous plant species, namely *Sesuvium portulacastrum, Wedelia biflora, Acanthus ebracteatus, Acrostichum aureum L.,* and *Acanthus ilicifolius L.,* collected from a mangrove forest in Samut Sakhon Province, Thailand, were screened for their capacity to adsorb MPs by their roots. *A. aureum, A. ilicifolius*, and *W. biflora*, which showed the highest efficiency in MPs removal, were selected for investigation of PP-MPs removal in a controlled laboratory experiment using a hydroponic system for 7 days at an initial concentration of 100 mg/L of PP. Although no significant difference was observed in PP-MPs removal between *A. ilicifolius* and *A. aureum*, *A. ilicifolius* showed a higher proportion of strongly adhered particles, whereas *W. biflora* showed significantly lower removal capacity. Three rhizobacterial strains were isolated from the mangrove soil, *Pseudomonas reactans, Pseudomonas gessardii*, and *Shewanella putrefaciens* were able to grow on PP-supplemented minimal medium. All strains could produce indole-3-acetic acid and exopolysaccharides. Based on these findings, *P. gessardii* was selected for inoculation with *A. ilicifolius* under PP-MP exposure in a hydroponic system to assess effects on root adsorption and plant growth. The results showed that inoculating *P. gessardii* with *A. ilicifolius* actively removed microplastics by 17%. Combining high MPs-removing mangrove herbaceous plants with beneficial rhizobacteria could provide a promising nature-based approach for remediating microplastic contamination in mangrove coastal environments.

Keywords: Mangrove ecosystem; Microplastics; Phytoremediation; Plant-microbe interactions; Rhizobacteria

Green Extraction and Isolation of Cellulose Nanofibrils from Kiam (*Cotylelobium melanoxylon*) Wood Waste

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ABSTRACT: *Cotylelobium melanoxylon,* commonly known as kiam wood, is a hardwood composed of major polymers, including cellulose, hemicellulose, and lignin, similar to other lignocellulosic biomass. This study investigates the extraction and characterization of cellulose and cellulose nanofibrils from *C. melanoxylon* waste, using extractive-free fibers obtained after Soxhlet extraction. Cellulose was subsequently extracted and purified through a delignification and bleaching process utilizing peracetic acid, resulting in a high alpha-cellulose yield of up to 70%. The resulting purified cellulose was then transformed into CNF via mechanical treatment using high-pressure homogenization. The morphological, structural, and chemical characteristics of the initial cellulose and the final CNF were comprehensively analyzed using FTIR, SEM, TEM, and XRD. These techniques confirmed the successful removal of lignin, significantly increasing the swelling and water-holding capacity of the fibers. Additionally, the isolated CNF exhibited a stable, well-dispersed suspension with a high zeta potential of up to -40 mV and a crystallinity of 65%. The findings demonstrate that *C. melanoxylon* is an effective, sustainable source for high-value CNF production, which can then be utilized to formulate effective edible coatings that extend the shelf life of perishable products. Furthermore, the application of these bio-based materials can decrease reliance on fossil-based synthetic polymers in the food packaging sector, aligning with current efforts to valorize lignocellulosic agricultural and forestry residues

Keywords: Biorefinery; Cellulose nanofibril; Green technology; Nanomaterials; Sustainable feedstock

Investigating the Potential of Transcription Factors in Multiple Stress Tolerance: a Way Forward for Stress-Resilient Crop Plants Under Climate Change Conditions

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ABSTRACT: Climate change poses an unprecedented threat to global food security, primarily through the intensification of different stresses such as drought, salinity, heat and cold. They adversely affect plant growth, leading to substantial yield losses in crops. Recent advances in plant molecular biology have revealed that stress tolerance is a complex trait regulated by multitude of genes and pathways. To engineer plants with numerous genes is a difficult task and it is highly needed to manipulate plant genomes with transcription factors (TFs) which regulate number of down-stream genes responsible to multiple stresses. So, the research was carried out to explore the potential of MYB, DREB, MT1A, AP2, AREB and ABRE TFs to tolerate multiples stresses. The maize plants were grown under laboratory conditions and were exposed to drought, salt and heavy metal (cadmium). Expression profile of TFs was developed at various stages of plant growth. All the TFs were found to be up-regulated under drought, salt and heavy metal stress in laboratory conditions. Antioxidant and ROS activities were also monitored during the experiment. Antioxidant (CAT, SOD, and POD) and ROS (MDA and H_2O_2) activities were increased with the increase of stress conditions, showing the incidence of stress to plants. All the results were significantly different in various treatments of different stresses when compared with control plants. Our results showed the importance of TFs and their potential use in developing environment-resilient plants under climate change conditions to tolerate multiple stresses. The information may also be useful to develop a mitigation strategy and potential use of TFs in engineering plants, over-expressing TFs. These plants may further be used in various breeding programs for sustainable resilience against multiple environmental stresses.

Keywords: Antioxidant enzymes, Climate change, Multiple environmental stress, ROS activity, Stress-resilience, Transcription factors

Development and Optimization of Sustainable Fish Feed Formulations Using High-Lipid Algae Species for Aquaculture

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ABSTRACT: Aquaculture has seen huge growth in recent decades, with the growing demand in many sectors. Traditional production of fish meals is largely based on wild fish, putting pressure on an overburdened marine resource, with over 90% fully utilized or overfished. This is especially worrying given the rising production costs and serves as a strong call to action for new, more sustainable and cost-effective protein sources. Its nutritional value, good growth and harvesting characteristics make Spirulina a promising alternative. Although algae-based feeds have potential, they also have some problems with water stability and leaching of nutrients, which can lead to a rapid breakdown of algae in water and reduce feed efficiency, thereby adversely affecting water quality. Thus, in this study, an algae based feed pellet was developed using starch as a natural binder to enhance water stability and cohesion of the pellet. The harvested culture solution for microalgae was mixed with different proportions of starch, heated to gelatinize it and then shaped as pellets. Crude protein, crude lipid and moisture content were the three parameters evaluated using proximate analysis. FTIR analysis of Sample 5 showed a broad absorption peak at 3340 cm^{-1}, typical of hydroxyl (OH) groups in the presence of moisture and hydrogen bonding, and a moderate absorption peak at 1632 cm^{-1}, which could be due to oxygen-containing functional groups or water bending vibrations. Water stability tests indicated that the pellets had greater stability (cohesiveness) with increased starch and less stability (cohesiveness) with decreasing starch levels. The results indicate that it is possible to obtain a nutritionally complete and water resistant algae based aquafeed that can be optimized in terms of starch content and process conditions to provide a sustainable and economical alternative that minimizes nutrient loss and environmental damage.

Keyword: Algae, Fish, Spirulina, Protein, Pellet

Single-Site Polarity Modulation Improves the Catalytic Efficiency and Thermostability of D-allulose 3-epimerase through Flexibility–Rigidity Rebalancing

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ABSTRACT: The delicate balance between localized flexibility and global structural rigidity is often fundamental to enzymatic efficiency. Here, we demonstrate that a single point mutation (E35H) in *Arthrobacter psychrolactophilus* D-allulose 3-epimerase (ApDAEase) yields a 1.4-fold increase in catalytic efficiency compared to the wild-type, driven by a 1.3-fold decrease in K_m and a 1.1-fold increase in k_{cat}. Structural dynamics were elucidated using molecular dynamics simulations based on models generated via AlphaFold 3. The simulations revealed that the E35H substitution weakens the local hydrogen-bonding network surrounding residue 35, thereby relaxing structural constraints near the active site. Root mean square fluctuation (RMSF) analysis confirmed increased localized flexibility at residue 35, contrasted with a reduction in overall structural fluctuations, suggesting a more stabilized global scaffold. Additionally, a newly identified interaction between E152 and the substrate's O1 atom provides a supplementary anchoring effect. Circular dichroism (CD) spectroscopy and thermal unfolding assays confirmed a modest increase in thermostability, elevating the melting temperature from 92.6 °C in the wild-type to 94.3 °C. Ultimately, these results identify residue 35 as a key functional hotspot where polarity shifts successfully recalibrate the flexibility-rigidity balance, offering critical mechanistic insights into the catalytic enhancement of ApDAEase.

Keyword: D-allulose 3-epimerase, *Arthrobacter psychrolactophilus*, rational mutation, catalytic activity, thermostability.

Development of Oil in Water Emulsion Formulations to Enhance the Efficiency of Vitamin D3 Encapsulation

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ABSTRACT: Vitamin D_3 deficiency remains a global public health concern. Vitamin D_3 plays an essential role in calcium regulation and bone health. Beyond these roles, inadequate vitamin D_3 status has been associated with type 2 diabetes, cardiovascular disease, and mental health disorders. However, vitamin D_3 is sensitive to factors such as light, heat, and oxygen, which may cause degradation during processing and storage. Oil-in-water emulsions are used as delivery systems to improve the stability of lipophilic bioactive compounds. In this study, oil-in-water emulsions containing 0.025 g of vitamin D_3 dissolved in rice bran oil were prepared using emulsifier systems to investigate emulsion stability. The formulations contained a high level of lecithin (F1), a low level of lecithin (F2), wall materials (Arabic gum, Hi-Cap® 100, and maltodextrin) without an additional emulsifier (F3), Tween 80 (F4), and pea protein hydrolysate (F5). The wall-material concentration was fixed at 20% (w/w) in all formulations. The high-lecithin formulation exhibited phase separation after pH adjustment and was therefore excluded from processing. The remaining formulations were processed by high-pressure homogenization and spray drying to produce vitamin D_3 microcapsule powders. The emulsions were evaluated for visual appearance and viscosity, while the powders were evaluated for solubility and encapsulation efficiency. High-pressure homogenization increased the viscosity of F2, F3, and F5, whereas F4 showed only a small change. During the short-term visual stability test, F3 showed the smallest visible change. Powder solubility ranged from 67.28 to 80.52%, with F3 showing the highest value. All powders exhibited high encapsulation efficiency, ranging from 99.61 to 99.82%, with no significant differences among the formulations. F3 combined the highest numerical solubility with encapsulation efficiency comparable to the other formulations without requiring an additional emulsifier. These findings suggest that the wall materials provided an emulsifying effect and that F3 is a promising formulation for further development.

Keyword: Vitamin D_3, Spray Drying, Emulsifier and Encapsulation Efficiency

Application of Ohmic Heating Pretreatment to Accelerate the Aging Process and Modulate the Bioactive Profile of Black Shallots

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ABSTRACT: Shallot (*Allium ascalonicum* L.) is a widely consumed Allium vegetable containing bioactive compounds, particularly phenolic compounds and flavonoids, which contribute to its antioxidant properties. The production of black shallot through controlled aging induces physicochemical and biochemical transformations, including the formation of reducing sugars and Maillard reactions, which contribute to its characteristic color, flavor, aroma, and functional properties. However, conventional black shallot production requires approximately 15 days of aging, resulting in extended processing time, high energy consumption, and increased production costs. This study investigated the application of ohmic heating as a pretreatment to facilitate biochemical transformations and shorten the aging period. Fresh shallots were subjected to ohmic heating at 60, 70, and 80°C for 15, 30, and 60 min, with the applied voltage varying between 90 and 120 V to maintain the target temperature, before aging. Ohmic pretreatment significantly increased reducing sugar content, while no significant differences were observed in total phenolic content (TPC), total flavonoid content (TFC), or antioxidant activity compared with untreated shallots. Following aging, ohmic pretreated shallots produced black shallots within 9 days, representing a 40% reduction in aging time compared with the conventional 15 days process, while maintaining comparable TPC, TFC, and antioxidant activity. These findings suggest that ohmic pretreatment enhances the availability of reducing sugars, potentially facilitating subsequent biochemical transformations during aging and shortening the aging period while maintaining the chemical properties of conventionally produced black shallot.

Keyword: Antioxidant activity, Black shallot, Ohmic heating and Reducing sugar

Evaluation of the Protective Effects of an Energy- and Electrolyte-Enhanced Mulberry Beverage Against Delayed Onset Muscle Soreness Through Redox

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ABSTRACT: Intense physical exercise promotes excessive generation of reactive oxygen species (ROS), leading to oxidative stress that damages muscle cells, triggers inflammation, this not only causes delayed onset muscle soreness but also impairs post-exercise recovery. This study aimed to evaluate the potential of an anthocyanin-rich mulberry beverage supplemented with energy sources and electrolytes to protect against DOMS by examining its antioxidant properties and redox-regulating mechanisms under oxidative stress conditions in C2C12 skeletal muscle cells. Mulberry aqueous extract was characterized for its antioxidant activity and phytochemical composition, focusing on free radical scavenging activity by the Ferric Reducing Antioxidant Power (FRAP), 2,2′-azinobis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) assays, total phenolic content, total flavonoid content, total anthocyanin content, and total soluble carbohydrate content. The extract was then formulated into a sports beverage by incorporating energy substrates and electrolytes. The protective activity of the final product was subsequently evaluated using a hydrogen peroxide (H_2O_2)-induced oxidative stress model in C2C12 myoblasts. The result showed that mulberry extract contained total anthocyanin content of 678.25 mg C3G/L, ABTS VCE of 0.00621 mg/mg, FRAP VCE of 0.648 µg/mL, total phenolic content of 1.12 mg GAE/mL and total flavonoid content of 0.00230 mg CE/g. The formulated post-exercise recovery beverage retained anthocyanin at 645.41 mg C3G/L, ABTS VCE of 0.00605 mg/mg, FRAP VCE of 0.609 µg/mL, total phenolic content of 0.99 mg GAE/mL and total flavonoid content of 0.00218 mg CE/g. These findings demonstrate that both the mulberry extract and the formulated post-exercise recovery beverage retained substantial levels of anthocyanins and exhibited antioxidant activity, suggesting their potential to alleviate exercise-induced DOMS. However, further cellular studies are required to confirm their protective effects and underlying mechanisms.

Keyword: Anthocyanins, Delayed Onset Muscle Soreness, Mulberry, Redox Homeostasis, Sports Beverage

Physicochemical Characterization and 2D *In Vitro* Wound Healing Evaluation of a Novel Tripeptide

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ABSTRACT: Chronic and non-healing wounds impose a substantial healthcare burden. Therapeutic peptides have emerged as promising bioactive agents capable of regulating key regenerative processes; however, the clinical application of longer and structurally complex peptides is often limited by rapid degradation, short half-life and poor bioavailability. Increasing attention has been directed towards short therapeutic peptides with minimal yet strategically designed amino acid sequences that retain biological activity while offering improved stability, simplified design and cost-effectiveness. In this study, a novel synthetic Lysine-Arginine-Isoleucine (Lys-Arg-Ile; KRI) tripeptide, designed from a minimal bioactive motif of the human cathelicidin antimicrobial peptide LL-37, was evaluated for its regenerative potential using a two-dimensional (2D) *in vitro* wound healing model. The physicochemical characteristics of the tripeptide were determined using high-performance liquid chromatography (HPLC), electrospray ionization mass spectrometry (ESI-MS), fourier-transform infrared spectroscopy (FTIR) and circular dichroism (CD) to assess the peptide purity, molecular weight, functional groups and secondary structure, respectively. The tripeptide exhibited high purity (>98%) by HPLC, an observed molecular weight of approximately 415 Da by ESI-MS, characteristic amide absorption bands by FTIR and a predominantly random coil secondary structure as determined by CD analysis. Dose-dependent evaluations were subsequently performed on human dermal fibroblasts (HDFs) using MTT, live/dead staining, and wound scratch assays to assess proliferative, cytocompatibility, and migratory effects, respectively. The tripeptide exhibited concentration-dependent activity, with 12.5-50 µg/ml promoting fibroblast viability and migration, while concentrations exceeding 100 µg/ml reduced cell viability. Live/Dead staining demonstrated 90-100% viable cells with minimal cell death at 12.5-50 µg/ml across 24 to 72 hours, whereas 100 µg/ml reduced viability to 74-89% with increased dead cells. Wound scratch assays further showed complete wound closure at 12.5-50 µg/ml after 24 hours, exceeding the untreated control (97.08%) and 100 µg/ml group (90.89%). Collectively, these findings support the KRI tripeptide as potential short peptide candidate for wound healing applications.

Keyword: Cytocompatibility; Physicochemical characterization; Short peptides; Wound healing

Effect of Peptide Sequence Length on the Physicochemical Properties and Biological Performance in Hyperglycaemic Wound Healing

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ABSTRACT: Hyperglycaemic wound healing, characterized by dysregulated tissue regeneration, persistent inflammation and elevated susceptibility to infection, remains a major healthcare challenge due to the limited therapeutic efficacy of current treatment approaches. Antimicrobial peptides (AMPs) represent promising biomolecular candidates for hyperglycaemic wound healing applications due to their multifunctional properties, including wound reepithelization and collagen synthesis activation, immunomodulation, antimicrobial activity and vascular regeneration. However, the relationship between peptide sequence length and biological functionality remains insufficiently characterized. This study evaluates the influence of peptide length on the physicochemical properties and biological performance of LL-37-derived peptides under hyperglycaemic wound conditions. The long (LL-37), medium (RI-10) and novel short peptides (KRI) were characterized with HPLC, LC-MS and FTIR to investigate sequence-dependent structural variation. All peptides recorded a high purity (≥ 98%) with their molecular weight successfully identified (LL-37: 4493 Da; RI-10: 1273 Da; KRI: 415 Da). The functional groups of the peptides were successfully characterized. The hyperglycaemic condition was induced in human dermal fibroblasts (HDFs) using high-glucose DMEM for at least three passages. Hyperglycaemic induction in HDFs was confirmed through morphological observations and senescence assays, where HDFs displayed elongated morphology and increased SA-β-Gal staining, indicating cellular senescence. The MTT, Live/Dead cell viability and scratch assays were conducted to assess the proliferative, cytotoxic and migratory effects of different sequences of peptides on hyperglycaemic HDFs, respectively. The short peptide exhibited no cytotoxicity and enhanced cellular proliferation at concentrations up to 12.5 µg/mL, with 98% live cells retained at 100 µg/mL, whereas the longer peptides demonstrated cytotoxic effects at concentrations above 100 µg/mL. Following that, all peptides showed a concentration-dependent migratory effect from 12.5 to 100 µg/mL on hyperglycaemia-induced HDFs. The findings demonstrate that peptide sequence length plays a critical role in determining the physicochemical properties of peptides. Ultimately, this research may contribute to the rational design and optimization of peptide-based biomaterials and therapeutic platforms for hyperglycaemic wound applications.

Keyword: Hyperglycaemic wounds, Antimicrobial peptides, Peptide sequence, Physicochemical characteristics, Biological properties

Cellulase-Assisted Enzymatic Remodeling of Bacterial Cellulose as a Scaffold for Tissue Engineering Applications

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ABSTRACT: Bacterial cellulose (BC) is a natural polymer synthesized by various bacteria. Notably, BC produced by *Komagataeibacter xylinus* has attracted considerable attention as a scaffold material for tissue engineering applications due to its outstanding physicochemical and biological properties, including high porosity, excellent water-holding capacity, biocompatibility, non-cytotoxicity, and a unique nanoscale fibrous structure. However, the direct use of native BC as a scaffold is limited by its densely entangled fiber structure, which restricts cell adhesion, migration, and proliferation. The objective of this study is to structurally modify BC using cellulase treatment in order to loosen the fiber network and increase surface area, thereby improving its suitability for cell attachment and migration. Surface morphology and structure was examined using scanning electron microscopy (SEM). Scaffold porosity was evaluated using a liquid displacement method. Crystallinity index was analyzed using wide angle x-ray scattering (WAXS). In addition, cytotoxicity and cell viability was assessed using the MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium) assay. Results stated that BC modified with cellulase exhibited an increase in the porosity and results in 97.0103, 97.9861 and 98.7270 of BC control, BC3 and BC6 respectively. The swelling ratio of scaffold showed an increase of 2,532, 3,332 and 4,376 of BC control, BC3 and BC6, respectively. SEM analysis revealed a progressively loosened fiber structure with increasing cellulase concentration. The evaluation of cytotoxicity and cell proliferation indicated that the cell viability was above 70 and 80% in both BC control and cellulase-treated, demonstrating that the modified BC scaffolds provide a more favorable environment for cell growth. These modified BC scaffolds will serve as a prototype biomaterial with a loosened fibrous architecture, effectively overcoming the structural limitations of native BC. Ultimately, the findings of this study are anticipated to provide a fundamental basis for further development of bacterial cellulose-based scaffolds for tissue engineering applications.

Keyword: Bacterial cellulose, Cellulase, In-situ modification, Scaffold, Tissue engineering

Recombinant Fibrinolytic Proteins: Production, Isolation and Application of 'Recombinant Lumbrokinase' Against Chemically Induced Thrombosis in Mice

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ABSTRACT: Cardiovascular Diseases (CVDs) have become the most leading cause of mortality. Certain factors like smoking, diabetes, lifestyle, high blood cholesterol, socio-economic stresses, age and inheritance may contribute as risk factors for CVDs. Various medicines including blood thinners, Beta blockers, ARBs, vasodilators, Calcium Channel blockers, Cholesterol-lowering drugs and fibrinolytics are frequently used. Fibrinolytic therapy is mostly devised in the cases of acute Myocardial Infarction (MI) and Stroke. Potent fibrinolytic agents as streptokinase, tissue Plasminogen activator, reteplase, urokinase and nattokinase are being administered in different areas of the world. Various drawbacks are associate with fibrinolytics including systemic lysis, hypotension, hypertension and high cost. To cover up the reported disadvantages, a novel fibrinolytic protein from the intestinal lining of earthworms has been identified and named as Lumbrokinase (LK). Here we report the expression, isolation and functional characterization of recombinant LK-6 in *E. coli*. For this purpose, codon optimized gene of LK-6 was expressed in strain BL21. Expression and the molecular size of LK-6 around 31KDa was confirmed by SDS-PAGE. rLK-6 was then purified using column chromatography and tested for its activity. Whole blood clot lysis assay showed the fibrinolytic activity of purified LK-6 to be 65%. It was active over a broad range of temperature (25° C to 50°C) and pH (3-9). *In-vivo* studies in mice confirmed the fibrinolytic activity of rLK-6 and showed 64% reduction in clot as compared to non-treated groups. PT, APTT and TT readings also indicated that rLK-6 has increased blood clotting time.

Keyword: Heart Diseases, Strokes, Fibrinolysis, Biopharmaceuticals.

Evolution of *Bacillus thuringiensis* Virulence During Passage through the Resistant and Susceptible Host

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ABSTRACT: *Bacillus thuringiensis* is one of the most common sources of biopesticide and gene modified crops used for pest management in the world. However, reduction or loss of virulence, morphological differentiation of *B. thuringiensis* when cultivated on an industrial scale, as well as the formation of pest populations resistant to biological insecticides, is a relevant area of research that requires the attention of scientists. Many cases of insect's resistance to *B. thuringiensis* were registered last decades. We experimentally selected a *Galleria mellonella* line over 40 generations for resistance against *B. thuringiensis*. The *B. thuringiensis* subsp. *galleriae* infection in susceptible and resistant populations of wax moth larvae was investigated to gain further insight into the "arms race" between *B. thuringiensis* virulence and insect defences. We found that a sub-population of highly virulent *B. thuringiensis* could survive in the resistant insects by disrupting the midgut microbiome and switching rapidly to a necrotrophic strategy, prior to sporulation in the cadaver. Arm race between virulence factors of *B. thuringiensis* and insect resistance is interesting example of coevolution in the field. Sequential passage, and isolation, of *B. thuringiensis* through resistant insects for developing highly virulent strains will be discussed in context of applied biotechnology for improvements of biological preparations.

Keyword: *Bacillus thuringiensis,* passages, virulence, biological pest control

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Encapsulation of Anti-Dengue Virus NS3 Monoclonal Antibody in PEG-PLGA Nanoparticles for Intracellular Delivery

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ABSTRACT: Dengue fever, an infectious disease caused by dengue virus (DENV), remains a significant global health challenge with no specific antiviral treatment available. The non-structural protein 3 (NS3) of DENV plays an essential role in viral replication, making it an attractive therapeutic target. Among potential therapeutic approaches, antibodies could play a vital role in reducing disease severity by targeting and neutralizing specific viral components. We hypothesize that antibody-mediated neutralization of viral components within the intracellular environment could lead to a significant reduction in viral production. However, delivery of antibodies to intracellular targets is hindered by their inability to cross the plasma membrane and their susceptibility to intracellular degradation. In this study, anti-DENV NS3 monoclonal antibody was encapsulated within poly (ethylene glycol)-*block*-poly(lactide-*co*-glycolide) (PEG-PLGA) nanoparticles using a solid-in-oil-in-water (S/O/W) emulsion method. Prior to encapsulation, the anti-NS3 mAb demonstrated specific reactivity to DENV NS3 protein across all four serotypes by showing a single band at approximately 70 kDa by Western blot. The resulting nanoparticles exhibited a hydrodynamic diameter of 106.7 ± 1.6 nm with acceptable polydispersity index (PDI < 0.2), a negatively charged surface, and an encapsulation efficiency of 28.79%. Transmission electron microscopy confirmed spherical morphology. Cytotoxicity assessment in immortalized hepatocyte-like cells (imHC) by MTT assay showed that all antibody-loaded nanoparticles formulations maintained cell viability above 70%, although additional biological replicates are required for further validation. Cellular uptake analysis demonstrated efficient and concentration-dependent intracellular internalization of the antibody-loaded nanoparticles in imHC cells, indicating effective intracellular delivery of the encapsulated antibody. These preliminary results suggest that PEG-PLGA nanoparticles represent a promising carrier platform for intracellular antibody delivery targeting non-structural viral proteins in dengue-infected cells.

Keywords: Dengue Virus; Polymeric Nanoparticles; PEG-PLGA; Monoclonal Antibody; Intracellular Delivery

Development and Evaluation of a Pumpkin Seed-Enriched Functional Cream Cheese for Modulating Risk Factors of Polyendocrine Metabolic Ovarian Syndrome

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ABSTRACT: Polyendocrine Metabolic Ovarian Syndrome (PMOS) is a complex endocrine and metabolic disorder associated with insulin resistance, oxidative stress, chronic inflammation, and hormonal imbalance. Dietary approaches incorporating nutrient and bioactive-rich foods have garnered substantial attention for mitigating metabolic dysfunction. Pumpkin seeds (*Cucurbita pepo*) emerge as a promising functional matrix owing to their dense nutritional profile and naturally occurring bioactive compounds. However, their application in fermented plant-based dairy alternatives remains limited. This study aimed to develop a fermented pumpkin seed-based cream cheese via lactic acid bacteria inoculation and evaluate its physicochemical, textural, and sensory characteristics as an initial step toward functional food development. Fermentation with 0.1% (w/w) Lyofast SYAB 1 yielded a final product pH of 4.1 within 6 h. Texture profile analysis showed a firmness of 5.190 ± 0.966 N and adhesiveness of 9.629 ± 1.481, indicating suitable spreadability. Just-About-Right evaluation (N=50) showed that while appearance (64%), aroma (62%), and texture (60%) reached satisfactory acceptance, flavor (38%) and cream cheese similarity (46%) fell below the benchmark. This indicates a critical need for formulation refinement to attenuate flavor intensity and enhance core cream cheese identity. These findings demonstrate the feasibility of developing a fermented pumpkin seed cream cheese with baseline properties. As this study did not quantify bioactives or evaluate PMOS-related biological activities in the final matrix, further research is required to characterize its precise bioactive profile and investigate its metabolic efficacy before its potential relevance to PMOS management can be established.

Keyword: Functional Food, Lactic Acid Bacteria, Plant-Based Cream Cheese, Polyendocrine Metabolic Ovarian Syndrome (PMOS), Pumpkin Seed

Fecal Microbiota Alterations Induced by Triphala Extract

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ABSTRACT: Diabetes mellitus is associated not only with impaired glucose metabolism but also with alterations in gut microbiota composition and microbial metabolic activity. Gut microbial imbalance may affect host metabolism through microbial metabolite production and nutrient utilization, suggesting that modulation of the gut microbiota could help support metabolic health in diabetic patients. This study investigated the potential of Triphala extract to modulate gut microbiota using a human gut model. Triphala extract, composed of *Terminalia chebula*, *Terminalia bellirica*, and *Phyllanthus emblica*, was tested in an *in vitro* fermentation of a human gut model inoculated with fecal microbiota from a diabetic female donor. Fermentation was conducted for 48 h with and without Triphala supplementation, followed by DNA extraction and shotgun metagenomic analysis to assess changes in microbial composition. At the phylum level, Triphala extract treatment was associated with a marked increase in Pseudomonadota from 2.89% to 51.04%, while Bacillota decreased from 49.01% to 22.99% compared with the control group. At the genus level, *Hungatella*, *Agathobaculum*, and *Bacteroides* showed higher relative abundance or better retention following Triphala treatment. These genera are known to contribute to beneficial gut metabolic activities, including complex carbohydrate degradation, short-chain fatty acid production, particularly butyrate, and maintenance of gut barrier function. In contrast, *Enterococcus* and *Clostridium* were reduced following Triphala extract treatment compared with the control. The reduction of *Enterococcus* and *Clostridium* may indicate decreased levels of potentially opportunistic bacteria and reduced risk of bacterial overgrowth associated with gut disturbance. Overall, these findings indicate that Triphala extract may contribute to restoring gut microbial balance and provide preliminary support for its potential use as a functional ingredient to modulate gut microbiota and metabolites in diabetic patients.

Keywords: Diabetes mellitus; fecal microbiota; *in vitro* human gut model; Triphala extract

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In Vitro Activity of a Co-Eluted Amphiphilic Crude Mixture Obtained from *Priestia aryabhattai* PTKU-123 Against *Phytophthora palmivora*

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ABSTRACT: To address the need for alternatives to chemically synthesized fungicides, this study explored the extraction and enrichment of amphiphilic crude mixture from *Priestia aryabhattai* PTKU-123 to evaluate their anti-oomycete potential against the plant pathogen *Phytophthora palmivora*. The fermentation broth was precipitated and harvested to obtain the unrefined extract. Following with the enrichment process using preparative thin-layer chromatography and solid-phase extraction, an unresolved co-eluted fraction was recovered. Post-hydrolysis gas chromatography-mass spectrometry analysis identified this as an amphiphilic crude mixture, revealing a dominant β-hydroxy fatty acid-linked constituent at a 68.6% relative abundance alongside other co-migrating variants. When tested at a low concentration of 200 mg/L, this co-eluted crude mixture exhibited exceptional anti-oomycete activity, inhibiting mycelial growth by 95.55%, which demonstrated an increase in potency compared to the unrefined extract. Additionally, the fraction demonstrated thermal stability whilst retaining their potent anti-oomycete properties even after 28 days of continuous exposure to 50 °C. These active, naturally co-eluting compounds may represent as promising candidates for developing effective bio-pesticides to manage oomycete diseases in tropical agriculture.

Keyword: Anti-oomycete activity; bio-pesticide; co-elution; *Priestia aryabhattai*; *Phytophthora palmivora*

Co-Solvent-Driven Structural Engineering of Rice Bran Oil-Based Oleogels Through Multidimensional Characterization: Advancing Solid Fat Mimetics in Food Biotechnology

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ABSTRACT: The transition towards the use of trans-fat-free solid fats obtained from plants is one of the key objectives in the field of food biotechnology. Herein, the implementation of nutrient-rich agricultural products, such as rice bran oil (RBO), and designing them in the form of oleogels provides an effective strategy in the preparation of desirable lipids. In this study, polyethylene glycol (PEG 200) has been used as a crystal habit modifier (CHM) in stearic acid and RBO-based oleogels. The formulations with PEG 200 (0-10% w/w) have been prepared through a systematic process of heat-cool treatment. Subsequently, various analytical techniques such as microscopy, colorimetry, visible reflectance spectroscopy, and hyperspectral imaging (HSI) have been used to analyze the underlying structure–property relationships. Microstructural analysis has demonstrated that PEG 200 at a concentration of 1.25% w/w has induced a significant morphological change from one-dimensional (1D) needle-like structures to highly branched crystalline networks. As the concentration of the CHM was increased, it was observed that needle-like morphologies reappeared in the intermediate concentrations (2.5%-7.5% w/w) along with an increase in the density of the oleogel matrices. Specifically, the formulation P200-1.00 (5% w/w PEG) had shown an optimal structural balance wherein an increased scattering of short wavelengths (blue band) had occurred owing to the highly interconnected solid matrix. HSI resulted in a spatial analysis that confirmed this optical alteration with a distinct and concentrated cluster of high scattering domains within the 5% w/w PEG formulation observed at 450 nm. This strong local scattering created an effective ‘umbrella’ over the endogenous RBO carotenoid pigments, thereby imparting a large increase in the macroscopic whiteness needed to successfully mimic solid fats. Conversely, incrementing the PEG concentration to 10% w/w led to a structural breakdown of fat crystals into bulky agglomerates. Therefore, the formulation with 5% w/w PEG 200 showed an optimal balance between network density and the whiteness required for solid fat formulation, thus emphasizing the potential of co-solvent engineering of natural lipids as value-added food ingredients for the development of functional foods.

Keywords: Oleogels; Crystal habit modification; Hyperspectral imaging; Solid fat mimetics; Food biotechnology.

Multiscale Investigation of Pectin-Mediated Structural Reinforcement and Shelf-Life Enhancement in Whole Wheat Bread

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ABSTRACT: Development of functional whole wheat bread (WWB) with improved quality and extended shelf-life remains a significant challenge in the bakery industry. This study has focused on understanding the influence of incorporating pectin in WWB for the purpose of examining the changes in physicochemical, microstructural, textural, and shelf-life characteristics of the WWB formulations. Varying pectin concentrations have been employed to develop the formulations, which have been designated as SP0 (control), SP1 (1% w/w), SP2 (2% w/w), SP3 (3% w/w), and SP4 (4% w/w). Pectin incorporation has significantly enhanced the quality of bread in a concentration-dependent manner. Upon addition of pectin, loaf volume increased from 807.64 cm^3 (SP0) to 1112.10 cm^3 and 1194.22 cm^3 in SP3 and SP4, respectively. However, SP3 and SP4 exhibited significant improvement in architecture and a finer and more uniform crumb. This change in architecture may be attributed to enhanced gas retention and increased dough stability caused by the incorporation of pectin. Further, the texture profile analysis has also shown a substantial crumb softening following pectin addition. Herein, the hardness of the crumb decreased from 1134.14 g in SP0 to 295.00 g and 272.62 g in SP3 and SP4 formulations, respectively. Moreover, stress-relaxation analysis also showed enhanced viscoelasticity and elastic recovery, indicating the development of a flexible network mediated by hydrocolloids. Additionally, sensory evaluation was conducted to validate the findings, and the results showed that SP4 got the highest texture and overall acceptability score (3.94 0.89). Based on the overall improvements in loaf volume, crumb structure, texture, sensory properties, and the efficiency of ingredient utilization, SP3 (3% w/w pectin) was selected as the optimum formula, achieving comparable results to SP4 at a lower concentration of pectin. Shelf-life studies have demonstrated that SP3 and SP4 formulations maintained freshness and were more structurally stable during storage. In this study, a clear link has been made between the microstructure induced by pectin, viscoelastic properties, sensorial characteristics, and storage properties. An attempt has been made to prove that pectin is a structure modifier that can improve bread quality parameters, including loaf volume, crumb texture, consumer acceptance, and storage properties, in a simultaneous way, while 3% (w/w) pectin was the optimum amount.

Keywords: Whole wheat bread; Pectin; Hydrocolloid; Sensory analysis; Shelf-life; Functional foods.

In-Silico Evaluation of *Moringa oleifera* and *Solanum americanum* Phytochemicals to Protect Red Blood Cell Membrane in Haemolytic Anemia: A Network Pharmacology Approach

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ABSTRACT: Disorders affecting red blood cell (RBC) membrane integrity, including sickle cell disease, stem from cytoskeletal destabilization and oxidative stress, resulting in haemolysis and reduced erythrocyte deformability. Although these conditions impact approximately 7–8 million individuals worldwide and significantly contribute to morbidity and mortality in endemic regions, effective multi-target therapeutic strategies remain scarce. In this study, we employed an integrative approach combining network pharmacology and molecular modeling to systematically evaluate the therapeutic potential of phytochemicals derived from *Moringa oleifera (MO) and Solanum americanum (SA)*. From an initial set of 178 bioactive compounds, subsequent ADME profiling, QSAR filtering, and density functional theory (DFT) optimization led to the identification of nine promising lead candidates. Target prediction analyses revealed 853 drug–protein interactions, with 10 intersecting disease-associated proteins. Protein–protein interaction network topology and enrichment analyses highlighted three key hub regulators of membrane stability: SLC4A1 (4YZF), EPB42 (7UZS), and ALAS2 (5QQR). Molecular docking and molecular dynamics simulations demonstrated highly stable ligand–protein complexes, exhibiting binding affinities up to −9.5 kcal/mol for notable phytoconstituents, including gossypetin, apigenin, luteolin, and hesperetin. These results suggest that these four bioactive compounds may serve as potential therapeutic agents for sickle cell anemia and related hemolytic disorders. Further *In-Vitro* and *In-Vivo* validation is required for the therapeutic's applications of the screened molecules. This study is exclusively *In-Silico* in nature.

Keywords: *Moringa oleifera*, Network pharmacology, Molecular docking, Molecular dynamics, RBC Membrane integrity.

Characterization, Purification and Media optimization of *S. cerevisiae* BHF5D35-2Δ*Ade*2 for Superoxide Dismutase Production

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ABSTRACT: Superoxide dismutase (SOD) is a potent antioxidant enzyme with growing demand as a bioactive ingredient in cosmetic and nutraceutical industries. As SOD in Thailand is predominantly imported, this study aimed to establish a domestic production platform by developing and characterizing a bioreactor-scale process for recombinant SOD using an engineered *Saccharomyces cerevisiae*. A chemically defined medium comprising yeast extract (15.0 g/L), ammonium nitrate (10.0 g/L), and glucose (10.0 g/L) was optimized for SOD production. Fed-batch fermentation in a 2 L bioreactor at 30°C, 200 rpm, and 1 vvm aeration over 24 h yielded a final cell density of OD_{600} = 27.132, with stationary phase onset at 18 h. The maximum SOD activity of 813.14 U/mL was observed at 12 h during the exponential growth phase, declining to 443.50 U/mL by 24 h due to proteolytic degradation. Purification by immobilized metal affinity chromatography (IMAC) via fast protein liquid chromatography (FPLC) yielded a specific activity of 9,691.38 U/mg. SDS-PAGE confirmed a protein band at approximately 32 kDa, consistent with the predicted molecular weight of SOD. Biochemical characterization revealed optimal activity at pH 8.0 in Tris-HCl buffer (717.93 ± 12.93 U/mL) and 30°C (695.20 ± 14.66 U/mL). Stability assays demonstrated highest residual activity under alkaline conditions (pH 8–9; up to 753.10 ± 12.23 U/mL), while the enzyme was thermolabile above 45°C with complete inactivation at 50°C within 1 h. These findings establish a viable laboratory-scale platform for recombinant SOD production and purification with well-defined biochemical properties, providing a foundation for process scale-up and further formulation with delivery systems for cosmeceutical applications.

Keyword: Superoxide dismutase, Antioxidant enzyme, Recombinant, *Saccharomyces cerevisiae*

SPIDERS DETECH: An AI Innovation for Classifying Spider Species via a LINE Chatbot

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ABSTRACT: In our environment, arachnids are commonly found, and some species can be dangerous. However, many people are unable to identify different spider species or respond appropriately when encountering them. Therefore, we developed an AI-based system to promote awareness and understanding of the danger levels associated with spiders. Our project focuses on detecting and classifying five common spider species: Brown Recluse, Black Widow, Cellar, Jumping, and Huntsman spiders. The system not only identifies spider species, but also provides information about danger levels, safety responses, and educational knowledge regarding dangerous arachnids commonly found around homes. Several deep learning models were tested, including VGG16, Xception, EfficientNetB0, and ResNet50. The models were trained using a dataset of 532 images across five classes, consisting of 306 training images, 124 validation images, and 102 testing images. Among the tested models, ResNet50 achieved the highest F1-score of 0.96, followed by EfficientNetB0 with 0.95, Xception with 0.91, and VGG16 with 0.86. Each model was trained for 30 epochs to achieve optimal performance. The system was developed using Python on Google Colab, while the "LINE" application serves as the main platform for user interaction. Heatmaps are also used to display important features detected by the AI. Users can upload a spider image through the "LINE" app, and the AI automatically provides the species name, confidence score, danger level, heatmap, and cautions. In the future, we aim to expand the dataset, improve accuracy, and provide more detailed warnings and safety recommendations regarding dangerous spiders.

Keyword: Arachnid Safety Awareness, Deep Learning, Image Recognition, LINE Chatbot, Spider Species Classification

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A Deep Learning-Based Smartphone Solution for Thai Jasmine Rice Quality Assessment

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ABSTRACT: Thai Jasmine rice (*Oryza sativa L.*) is globally renowned for its premium quality, long slender grains, and distinctive aroma, making it both a staple food and a major export commodity for Thailand. However, quality degradation from broken grains, chalky kernels, and discolored grains—whether from adulteration, improper storage, or poor processing—compromises national standards, market value, and consumer health. While precise quality assessment exists in large-scale laboratory facilities, everyday consumers, small restaurant owners, and local vendors lack accessible, affordable tools for real-time quality verification. This study addresses this gap by developing a smartphone-based rice quality assessment system integrated with a LINE Official Chatbot, enabling instant quality evaluation without specialized equipment. A custom dataset of 506 images was compiled from curated internet sources and categorized into four classes: Perfect (117 images), Broken (174 images), Brown/Yellow (112 images), and Chalky (103 images), aligned with internationally recognized defect criteria established by the International Rice Research Institute (IRRI) and ISO 7301 standards. Broken grains (fragments <75% of whole kernel length) reduce commercial value and cooking quality; chalky grains (kernels with ≥50% opaque area) result from incomplete starch gelatinization, affecting texture and palatability; and yellow-brown discolored grains indicate heat damage or fungal contamination, historically linked to mycotoxin health risks. The dataset was split into training (306), validation (101), and testing (99) sets. To overcome the limited dataset size, extensive data augmentation techniques were applied, including rotation, horizontal and vertical flipping, brightness and contrast adjustments, and color space transformations to simulate diverse real-world smartphone capture conditions. Additionally, transfer learning was employed using four pre-trained deep learning architectures—ResNet-50, VGG, Xception, and EfficientNetB0—leveraging knowledge from ImageNet's millions of images to enable effective feature extraction with limited domain-specific data. Model performance was evaluated using F1 scores across the three defect categories. ResNet-50 achieved the highest performance for Broken grain detection (F1 = 0.9819), EfficientNetB0 excelled in Chalky grain identification (F1 = 1.0), and Xception performed best for Brown/ Yellow grain detection (F1 = 0.9555). These three specialized models were successfully embedded into a LINE Official Chatbot interface. Users simply upload a photograph of their rice sample, and the system evaluates it against the three defect criteria, generating an intuitive quality score: 3/3 (perfect quality), 2/3 (acceptable), 1/3 (fair), or 0/3 (poor quality), along with specific defect notifications and health warnings when applicable. This innovation democratizes rice quality assessment by transforming smartphones into portable quality assurance tools accessible to non-expert users. The system enables consumers to verify authenticity and safety before cooking, helps restaurant owners ensure premium grain quality, and allows small vendors to transparently demonstrate product quality to buyers. Future development will focus on enhancing contaminant detection capabilities, implementing automatic grain counting algorithms, and expanding the system to support diverse rice varieties beyond Thai Jasmine rice, contributing to improved food safety standards and agricultural quality control across the rice supply chain.

Keywords: Deep learning; Image classification; LINE Bot; Thai Jasmine rice, Quality assessment

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Deep Learning-Based Skin Disease Classification Chatbot

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ABSTRACT: Skin diseases are common health problems in Thailand due to the hot climate, pollution, and genetic factors. Every year, many Thai people suffer from various skin conditions that affect not only physical health but also mental well-being and self-confidence. However, access to dermatologists remains difficult because of high medical costs, travel limitations, a shortage of specialists, and discomfort with hospital visits. To address these challenges, this project developed a LINE Chatbot embedded with a well-trained deep learning model for preliminary skin disease assessment and basic suggestions. The system allows users to upload skin images through mobile phones, making early screening more convenient and accessible. In its current stage, the system can detect Atopic Dermatitis, Chickenpox, Cellulitis, Ringworm, Urticaria, and Shingles, all of which are the skin diseases commonly found in Thailand. The project applies Deep Learning and Convolutional Neural Network (CNN) technology using Python on Google Colab. The classification utilizes four distinct pre-trained models, each trained using a standardized training, validation, and test method over 30 epochs. To facilitate this, a dataset of 892 images was divided into training (609 images), validation (164 images), and test (119 images) sets. Model performance was evaluated using Heat Maps, Confusion Matrices, and F1 Scores. Among the four models, ResNet50 achieved the highest F1 score at 91.19%, demonstrating the best overall performance. Xception ranked second with 84.40%, followed by EfficientNetB0 at 74.78%, while VGG16 showed the lowest F1 score at 54.85%. The trained model was integrated into the LINE Chatbot, enabling automatic image analysis and prediction of possible disease classes. This innovation is designed for people with early skin symptoms or those at risk of skin diseases, helping reduce medical expenses and travel difficulties while providing fast preliminary assessment. However, the current chatbot does not cover all skin diseases in Thailand. Future development will include more detectable diseases, normal skin data, and higher-quality datasets to further improve accuracy and system performance.

Keyword: Artificial Intelligence, Deep Learning, Image Classification, Line Chatbot, Skin Diseases

Evaluation of Antioxidant Activity, Total Phenolic Content, and Total Flavonoid Content of *Phyllanthus emblica and Garcinia mangostana* Extracts for Potential Biotechnological Applications in Herbal Oral Healthcare

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ABSTRACT: Medicinal plants are important sources of bioactive compounds with significant potential for biotechnological and healthcare applications. *Phyllanthus emblica* and *Garcinia mangostana* have been widely utilized in traditional medicine due to their antioxidant and antimicrobial properties. Natural antioxidants derived from medicinal plants have gained increasing attention in molecular biotechnology and nanobiotechnology for the development of sustainable healthcare products and bioactive formulations. This study aimed to evaluate and compare the antioxidant activity, total phenolic content (TPC), and total flavonoid content (TFC) of *P. emblica* and *G. mangostana* extracts for their potential application in herbal oral healthcare biotechnology. Dried plant materials were extracted using 90% ethanol as the extraction solvent. Antioxidant activity was determined using 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2′-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) radical scavenging assays. TPC and TFC were analyzed using standard colorimetric methods and expressed as milligrams gallic acid equivalent per gram extract and milligrams quercetin equivalent per gram extract, respectively. *P. emblica* demonstrated stronger antioxidant activity than *G. mangostana*, with lower half maximal inhibitory concentration (IC_{50}) values for both the DPPH (29.29 ± 0.582 and 75.82 ± 0.614 µg/mL, respectively) and ABTS assays (15.16 ± 0.243 and 41.71 ± 0.302 µg/mL, respectively). Furthermore, *P. emblica* exhibited higher TPC (535.42 ± 3.752 mg gallic acid equivalent/g extract), while *G. mangostana* showed higher TFC (64.25 ± 2.682 mg quercetin equivalent/g extract). The findings suggest that phenolic compounds may contribute substantially to the antioxidant potential. These results support the potential utilization of medicinal plant extracts as sustainable bioactive materials for future biotechnological applications, including herbal oral healthcare formulations and natural antioxidant-based delivery systems.

Keywords: ABTS, Antioxidant activity, Biotechnology, DPPH, *Garcinia mangostana*, *Phyllanthus emblica*

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Bid by Bit: A Micro:bit-Based Wearable Device for Lower-Limb Motion Monitoring and Rehabilitation

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ABSTRACT: Falls are a major global health concern and the second leading cause of unintentional injury deaths worldwide, with older adults being especially vulnerable due to declines in lower-limb muscle strength, postural balance, and musculoskeletal function. While targeted physiotherapy can mitigate these fall risks and preserve independence, proper technique and long-term adherence during unsupervised home exercise remains a significant clinical challenge. To address this gap, we developed “Bid by Bit,” an affordable smart wearable device, designed to facilitate safe, accessible, and high-quality home-based physical therapy. Utilizing Micro:bit V2 technology and machine learning, the wearable system focuses on monitoring three core lower-body exercises crucial for mobility: straight-leg and lying-leg raises, which engage both the hip flexors and quadriceps; side-lying leg raises for hip stability; and lying knee bends for joint flexibility. Real-time motion data collected via an integrated accelerometer is processed by trained machine learning models to accurately recognize movement patterns, differentiate execution quality, and detect errors. Acting as an interactive "Personal Coach," the device provides immediate audio-visual feedback and displays a live movement accuracy percentage on both the hardware interface and a synchronized Blynk Dashboard. In addition, the system actively prioritizes patient safety and tailored recovery; it prevents overexertion by automatically limiting daily sets and repetitions, while offering personalized configurations for pain-limit settings and individual calibration. Ultimately, “Bid by bit” successfully tracks long-term performance progress and securely stores motion data for future clinical analysis, offering a highly scalable, low-cost solution to enhance rehabilitation compliance and significantly reduce elderly fall risks. Abstract text in 12 pt Times New Roman normal, justify alignment, single space, and single paragraph.

Keywords: Elderly; Fall risks; Micro: bit technology; Rehabilitation; Wearable device

A Preliminary Study of Liquid Biopsy-Based Detection of Epidermal Growth Factor Receptor Mutations Using a Surface Acoustic Wave Biosensor

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ABSTRACT: Lung cancer remains one of the leading causes of cancer-related deaths worldwide, with non-small cell lung cancer accounting for more than 80% of cases. Mutations in the Epidermal Growth Factor Receptor (EGFR) gene are important biomarkers for targeted therapy selection. This study investigated the potential of a Surface Acoustic Wave biosensor for label-free detection of EGFR mutations in plasma samples. The biosensor operated through DNA hybridization between probes and complementary target DNA, which produced measurable phase shift responses due to mass loading on the sensing surface. Two clinically relevant EGFR mutations, Exon 18 and Exon 19 deletion, were evaluated. Experimental parameters, including incubation time, probe concentration, and target concentration, were systematically optimized to improve biosensor response. Results showed a detection of both EGFR mutations from plasma samples under label-free conditions with minimal reagent consumption. Phase shift differences between negative controls and mutation-positive samples confirmed the feasibility of mutation detection using the proposed platform. A detection cutoff derived from the mean plus three standard deviations of the negative control responses (8.92°) was applied to distinguish mutation-positive samples, and mutation-positive samples produced phase shift magnitudes approximately 2.8- to 3.0-fold higher than the negative control on average. Exon 19 samples showed more distinguishable responses than Exon 18 samples, which indicated better selectivity under the current experimental conditions. However, variations in phase shift responses among plasma samples showed no clear relationship with Ct values under the current experimental conditions. As this study represents a preliminary feasibility assessment using plasma samples rather than a synthetic target dilution series, analytical parameters such as the limit of detection, linear detection range, and analytical sensitivity could not be determined under the current experimental design. Therefore, additional studies with larger numbers of plasma samples are required to further evaluate biosensor sensitivity, selectivity, and quantitative detection capability.

Keywords: EGFR mutations; Exon 18 G719X; Exon 19 deletion; Non-small cell lung cancer (NSCLC); SH-SAW biosensor

A Low-Carbon Biochar Module for Nitrogen Reduction, Eutrophication Mitigation, and Sustainable Urban Water Resilience

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ABSTRACT: Bangkok's urban canals are affected by nitrogen and organic pollution, leading to eutrophication and ecological degradation. This study developed a low-carbon biochar module for nitrogen reduction using a 54-L solar-powered, biochar-based floating moving bed biofilm reactor (MBBR) as a decentralized wastewater treatment solution. The system used ring-shaped bamboo biochar as a microbial biocarrier and applied intermittent aeration powered entirely by an off-grid solar energy system without external electricity input. During startup, aeration schedules were adjusted to balance nitrate removal with solar energy availability; the 8 h aeration and 16 h non-aeration cycle showed the most favorable performance-energy balance. The module was evaluated using urban canal water during a 14-day startup period followed by a 7-day validation phase. Nitrate, biochemical oxygen demand (BOD), pH, dissolved oxygen, and oxidation-reduction potential (ORP) were monitored to assess performance and stability. Average nitrate removal reached 70–75%, with a maximum of 88%. Influent nitrate decreased from approximately 15 mg/L to 3–6 mg/L, while BOD decreased from about 30 mg/L to 3.8 mg/L. ORP shifted from positive values above +100 mV during aerobic periods to negative values below −50 mV during anoxic periods, indicating alternating aerobic-anoxic conditions that may support simultaneous nitrification-denitrification and alkalinity recovery. An indicative global warming potential (GWP) reduction estimate suggested 21.18–22.63 kg CO_2-eq module^{-1} year^{-1} from intermittent aeration, off-grid solar operation, and potential indirect methane and nitrous oxide reductions, excluding biochar. Including biochar carbon retention increased the unverified estimated benefit to 24.57–26.02 kg CO_2-eq per module. Longer-term operation, repeated trials, control comparisons, and additional nitrogen species data are recommended to confirm the mechanism and scalability. Overall, this study demonstrates the potential of solar-powered biochar-based MBBR technology as a decentralized, low-carbon approach for improving urban canal water quality.

Keywords: Biochar, Decentralized Wastewater Treatment (DWWT), Intermittent Aeration, Nitrogen Removal, Oxidation-Reduction Potential (ORP)

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KneeHab Pro: A Wearable Motion Tracking System for Post Knee Surgery Rehabilitation

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ABSTRACT: Musculoskeletal knee injuries are a major source of long-term pain, disability, and healthcare expenditure worldwide. A critical limitation of current post-surgical recovery is that much of rehabilitation occurs unsupervised outside clinical facilities, contributing to poor exercise quality, low patient adherence, and an increased risk of reinjury. This study introduces KneeHab Pro, a low-cost wearable motion-tracking system designed to support home-based knee rehabilitation. The hardware comprises a Seeed Studio XIAO ESP32-C3 microcontroller, an Adafruit BNO085 nine-degree-of-freedom inertial measurement unit, a 3.7 V 500 mAh battery, and an Adafruit SPI MicroSD breakout. Synchronized sensors positioned on the thigh and shin continuously capture lower-limb orientation and movement data. The system supports two operating configurations: local data logging for long-duration assessment of recovery trends and real-time Bluetooth streaming to a patient mobile application and clinician web dashboard. The mobile application provides personalized rehabilitation exercises, guided range-of-motion measurements, and real-time movement feedback, while the clinician dashboard enables healthcare providers to monitor recovery data remotely, assign rehabilitation goals and exercise plans, and provide direct feedback. Raw inertial data are processed using a recursive low-pass filtering and kinematic analysis pipeline that calculates numerical metrics including knee joint angle, range of motion, angular velocity, movement smoothness, exercise repetitions, and exercise completion. These algorithmically calculated values form the basis of all displayed results and progress assessments. A Large Language Model is used only within the patient application to condense these precomputed medical metrics and clinician-provided information into clear, understandable progress summaries. It does not calculate measurements, diagnose conditions, or independently interpret raw sensor data. Patient movement data are protected using Fernet symmetric encryption to support the secure handling of sensitive rehabilitation information. KneeHab Pro therefore enables remote patient monitoring, real-time feedback, and at-home range-of-motion assessment beyond the limitations of periodic in-clinic measurements.

Keywords: Knee rehabilitation; Inertial measurement unit, Range of motion, Remote patient monitoring; Wearable sensor

AI-Engineered Nanoproteins: A De Novo Approach to Inhibit Hantavirus Transmission

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ABSTRACT: Andes virus (ANDV) is a highly pathogenic virus capable of causing severe Hantavirus Cardiopulmonary Syndrome (HCPS), presenting a critical threat to global public health. While monoclonal antibodies offer a traditional therapeutic pathway, their development and production are time-consuming, costly, and often limiting their accessibility. To overcome these limitations, this study proposes the development of *de novo* engineered nanoproteins binders targeted directly at the viral fusion loop of the ANDV Gc glycoprotein, a highly conserved region essential for host cell entry. By isolating the structural coordinates of the Gc glycoprotein, the fusion loop and its critical hotspots residues were mapped, RFdiffusion was used to design three-dimensional backbone structures that fit the specific epitope, the conditions used were iterations:200, num_designs:8, and hotspots included. Remarkably, the generated scaffolds achieved the best Root-Mean-Square Deviation (RMSD) of just 0.13 Å (PDB ID: 6Y5W) and 0.12 Å (PDB ID: 6Y5F), indicating highly stable and precise generation. ProteinMPNN was deployed to optimize the amino acid sequences to ensure stability and folding efficiency. Molecular Dynamic (MD) was applied to analyze movements of the molecules in real condition to verify binders' efficiency. For future downstream applications, these binders can be expressed using bacterial or yeast expression systems to validate their binding efficiency (EC50 and KD) in laboratory assays, including Enzyme-Linked Immunosorbent Assay (ELISA) and Bio-Layer Interferometry (BLI). Ultimately, these stable nanoproteins hold immense potential for translation into innovative medical countermeasures, such as therapeutic nasal sprays, designed to effectively block viral-host cell attachment and neutralize infection at the primary site of entry.

Keywords: Andes virus; De novo protein design; Fusion loop binder; Gc glycoprotein

Evaluation of CRISPR/Cas12f-Mediated Genome Editing Targeting the BCL11A Enhancer in HEK293T Cells

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ABSTRACT: β-thalassemia is a hereditary blood disorder caused by reduced or absent β-globin production, resulting in chronic anemia and severe clinical complications. Reactivation of fetal hemoglobin (HbF) through disruption of the erythroid-specific BCL11A enhancer has emerged as a promising therapeutic strategy. While CRISPR/Cas9-based approaches have demonstrated clinical success, their large-size delivery limits using viral vectors. Cas12f is a recently identified compact CRISPR nuclease that may provide advantages for genome-editing applications requiring efficient delivery. This study aimed to evaluate the feasibility of Cas12f-mediated genome editing at the BCL11A erythroid enhancer in human embryonic kidney 293T (HEK293T) cells. Three guide RNAs (gRNAs) targeting the BCL11A enhancer were designed and cloned into two Cas12f expression vector backbones, HKRA and YHAM, corresponding to different engineered Cas12f variants. Recombinant plasmids were validated by Sanger sequencing and transiently transfected into HEK293T cells. Genome editing activity was assessed by PCR amplification of the target loci followed by a T7 Endonuclease I (T7E1) mismatch assay, and by Sanger sequencing followed by Tracking of Indels by Decomposition (TIDE) analysis. Correct gRNA insertion was confirmed for all constructs. T7E1 analysis revealed detectable indel formation at the target site, with editing efficiencies ranging from 4.08-12.10%, depending on the gRNA and Cas12f variant. Sanger sequencing showed mixed chromatogram signals near the predicted cleavage site, supporting successful genome modification, while TIDE analysis detected low but measurable indel frequencies ranging from 0.6-3.7%. These findings demonstrate that Cas12f can mediate targeted genome editing of the BCL11A enhancer in human cells and support its potential as a compact alternative to larger CRISPR nucleases. Further optimization and validation in erythroid cell models are required to assess its therapeutic applicability for β-thalassemia gene therapy.

Keywords: BCL11A enhancer; CRISPR/Cas12f; Fetal hemoglobin; Genome editing; β-thalassemia

Gelatin/agar Film Combined with *Psidium cattleianum* Leaves Carbon Dots for Food Preservation

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ABSTRACT: This research created sustainable bioplastic films through integrating carbon dots (CDs) derived from strawberry guava leaves (*Psidium cattleianum*) into a gelatin/agar matrix. The CDs were made using an eco-friendly hydrothermal technique. UV-Vis spectroscopy and blue fluorescence upon UV irradiation confirmed that strawberry guava leaves underwent successful carbonization. Hydrothermal conditions, especially temperature and alkaline pH, influenced fluorescence behavior by promoting the synthesis of hydroxyl (OH) and amino (NH_2) functional groups linked to luminescence properties. Fourier-transform infrared spectroscopy (FTIR) proved the formation of GA/AG composite films with CDs. Characteristic functional groups, such as O-H, N-H, and C=O bonding, indicated the creation of carbonaceous structures and surface functionalization in CDs. The composite films showed a broad absorption band at 3200-3400 cm^{-1} and a bathochromic shift of the amide band (from 3300 to 3280 cm^{-1}), confirming strong intermolecular hydrogen bonding and compatibility between gelatin and agar. Increasing the agar content greatly improved film performance, as increasing the GA/AG ratio from 6:1 to 6:5 increased film thickness from 0.087 ± 0.004 to 0.120 ± 0.003 mm, tensile strength from 0.77 ± 0.024 to 2.20 ± 0.347 MPa, and reduced water vapor transfer rate and permeability. Overall, agar reinforcement increased the film's mechanical strength and moisture barrier qualities. Combined with the functional properties of strawberry guava leaf-derived CDs, the produced films show remarkable potential for future active packaging applications.

Keywords: Agar; Bioplastic film; Carbon dots; Gelatin; Hydrothermal; *Psidium cattleianum* leaves

Population Dynamics of Ammonia-Oxidizing and Nitrite-Oxidizing Bacteria in Outdoor Shrimp Culture Ponds

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ABSTRACT: Nitrification is a key process governing water quality in shrimp aquaculture, sequentially converting toxic ammonia and nitrite into nitrate and thereby protecting animal health, growth, and survival. This two-step process depends on ammonia-oxidizing bacteria (AOB), such as *Nitrosomonas* spp., which convert ammonia to nitrite, and nitrite-oxidizing bacteria (NOB), such as *Nitrobacter* spp., which convert nitrite to nitrate. In outdoor earthen ponds, these communities are continuously exposed to fluctuating temperature, sunlight, salinity, and organic loading, yet their dynamics over a production cycle remain poorly characterized. This study quantified the abundance and tracked the dynamics of AOB and NOB in open-air outdoor ponds at Chaipattana Foundation demonstration shrimp farm (Chachoengsao, Thailand) managed without chemical pesticides or commercial probiotics. A SYBR Green real-time PCR assay was developed using two primer sets specific to AOB and NOB marker genes and applied to 69 pond-water samples collected across the culture period. Both bacterial groups were consistently detected, and their abundance and diversity varied among ponds and sampling times, revealing a dynamic nitrifying community that shifted with the changing nitrogen load of the ponds. The continuous presence and balance of AOB and NOB corresponded with effective on-farm nitrogen-waste management, stable water quality, and healthy cultured animals. These findings demonstrate that SYBR Green real-time PCR is a rapid and sensitive tool for monitoring temporal changes in nitrifier gene abundance in outdoor shrimp ponds, providing a practical molecular indicator that can support water-quality management and more sustainable shrimp production.

Keywords: Ammonia-oxidizing bacteria; Nitrite-oxidizing bacteria; Nitrification; Real-time PCR; Shrimp pond water quality

Development of a SYBR Green Real-Time PCR Assay Targeting the *amoA* and *nxrB* Genes for Monitoring Nitrifying Bacteria in a Recirculating Aquaculture System (RAS)

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ABSTRACT: Water quality is critical to shrimp health and productivity, and the accumulation of toxic ammonia and nitrite from excess feed and excretory waste is a major constraint in intensive culture. These nitrogenous compounds are removed by autotrophic nitrification, in which ammonia-oxidizing bacteria (AOB) convert ammonia to nitrite and nitrite-oxidizing bacteria (NOB) convert nitrite to nitrate. Rapid, accurate monitoring of these functional groups, however, remains limited in aquaculture. This study developed and validated a SYBR Green real-time PCR assay targeting the *amoA* and *nxrB* genes, the functional marker genes of AOB and NOB, respectively, to monitor nitrifying bacterial populations in a Recirculating Aquaculture System (RAS) stocked with Pacific white shrimp (*Litopenaeus vannamei*) at Rajamangala University of Technology Tawan-ok (Chonburi, Thailand). Archived water samples from the culture cycle were filtered through a 0.22 µm membrane filter to collect the bacterial community, and genomic DNA was extracted. Seven newly designed short-amplicon primer pairs were screened against cloned *amoA* and *nxrB* plasmid standards, and one pair per gene was selected: *amoA* F1/R1 (180 bp) and *nxrB* F2/R1 (132 bp). Both pairs generated a single amplicon of the expected size on agarose gel electrophoresis and a single melt peak, with no specific amplification in no-template controls. Applied to the field-derived DNA, both genes were reliably detected, with Cq values of 22.4–27.7 for *amoA* and 22.7–23.4 for *nxrB*, and melt peaks (82.5–83.0 °C and 85.0–85.5 °C, respectively) identical to those of the corresponding plasmid controls, confirming target specificity against a complex environmental background. These findings demonstrate that *amoA*- and *nxrB*-targeted SYBR Green real-time PCR is a rapid and reliable tool for monitoring nitrification, supporting water-quality management and sustainable shrimp production in closed indoor systems. Absolute quantification against plasmid standard curves across the full culture cycle is in progress.

Keywords: *amoA* gene; Nitrifying bacteria; *nxrB* gene; Real-time PCR, Recirculating Aquaculture System (RAS)

Valorization of Sweet Sorghum Juice for Sustainable Protein Production Through Co-cultivation of Microalgae and Yeast Cells

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ABSTRACT: Microalgae are recognized as a highly promising feedstock due to their ability to synthesize a diverse array of high-value bioproducts, including lipids, proteins, carbohydrates, carotenoids, and other bioactive compounds. Especially, they represent an excellent alternative protein source, outperforming traditional crop and livestock systems in protein yield. This study aimed to evaluate the protein production of microalgae locally isolated from Si Than Lake (Khon Kaen University, Thailand). A single isolate, designated as *Chlorella* sp. SR-4, was previously recovered. In subsequent growth evaluation, mixotrophic cultivation of *Chlorella* sp. SR-4 outperformed heterotrophic cultivation a nearly five-fold increase, achieving a cell density of 7.83×10^6 cells/ml after 7 days of cultivation. Mixotrophic cultivation was selected to evaluate the growth and protein productivity of *Chlorella* sp. SR-4 using sweet sorghum juice as a carbon source. While a total sugar content of 5.0 g/l maximized biomass proliferation, a higher total sugar content of 15.0 g/l was required to enhance protein production, resulting in a high protein yield of 8.30 %(w/w). To further improve protein yield, a co-culture system pairing the isolated microalgae with the yeast *Saccharomyces cerevisiae* DBKKU-Y-53 at a 20:1 was detected. When grown in sweet sorghum juice at a total sugar content of 15.0 g/l, the co-culture achieved the higher protein yield of 32.60%(w/w), which was approximately four-fold more than yield of the monoculture. Based on these findings, this co-cultivation of microalgae and yeast strategy using sweet sorghum juice offers a highly viable approach to valorizing agricultural resources and producing high-value proteins.

Keywords: *Chlorella* sp.; Co-cultivation; Protein production; *Saccharomyces cerevisiae;* Sweet sorghum juice

Effect of Maltose Concentration on the Production of Long-Chain Isomaltooligosaccharides by *Bacillus subtilis* strain AP-1

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ABSTRACT: This study investigated the effect of initial maltose concentration (50–200 g/L) as a carbon source on the production of a series of long-chain isomaltooligosaccharides (IMOs) without glucose and maltose contamination, using whole cells of *Bacillus subtilis* strain AP-1. Fermentations were conducted in Berg's mineral salt medium under aerobic conditions at 37 °C and 200 rpm. IMO profiles over time were monitored via thin-layer chromatography (TLC) and high-performance liquid chromatography (HPLC), while final product yields were quantified gravimetrically. An evaluation of process efficiency revealed that complete depletion of residual glucose was achieved at lower initial maltose levels of 50 and 80 g/L within 36 h (1.5 days) and 54 h (2.25 days), yielding 36.33 and 58.60 g/L of IMOs, respectively. Although increasing the initial maltose loading from 80 to 200 g/L successfully achieved the highest IMOs concentration of 157.67 ± 0.08 g/L, the required cultivation time was substantially prolonged to 17 days. Consequently, the optimal productivity of 26.04 ± 0.04 g/L/day was achieved at 80 g/L of maltose, whereas higher maltose loadings (100–200 g/L) led to a marked decrease in productivity, ranging from 8.22 ± 0.01 to 13.95 ± 0.03 g/L/day. Under the selected operating condition, HPLC analysis confirmed no detectable residual glucose and maltose, with the oligomeric series spanning at least DP10. These findings demonstrate that an initial maltose concentration of 80 g/L represents an optimal operating condition, providing high productivity with a relatively short cultivation time and serving as a promising baseline for further process development and scale-up studies.

Keywords: *Bacillus subtilis*; Isomaltooligosaccharides; Maltose; Prebiotic

Production of Mannan-oligosaccharides from Soybean Residues by Probiotic *Bacillus tequilensis* PLM1

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ABSTRACT: Soybean residue is an abundant and low-cost by-product generated from the soy sauce industry. It contains high amounts of proteins and carbohydrates, making it a promising substrate for the production of bioactive oligosaccharides. Mannan-oligosaccharides (MOSs) have attracted considerable attention due to their prebiotic properties and their applications in functional foods, dietary supplements, and pharmaceutical products. However, the complex structure of soybean residue limits its biodegradation by common microorganisms and results in heterogeneous oligosaccharide products. Therefore, this study aimed to investigate the potential of enzymes produced by *Bacillus tequilensis* strain PLM1 for the bioconversion of soybean residue into oligosaccharides. Crude enzyme extracts obtained from cultivation in mineral salt medium (MS) supplemented with soybean residue as a carbon source at 37°C exhibited the highest mannanase activity (568.72 ± 10.85 U/g protein), followed by pectinase, xylanase, and cellulase activities. High-performance liquid chromatography (HPLC) analysis revealed that increasing soybean residue concentrations to 5, 8, and 10 (w/v) enhanced MOSs with a degree of polymerization (DP) of 4–5 were detected. These results demonstrated the capability of *B. tequilensis* PLM1 enzymes to hydrolyze hemicellulose in soybean residue for oligosaccharide production. Furthermore, *B. tequilensis* PLM1 exhibited a high survival rate under simulated gastrointestinal conditions (95.00 ± 0.08%), indicating its probiotic potential. Owing to its efficient soybean residue-degrading capability, the strain effectively hydrolyzed cell wall polysaccharides and mannan, enabling the production of MOSs. Collectively, these results demonstrate the feasibility of using *B. tequilensis* PLM1 as a promising biocatalyst for the valorization of soybean residue and the co-production of probiotic bacteria and prebiotic MOSs. This study provides a sustainable strategy for converting soybean residue into value-added prebiotic oligosaccharides with potential applications in functional foods and health-related products. Further optimization of the hydrolysis process and biological validation of the produced MOSs are required to support their practical applications.

Keywords: *Bacillus tequilensis*, Mannan-oligosaccharides, Prebiotics, Soybean residue

Genomic Resequencing Reveals Genetic Diversity and Population Structure of Durian in Uttaradit Province, Thailand

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ABSTRACT: Durian (*Durio zibethinus* L.) is an important economic fruit in Southeast Asia, particularly in Thailand, the world's largest durian exporter. Currently, only a few durian varieties are commercially cultivated, resulting in a decrease in the diversity of other durian varieties. However, in Uttaradit province, durians were propagated from seeds, which might lead to higher genetic diversity than in typical commercial growing areas. For this reason, the objective of this research was to assess the population structure and genetic diversity of thirty durian varieties in the Uttaradit province. The results revealed 26,793,798 SNPs across the genome, providing genome-wide markers for characterizing the genetic diversity of durian in the study area. Population structure analysis using IBS, phylogenetic tree, and PCA revealed three genetic clusters: group 1 (ID1-ID5, ID7, ID9-ID19, ID22, and ID25-ID30); group 2 (ID6 and ID8); and group 3 (ID20, ID21, ID23, and ID24). Furthermore, identified two ancestral sub-populations (K = 2). However, despite the clear classification of these population groups, the overall genetic differentiation of the 30 durian varieties was generally low to moderate. This study enhances our understanding of the population structure and genetic diversity of durian in Uttaradit province and can serve as a basis for future genetic resource conservation, germplasm management, and durian breeding programs.

Keyword: Durian; Uttaradit province; Population structure; Genome analysis; Single nucleotide polymorphisms (SNPs)

Postbiotic Potential of Cell-Free Supernatants from Khao-mak Microbial Isolates: Antimicrobial Activity and Stability

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ABSTRACT: Growing demand for natural antimicrobial agents has increased interest in postbiotics derived from fermented foods. Khao-mak, a traditional Thai fermented rice dessert, serves as a rich source of diverse microbial communities with potential bioactive properties. This study evaluated the antimicrobial activity, thermal and pH stability, and minimum inhibitory concentrations (MIC) of cell-free supernatants (CFS) from Khao-mak microbial isolates against *Escherichia coli* K12 and *Bacillus subtilis* CU1065. Ten bacterial and ten yeast isolates were isolated and screened using the agar well diffusion method. Yeast isolates exhibited no inhibitory effects, while several bacterial isolates demonstrated significant antibacterial activity: L02, L05, L07, and L08 inhibited *E. coli*, and L02, L07, and L08 were active against *B. subtilis*. CFS from the promising isolates were freeze-dried and reconstituted for further characterization. Thermal stability testing at 60°C, 80°C, and 100°C showed that L02 and L07 maintained complete stability against *E. coli* ($p \geq 0.05$), whereas L08 exhibited a significant decrease above 60°C ($p < 0.05$). Against *B. subtilis*, L02 and L08 retained full heat tolerance up to 100°C, while L07 showed a slight reduction at higher temperatures ($p < 0.05$). CFS demonstrated excellent stability across pH 2.0–9.0; L08 achieved maximum inhibition against *E. coli* at pH 7.0 (1.70±0.10 cm), and L02 peaked against *B. subtilis* at pH 2.0 (1.83±0.06 cm). MIC determination indicated that L07 had the strongest potency against *E. coli* K12 (MIC = 0.07 g/mL), while all three isolates exhibited an identical MIC of 0.13 g/mL against *B. subtilis* CU1065. These findings highlight the postbiotic potential of CFS from Khao-mak microbial isolates, demonstrating heat- and pH-stable antimicrobial properties with efficacy dependent on the isolate and pathogen.

Keywords: Antimicrobial activity; Cell-free supernatant; Heat stability; Khao-mak; pH stability

Nested Recombinase Polymerase Amplification Coupled with a CRISPR-Cas12a Assay for Sensitive and Specific Detection of *Streptococcus iniae* in Fish

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ABSTRACT: *Streptococcus iniae* is one of the major pathogens in fish, causing Streptococcosis that results in massive fish mortalities and economic losses. Rapid diagnostic methods are crucial for early detection and prevention of this disease, but conventional molecular approaches often require laboratory settings and trained personnel, making field implementation challenging. In this study, we developed an integrated CRISPR-Cas12a platform for rapid, sensitive *S. iniae* detection that can be completed at 37ºC within one hour. Specifically, this assay uses one-tube nested RPA to amplify target DNA, followed by the CRISPR-Cas12a assay to detect the target sequence, generating strong fluorescence that can be observed by the naked eye. While the conventional RPA-Cas12a protocol failed to attain the expected sensitivity, using the one-tube RPA allowed the CRISPR detection assay to achieve high analytical sensitivity, detecting as few as 10^2 copies of target DNA, without cross-reactivity observed in other *Streptococcus* species or fish-related pathogens. Furthermore, the clinical validation using both field and artificially spiked samples exhibited 100% diagnostic accuracy. Collectively, the results confirm that our assay is a rapid, highly sensitive, and specific field-deployable diagnostic tool for *S. iniae* detection, providing early protection and prevention of Streptococcosis in aquaculture.

Keywords: CRISPR-Cas12a; Diagnosis; RPA; *Streptococcus iniae*; Tilapia

Rapid CRISPR-Based Detection Platform for Species-Specific Identification of *Edwardsiella* Bacteria

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ABSTRACT: Sudden outbreaks of bacterial pathogens in aquaculture represent a persistent threat to productivity and economic sustainability. Among the most pressing concerns are *Edwardsiella tarda* and *Edwardsiella ictaluri*, two pathogens capable of infecting both freshwater and saltwater fish species and, in rare cases, causing disease in humans. However, existing detection methods often lack the speed and accessibility required for routine, onsite surveillance. In this study, we developed a DNA detection platform based on a CRISPR-Cas12a assay combined with Recombinase Polymerase Amplification (RPA), referred to as the RPA-Cas12a assay, for the detection of both *E. tarda* and *E. ictaluri*. This assay detects as few as 100 copies of target DNA from both bacteria. No cross-reactivity was observed with closely related *Edwardsiella* species, nor with a panel of other fish-associated bacterial and viral pathogens. Validation using clinical samples confirmed a 100% diagnostic accuracy of the developed RPA-Cas12a assays. Importantly, the assay operates isothermally at 37°C and generates visual readouts within 50 minutes, removing the need for specialized equipment. Overall, this RPA-Cas12a assay provides a rapid, sensitive, and highly specific point-of-care tool for maintaining proactive, biosecure aquaculture systems.

Keywords: CRISPR-Cas12a, *Edwardsiella tarda*, *Edwardsiella ictaluri*, Fish, RPA

Whole Genome Characterization of *Streptomyces angustmyceticus* as a Potential Biological Control Agent Against Southern Blight Disease Caused by *Agroathelia rolfsii*

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ABSTRACT: Southern blight caused by *Agroathelia rolfsii* is an economically important soil-borne disease of many crops worldwide causing severe yield losses and decreased agricultural productivity. The widespread use of chemical fungicides for disease control has raised concerns about environmental pollution, pathogen resistance, and adverse effects on soil health and beneficial microorganisms. Thus, biological control using antagonistic microbes has become a sustainable approach, especially those belonging to the genus *Streptomyces*. *Streptomyces* spp. are known to be potent biocontrol agents due to their ability to produce several bioactive secondary metabolites that have significant antifungal activity against many phytopathogenic fungi. In this study, genetic and biological investigations were performed on *Streptomyces angustmyceticus* isolated from agricultural soil in southern Thailand to examine its antifungal potential against *A. rolfsii*. For genetic characterization, the isolate was subjected to whole-genome sequencing using the Illumina platform. The draft genome was 8.22 Mb with a GC content of 72.21% and showed high completeness (98.3% BUSCO). Genome analysis identified 32 putative biosynthetic gene clusters (BGCs) associated with the production of antimicrobial and antifungal secondary metabolites, including polyketides, non-ribosomal peptides, terpenes, and siderophores. In a biological investigation, the antifungal activity of *S. angustmyceticus* against *A. rolfsii* was examined by the toxic-medium method using different concentrations of culture filtrate (1%, 2%, 5%, 10%, and 20%). The results demonstrated a concentration-dependent inhibition of *A. rolfsii* mycelial growth, with higher concentrations showing significantly greater antifungal activity. These findings suggest that extracellular metabolites produced by *S. angustmyceticus* contribute substantially to fungal suppression. The integration of genomic characterization and antifungal assays highlights the potential of *S. angustmyceticus* as a promising biocontrol agent for sustainable management of southern blight disease. This study also provides genomic insights supporting the future development of environmentally friendly strategies for crop protection and sustainable agriculture.

Keywords: *Agroathelia rolfsii;* Biological contro; Biosynthetic gene clusters; *Streptomyces angustmyceticus;* Whole-genome sequencing

Substantial Catalytic Enhancement of D-allulose 3-epimerase from *Arthrobacter psychrolactophilus*: A Sustainable Chitosan Immobilization Strategy for Production of Low-Calorie Sweetener

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ABSTRACT: D-allulose, a low-calorie rare sugar, has gained significant industrial interest; however, cost-effective enzymatic production remains a bottleneck. Enzyme immobilization offers a promising approach to enhance the overall catalytic efficiency and operational feasibility of bioprocesses. While D-allulose 3-epimerase is conventionally immobilized on expensive synthetic resins or inorganic supports, there is a growing demand for sustainable alternatives. Chitosan—an abundant, inexpensive, and biocompatible natural biopolymer—emerges as an ideal support matrix. Therefore, this study aims to optimize the immobilization of recombinant *Arthrobacter psychrolactophilus* D-allulose 3-epimerase (ApDAEase) onto chitosan beads to maximize its catalytic performance. The immobilization was conducted using a glutaraldehyde cross-linking method. Specifically, the chitosan beads were formulated using a syringe dropping technique with a 2% chitosan concentration dissolved in 1% acetic acid. The resulting matrix was subsequently activated using 0.25% glutaraldehyde for 3 hours, followed by an enzyme loading phase optimized for 4 hours. Direct comparative analysis between the free and immobilized enzyme systems demonstrated that the optimized microenvironment within the porous chitosan matrix successfully preserved the functional conformation of the active site. Under these established optimum conditions, the chitosan-immobilized ApDAEase exhibited a remarkable nearly 19-fold increase in catalytic activity compared to its free counterpart. In conclusion, this optimized immobilization strategy provides a highly efficient, cost-effective, and robust biocatalytic platform, demonstrating strong potential for the scalable production of D-allulose.

Keywords: Chitosan beads; D-allulose 3-epimerase; D-allulose; Enzyme immobilization; Glutaraldehyde cross-linking

Preparation and Characterization of Mealworm-Contained Rice Starch Soft Foods for Older Adults with Dysphagia

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ABSTRACT: Sustainable protein sources have attracted considerable interest in the development of functional foods designed to meet both nutritional and textural requirements for aging populations. In this study, rice starch-based soft foods containing mealworm powder were developed to investigate the effects of mealworm powder content (0.0 –5.0 wt%) on the physicochemical and rheological properties of dysphagia-friendly formulations. A gelatinized rice matrix was prepared under controlled thermal conditions, followed by mealworm incorporation during the cooling stage. The resulting formulations were characterized by microstructural, thermal, and rheological analyses. The effects of mealworm incorporation on the structural characteristics and flow behavior of the food formulations were investigated using rheological analyses across a range of shear rates (1–1000 s-1) relevant to oral processing and chewing. The results demonstrated that increasing mealworm content altered the intermolecular interactions of the rice starch matrix, resulting in changes in thermal stability, viscosity, and viscoelastic properties. The formulations exhibited rheological characteristics consistent with the texture requirements for pureed foods defined by the International Dysphagia Diet Standardization Initiative (IDDSI), suggesting their suitability for safe swallowing. These findings highlight the potential of mealworm-enriched rice starch systems as sustainable, protein-fortified soft foods for elderly individuals with dysphagia.

Keywords Age-friendly soft food; Dysphagia, rheological property, Mealworm powder; Viscoelasticity

Isolation and Characterization of α-1, 3-Glucanase from Alkaliphilic Bacterium, *Alkalihalobacillus* sp.

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ABSTRACT: Various kinds of oligo saccharides have been recognized to be useful for physiologically functional food ingredients. The authors have been interested in the application of α-1,3-glucan oligosaccharides to food. To develop efficient enzymatic production of α-1,3-glucan oligo saccharides, α-1,3-glucanases capable of hydrolyzing α-1,3-glucan under alkali condition where α-1,3-glucan can be retained in solubilized condition were examined in the various microbial samples. As a result of extensive screening, several bacteria were grown on the agar medium containing α-1,3-glucan as a carbon source at pH 10. Among these isolates, the strain RTS232 exhibited highest activity at pH 10 where α-1,3-glucan was partially solubilized. Based on 16SrRNA sequence analysis, it was classified in *Alkalihalobacillus pseudoalcalophilus*. It was designated to be *A. pseudoalcalophilus* RTS232 and used for further study. The enzyme was extracellularly produced in the culture medium containing α-1,3-glucan as a main carbon source and homogenously purified through Butyl-cellufine and HiTrap Q HP column chromatography. The purified enzyme showed a specific activity of 4.08 U/mg with 57.8-fold purification. The enzyme exhibited maximum activity at pH 9.0 and an optimal temperature of 50°C. It was stable in a pH range of 7.0–9.5 (retaining greater than 95% activity) and retained 90% residual activity after heat treatment up to 45°C. The main hydrolysis product from α-1,3-glucan was a tetra-oligosaccharide. It showed the highest activity toward α-1,3-glucan, with slight activity toward α-1,6-glucan. Further study will clarify the production efficiency of tetra-oligosaccharide from α-1,3-glucan using the enzyme. This is the first report regarding α-1,3-glucanase from alkaliphilic *A. pseudoalcalophilus*.

Keywords: α-1,3-glucan; α-1,3-glucanase; Alkaliphilic; *Alkalihahobacillus*; Oligosaccharide

Optimal Condition for Mycelial Growth of Ectomycorrhizal Mushroom Het Ra-ngok Lueang (*Amanita javanica*)

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ABSTRACT: *Amanita javanica*, commonly known as Het Ra-ngok Lueang, is a highly popular and delicious edible ectomycorrhizal mushroom that commands high market prices. It forms mutualistic symbioses with dipterocarp trees and plays a critical role in forest restoration under challenging environmental conditions. However, laboratory cultivation remains challenging due to fastidious growth requirements. The objective of this study was to optimize the culture media, nutritional components, and initial pH levels to enhance the mycelial growth of *A. javanica*. To identify the most suitable basal medium, *A. javanica* strain KK was screened on eight solid media, including MMN, ½MMN, PDA, ½PDA, MEA, ½MEA, Heli medium, and ammonium chloride glucose agar. Among these, ½MMN agar at pH 5.3 was the most effective medium for supporting mycelial growth. Subsequently, nutrient optimization using a Response Surface Methodology (RSM) based on a Central Composite Design (CCD) revealed that the interactive effects of glucose and malt extract followed a significant quadratic model (p = 0.0109, R^2 = 0.9135). The RSM analysis identified a ½ MMN medium supplemented with 0.05% glucose and 0.10% malt extract as the optimal nutrient formulation. Following this nutrient optimization, evaluation of initial pH conditions identified pH 5.0 as the most effective level for supporting optimal growth, yielding a maximum colony diameter of 4.50–4.95 cm after 35 days of cultivation. In conclusion, these findings provide practical knowledge for producing high-quality mycelial inoculum to colonize host plant roots, facilitating successful dipterocarp reforestation and ultimately yielding edible wild mushrooms for sustainable local consumption.

Keywords: Central Composite Design; Dipterocarpaceae; Fungal biotechnology; Inoculum production, Reforestation.

D-Tagatose Production Using Recombinant L-Arabinose Isomerase from *Cellulomonas Palmilytica*

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ABSTRACT: D-Tagatose is a rare sugar widely recognized as a low-calorie sweetener and functional food ingredient. This study aimed to produce D-tagatose from D-galactose using recombinant L-arabinose isomerase from *Cellulomonas palmilytica* strain EW123 (CpL-AI) and to optimize the reaction conditions for enzymatic bioconversion. The *CpL-AI* gene was successfully cloned and heterologously expressed in *Escherichia coli*. SDS–PAGE analysis confirmed recombinant enzyme expression with an approximate molecular weight of 58.98 kDa. Biochemical characterization revealed that CpL-AI exhibited optimal activity at 50 °C and pH 8.0 in 50 mM sodium phosphate buffer. Among the tested metal ions, Mn^{2+} and Co^{2+} significantly enhanced enzyme activity, whereas Zn^{2+} strongly inhibited catalytic activity. Because Mn^{2+} is more suitable for food-related applications, it was selected for further optimization, with 1.0 mM identified as the optimal concentration. D-Tagatose production increased progressively with reaction time and reached a maximum conversion yield of 26.39% after 24 h under optimized conditions. These findings demonstrate that recombinant CpL-AI exhibits favorable catalytic activity for D-tagatose production and highlight its potential for sustainable rare sugar production in the food and biotechnological industries.

Keywords: *Cellulomonas palmilytica*; D-tagatose; Low-calorie Sweetener; L-arabinose Isomerase; Rare Sugar

Evaluation of Factors Affecting Phase Separation in Pickering Emulsions Stabilized by *Microbacterium esteraromaticum* SBS1-7

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ABSTRACT: *Microbacterium esteraromaticum* SBS1-7, a Gram-positive, non-pathogenic bacterium, has been proven for its ability to degrade monocyclic aromatic hydrocarbons (i.e., BTEX) as well as polycyclic aromatic hydrocarbons (PAHs) such as naphthalene (2 aromatic rings). In order to evaluate an ability of SBS1-7 to degrade phenanthrene (3 aromatic rings), the solvent extraction technique was used to quantify the residual phenanthrene. However, SBS1-7 exhibited a unique ability to stabilize the Pickering emulsions. The highly stable emulsion hindered the solvent extraction and quantification of the residual phenanthrene. This study aimed to develop an extraction technique that can destabilized the emulsion formed by SBS1-7. The SBS1-7 cells exposed with phenanthrene were used for emulsion preparation. Many parameters (i.e., temperature, centrifugation time, NaCl supplementation, and types of extracting solvent) were evaluated in detail. In addition, to confirm the SBS1-7's ability as a Pickering emulsions stabilizer, the emulsion stabilized by Safranin-O stained SBS1-7 was visualized under microscope. The emulsion was destabilized by centrifugation time and NaCl supplementation, while temperature (4 and 8°C) and the change of extracting solvent (*n*-heptane, *n*-octane, *n*-nonane, *n*-decane, *n*-dodecane, *n*-tridecane, and *n*-tetradecane) could not destabilize the emulsion. Furthermore, the stained SBS1-7 cells could be observed on the surface of tetradecane droplets, confirming its ability to stabilize the Pickering emulsions.

Keywords: Emulsion destabilization; *Microbacterium esteraromaticum*; Pickering emulsions

Analysis of the Growth of Lactic Acid Bacteria Producing D-Serine Under Controlled pH Conditions and the Expression of Genes Related to Serine Metabolism

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ABSTRACT: Through a screening of D-serine (D-Ser)-producing lactic acid bacteria, we isolated *Lactococcus* sp. strain 0710 and determined its genome sequence. This strain possesses a serine racemase catalyzing the serine racemization. Because a larger biomass is advantageous for utilizing bacterial cells as a catalyst, we investigated cultivation methods to optimize cell yield. To mitigate the rapid pH drop caused by lactic acid accumulation, the strain was cultured in MRS medium supplemented with either 0.1 M potassium phosphate buffer (MRS/KPB) or PIPES buffer at pH 7.2. The final OD_{600} increased 1.4-fold and 1.3-fold, respectively, compared to MRS alone, though the terminal pH remained at 4.4 in both conditions. Notably, the growth rate in MRS/KPB was 1.46-fold higher than in MRS. When the culture supernatant from the end of MRS cultivation was neutralized, sterilized, and reused as a medium, it supported a cell yield of approximately 60% of that achieved in fresh MRS at pH 6.78. These results suggest that growth arrest in standard MRS is primarily driven by acidification, whereas under buffered conditions, it is likely caused by nutrient depletion or elevated osmotic pressure. When L-Ser was racemized using cells grown in MRS/KPB, unwanted pyruvate production—absent in MRS-grown cells—was detected, resulting in a decreased D-Ser yield. To investigate this, RT-PCR was used to analyze the transcription levels of *sdaA*, *sdaB*, and *ilv*, which encode L-Ser-degrading enzymes. Interestingly, adding buffering capacity to the medium decreased the transcription levels of these genes relative to the internal standard, *rpoD*. We are currently investigating how the culture medium influences serine racemase expression and activity.

Keywords: Acid stress; D-Ser; *sdaA*; *sdaB*; *ilvA*; Lactic acid bacteria

Identification and Functional Analysis of Serine Racemase Genes in D-Serine Producing Lactic Acid Bacteria

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ABSTRACT: D-Serine (D-Ser) functions as a co-agonist of N-methyl-D-aspartate glutamate receptors in the mammalian brain, and plays critical roles in cortical memory and learning, cerebellar motor skill acquisition, and various neurological disorders. Given these functions, D-Ser holds potential as a unique functional food ingredient; however, it is not approved as a food additive in Japan. On the other hand, D-Ser produced by lactic acid bacteria during food processing is considered a natural product and is exempt from such regulations. In this study, we screened D-Ser-producing lactic acid bacteria and identified *Lactococcus* sp. strain 0710, which exhibits serine racemase activity. The serine racemase gene was cloned and expressed in Escherichia coli, and the purified enzyme was characterized. Its primary structure shows homology to bacterial alanine racemases dependent on pyridoxal 5'-phosphate (PLP), a coenzyme form of vitamin B6. The purified enzyme catalyzes the PLP-dependent racemization of both alanine and serine. To clarify the reaction characteristics of this enzyme, the effects of temperature and pH on its activity were evaluated. The results confirmed that this enzyme exhibited the highest activity at 40°C and pH 7.5. Notably, the enzyme features a unique subunit structure: both blue native PAGE and gel filtration chromatography indicated a tetrameric form, contrasting with most previously reported dimeric alanine and serine racemases. Here, we report the enzymological properties of the Ala/Ser racemase from *Lactococcus* sp. 0710 and discuss the structural basis enabling its serine racemization activity.

Keywords: Alanine Racemase;D-amino acid; D-Serine; Serine Racemase

Roles of Aspartate-Beta-Decarboxylases in Aspartate Metabolism of *Acetobacter pasteurianus* SKU1108

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ABSTRACT: Aspartic acid is an important intermediate product in amino acid metabolism and plays various physiological roles in cells. Aspartic acid is involved not only as a constituent of proteins, but also in energy metabolism. Previous studies have shown that acetic acid bacterium *Acetobacter pasteurianus* consumed L-aspartic acid (Asp) and produced L-alanine (Ala) during vinegar brewing process. It is also known that the same amino acid conversion occurs in soy sauce lactic acid bacteria (*Tetragenococcus halophilus*). In *T. halophilus*, the intracellular Asp is decarboxylated by aspartate-β-decarboxylase (AspD) and consumes intracellular H^+, resulting in the production of Ala and CO_2. The pH difference between inside and outside the cell is used for ATP generation. We hypothesized that the similar ATP generation system coupling the conversion of Asp to Ala could happen in the *A. pasteurianus*. Genome analysis of *A. pasteurianus* SKU1108 identified two putative AspD homologs, AspD1 (529 aa) and AspD2 (538 aa), which shared 62.7% amino acid sequence identity. In addition, a putative aspartate transporter, AspT (563 aa), was identified. Such an efficient energy-generating pathway might be a strategy for acetic acid bacteria to obtain energy efficiently during the fermentation process and is an important factor in understanding the metabolism of acetic acid bacteria. In the present study, we constructed expression plasmid of AspD1 gene and obtained the recombinant enzyme in *Escherichia coli*. Recombinant AspD1 was highly purified using Nickel affinity column chromatography and its enzymatic properties, including the optimal pH and temperature stability, were characterized. The optimal pH and temperature of AspD1 were pH 6.0 and 40°C, respectively. These findings suggest the involvement of AspD1 in Asp metabolism in *A. pasteurianus*.

Keywords: Aspartate-β-decarboxylase; Aspartic acid metabolism; *Acetobacter pasteurianus* SKU110

Structural Basis for the High Catalytic Efficiency of the Iron-Dependent Xylose Isomerase from *Lactococcus lactis* IO-1

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ABSTRACT: Xylose isomerase (XI) is a metalloenzyme found in bacteria and some fungi that converts the pentose sugar D-xylose to D-xylulose through a reversible reaction. Group II XIs are characterized by an extended N-terminus, and complete structural interactions between the core domains and the terminal tails of adjacent subunits are essential to the function of these XIs. Due to its ability to isomerize D-xylose to D-xylulose, XIs offer the distinct advantage for heterologous expression in *Saccharomyces cerevisiae* for developing microbial cell factories that produce several high-value products. Until now, XI from *Piromyces* sp. E2 has been widely used as a reference enzyme due to its strong catalytic activity and efficient expression in yeast. However, the *Lactococcus lactis* IO-1 XI fundamentally challenges this benchmark with a documented Km of 2.25 mM and a kcat of 184 s^{-1} that yields vastly superior catalytic velocity. Notably, our crystallographic analysis revealed that this enzyme uniquely coordinates with iron within its active site, offering a potential structural rationale for its high catalytic efficiency. This was further confirmed by metal ion replacement assays, in which the relative activity increased with ferrous ions (Fe^{2+}). To the best of our knowledge, this represents the first report of an iron-dependent xylose isomerase. This novelty paves the way for heterologous expression in *S. cerevisiae* for accelerated bioethanol production and sustainable green chemistry. Further anomalous difference Fourier mapping will provide insights on the iron occupancy inside the structural conformation of the active site.

Keywords: Bioethanol production; Metalloenzyme; Xylose isomerase

Development of a Paper-Based Test Strip for Colorimetric Detection of Cholinesterase Activity in Canine Serum

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ABSTRACT: Organophosphate and carbamate pesticide poisoning is a common cause of canine intoxication, and is reflected biochemically by a marked reduction in serum cholinesterase activity. Conventional detection relies on Ellman's assay, which requires freshly prepared reagents, temperature control, and laboratory spectrophotometry, limiting its use in field settings. This study aimed to develop a portable paper-based test strip for the colorimetric detection of reduced cholinesterase activity following toxicant exposure in blood samples of dogs presented for necropsy. The strip employed a two-zone dip-format design in which 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB) was immobilized in a chitosan gel on one zone and butyrylthiocholine iodide (BuChI) substrate was stabilized with polyvinylpyrrolidone (PVP-40) and sucrose on a separate zone, with a physical gap separating the two reagents to prevent premature reaction during storage. Upon application of serum mixed with phosphate buffer (pH 8.0), active cholinesterase hydrolyzed BuChI to thiocholine, which reacted with DTNB to produce a yellow product quantified by image analysis (ImageJ). Key parameters were systematically optimized, including DTNB concentration, incubation temperature, and sample volume. A DTNB concentration of 0.08 M dissolved in absolute ethanol provided the strongest and most stable signal, and observable colorimetric reaction within 2-3 minutes. The optimized prototype produced a clear, measurable yellow signal correlating with enzyme activity. Analytical validation of reduced cholinesterase activity is planned by spiking healthy canine serum in vitro with organophosphate and carbamate and comparing the strip against the reference Ellman's assay, with clinical canine serum samples to be incorporated subsequently. The shelf-life stability of the assembled strip will also be determined under room-temperature storage. These findings demonstrate the feasibility of a rapid, low-cost, and field-deployable strip for screening cholinesterase activity, supporting its potential application in the preliminary screening of pesticide poisoning in dogs.

Keywords: Canine serum; Cholinesterase; Ellman's assay; Paper-based strip; Pesticide poisoning

Valorization of Soybean Processing Residue as an Alternative Nitrogen Source for Enhanced Dark Fermentative Biohydrogen Production

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ABSTRACT: Dark fermentative biohydrogen production from agricultural residues has emerged as a promising strategy for sustainable renewable energy generation. Among the critical factors affecting hydrogen fermentation, nitrogen sources play an essential role in microbial growth, intracellular metabolism, enzyme biosynthesis, and substrate degradation efficiency. However, conventional nitrogen supplements, such as yeast extract and peptone, are expensive and limit the economic feasibility of industrial-scale biohydrogen production. This study investigated soybean meal (SBM), an abundant agro-industrial byproduct, as an alternative low-cost organic nitrogen source for biohydrogen production by *Thermoanaerobacterium saccharolyticum* TH05 under thermophilic anaerobic conditions at 55 °C. Soybean meal contained high levels of protein (47.78%), nitrogen (7.32%), hemicellulose (9.32%), and cellulose (5.76%), indicating its suitability as both a nitrogen source and a carbon precursor. Efficient degradation of these complex polymers by extracellular enzymes is essential for releasing fermentable sugars and supporting biological hydrogen production. The results revealed that SBM concentrations ranging from 0% to 8% (w/v) were evaluated, with 4% SBM achieving the highest hydrogen yield of 15.3 ± 0.47 mL H_2 g^{-1} TS after 120 h. This was accompanied by increased ethanol (1.47 g L^{-1}) and butyric acid (1.70 g L^{-1}) production. Residual nitrogen decreased from 1.52 to 0.04 g L^{-1} in the 4% SBM treatment, indicating efficient nitrogen assimilation. Enhanced amylase, cellulase, and xylanase activities further promoted carbohydrate hydrolysis and substrate conversion. In contrast, excessive SBM supplementation reduced hydrogen productivity, likely due to nitrogen overload and metabolic imbalance. These findings demonstrate the strong potential of soybean meal as a sustainable and cost-effective organic nitrogen source for thermophilic biohydrogen production while simultaneously promoting agricultural waste valorization.

Keywords: Biohydrogen; Dark fermentation; Soybean meal; Organic nitrogen source; *Thermoanaerobacterium saccharolyticum*; Waste valorization

Isolation and Identification of Thermoacidophilic Bacteria for Accelerated Food Waste Degradation

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ABSTRACT: Food waste is a major global environmental concern due to its contribution to greenhouse gas emissions, resource depletion, and economic losses. Conventional composting systems often generate unpleasant odors because they operate under neutral to alkaline conditions. This study aimed to isolate and identify thermoacidophilic bacteria with potential application in acidulocomposting, a composting process conducted under acidic and thermophilic conditions (pH 4.0–6.5 and 50–60°C) to improve degradation efficiency and reduce odor emissions. Six thermoacidophilic bacterial isolates were obtained from soil samples and screened for extracellular enzyme production on substrate-specific agar media at pH 4.5 and 50°C. Enzymatic activity was determined using the Enzymatic Index (EI). Xylanase activity was detected in all isolates, with BCMD42 exhibiting the highest activity (EI = 1.71). Cellulase, protease, and lipase activities were variably detected among the isolates, with G2.2 and H2.1 showing the highest cellulase (EI = 1.38) and lipase (EI = 2.00) activities, respectively, while no amylase activity was observed. Molecular identification based on full-length 16S rRNA gene sequencing revealed that isolate B313 was closely related to *Tuberibacillus calidus* (99.93% similarity), whereas isolates C1C, G2.2, H2.1, and C1A were closely related to *Alicyclobacillus pomorum* (99.06–99.50% similarity). In addition, isolate BCMD42 showed 98.64% similarity to *Alicyclobacillus herbarius*, suggesting that it may represent a genetically distinct strain within the genus *Alicyclobacillus*. These findings demonstrate the potential of thermoacidophilic bacteria as promising candidates for acidulocomposting by producing extracellular enzymes involved in the degradation of lignocellulosic and organic substrates. Their application may contribute to the development of more efficient and environmentally friendly food waste composting systems with reduced odor emissions.

Keywords: Acidulocomposting, Bacterial identification, Extracellular enzymes, Food waste degradation, Thermoacidophilic bacteria

Evaluation of Culture–Substrate Compatibility and Hydraulic Retention Time for Enhanced Biohydrogen Production

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ABSTRACT: Biohydrogen is a promising carbon-neutral energy carrier with high energy density. In Thailand, abundant organic waste and biomass residues remain underutilized. Dark fermentation provides an advantageous technology for energy conversion. This study evaluated biohydrogen production potential using pure cultures (*Klebsiella aerogenes* (a.k.a. *Enterobacter aerogenes*) and *Clostridium butyricum*) and anaerobic digestion (AD) sludge across various substrates, including glucose, glycerol, and oil, under mesophilic conditions in batch mode. Results indicated each culture achieved its maximum hydrogen yield when paired with its optimal substrate, with glucose and glycerol being optimal for *C. butyricum* (1.0 mol H_2/mol glucose) and *K. aerogenes*, respectively. Furthermore, this study developed a semi-continuous fermentation process to investigate the impacts of Hydraulic Retention Time (HRT) at 2 – 4 days. The results demonstrated that a 2-day HRT successfully stabilized the system pH, leading to a 47% yield increase to 1.5 mol H_2/mol glucose. This optimized yield represents 76% of the theoretical potential for the dominant butyrate metabolic pathway. These established operational conditions provide a critical baseline for biomass applications to evaluate commercial feasibility of industrial scale biohydrogen production in the future.

Keywords: Biohydrogen; Dark fermentation; Hydraulic retention time; Semi-continuous fermentation

Valorization of Corn Tassel Agro-Residues: Polyphenol Recovery and Cosmetic Potential via Conventional and Ultrasound-Assisted Extractions

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ABSTRACT: This study aimed to valorize corn tassel residues (T-CARs) as a sustainable source of bioactive ingredients for cosmetic applications. T-CARs were extracted using two extraction methods: conventional extraction (CE, 24 h) and ultrasound-assisted extraction (UAE, 30 min), utilizing three solvents (deionized water, 80% methanol, and 80% ethanol). The extracts were evaluated for their polyphenol (total phenolic–TPC and flavonoid–TFC contents) and cosmetic potentials, including antioxidant, anti-tyrosinase and anti-acnes activities. Additionally, cytotoxicity against human keratinocyte (HaCAT) cells was determined to ensure safety for cosmetics. Results indicated that CE generally yielded higher polyphenol contents compared to UAE. The significantly highest TPC was found in the methanolic and ethanolic CE extracts (791.9 ± 6.3 and 773.7 ± 17.2 mg GAE/g extract, respectively) while the ethanolic CE extract exhibited the highest TFC (570.8 ± 3.8 mg QE/g extract). Evaluation of cosmetic potential showed a diverse bioactivity profile among the extracts. The ethanolic UAE extract showed the highest ABTS and FRAP antioxidant activities (4,171.5 ± 47.8 and 749.3 ± 15.4 mg TEAC/g extract, respectively; $p<0.05$), whereas the methanolic and aqueous CE extracts exhibited the highest DPPH scavenging (756.8 ± 21.7 mg TEAC/g extract; $p<0.05$) and anti-tyrosinase activity (23.9 ± 3.6 %inhibition; $p<0.05$), respectively. Furthermore, the ethanolic CE extracts demonstrated significant anti-microbial efficacy against *Cutibacterium acnes* as anti-acne (MIC 12.5 mg/mL and MBC 25.0 mg/mL). The ethanolic corn tassels CE extract showed no toxicity at concentrations of 0.5 and 1.0 mg/mL (> 90% cell viability). In conclusion, this study validates the valorization of T-CARs, especially the ethanolic CE extract, as safe and promising bioactive ingredients for cosmetic applications.

Keywords: Agro-residues; Corn Tassels; Cosmetic; Polyphenols; Valorization

Antioxidant and Antimicrobial Activities of Crude Extracts from *Phellinus* sp.

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ABSTRACT: *Phellinus* sp., a member of the Hymenochaetaceae family, is a medicinal mushroom traditionally used in East Asia, which has gained significant attention for its diverse pharmacological properties. Bioactive compounds isolated from *Phellinus* sp., including polysaccharides and polyphenolic compounds such as hispolon, caffeic acid, and inoscavin A, have been reported to exhibit immunomodulatory, antioxidant, antibacterial, and anticancer activities. In this study, *Phellinus* sp. was extracted using three solvent systems: distilled water (DW), 60% ethanol, and 95% ethanol. Total phenolic content (TPC) was determined using the Folin–Ciocalteu method, with gallic acid as the standard reference, yielding values of 63.73 ± 3.49, 94.13 ± 3.84, and 35.88 ± 4.36 mg GAE/g extract for the DW, 60% ethanol, and 95% ethanol extracts, respectively. The 60% ethanol extract showed the highest TPC among all tested extracts. Antioxidant activities were evaluated using DPPH radical scavenging and ABTS assays, with gallic acid as the standard reference. The 95% ethanol extract demonstrated the strongest DPPH scavenging activity (IC_{50} = 28.98 ± 2.04 µg/mL), while the DW extract showed the strongest ABTS activity (IC_{50} = 13.70 ± 0.58 µg/mL). Antimicrobial activity was assessed using the agar well diffusion method at concentrations ranging from 50 to 200 mg/mL. All extracts exhibited antibacterial activity against *Escherichia coli* and *Staphylococcus aureus*. For antifungal activity, the extracts exhibited inhibitory activity against *Aspergillus* sp. but not against *Penicillium* sp. under the same conditions. These findings suggest that *Phellinus* sp. extracts possess notable antioxidant, antibacterial, and antifungal activities, highlighting their potential as natural bioactive sources for the development of functional products and future therapeutic applications.

Keywords: Antimicrobial; Antioxidant; Bioactive compounds; Medicinal mushroom; *Phellinus* sp.

In Vitro Generation of Multispecific Cytotoxic T Lymphocytes Targeting GD2, PRAME, and PD-L1

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ABSTRACT: Neuroblastoma (NB) is the most common extracranial solid tumor of the sympathetic nervous system and frequently evades immune clearance. High-risk NB carries a 5-year event-free survival rate below 50%, with high rates of relapse following complete remission. While cytotoxic T lymphocytes (CTLs) offer a promising immunotherapeutic approach for solid tumors *via* targeted cytolytic activity, NB evades immune clearance through multiple mechanisms. NB cells express tumor-associated antigens (TAAs) such as GD2 ganglioside and preferentially expressed antigen in melanoma (PRAME), which drive tumorigenesis. Additionally, NB cells express high levels of programmed death ligand 1 (PD-L1), which binds to PD-1 on effector T cells, thereby inducing T cell exhaustion. To address this, we developed multi-specific CTLs designed to simultaneously target GD2, PRAME, and PD-L1. Monocyte-derived dendritic cells (mDCs) were pulsed with a peptide mixture of these three targets and co-cultured with naïve T lymphocytes. These T cells were subsequently re-stimulated using those artificial antigen-presenting cells to drive the clonal expansion of multi-CTL lines. This protocol successfully generated a robust expandable population of multi-specific CTLs, demonstrating the feasibility of a tri-targeted approach and establishing these cells as warranted candidates for advanced neuroblastoma immunotherapy.

Keywords: Cancer immunotherapy; Dendritic cells; Neuroblastoma; GD2; PRAME; PD-L1

Cloning, Heterologous Expression, and Purification of Sphingomyelinase of *Staphylococcus epidermidis*

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ABSTRACT: Sphingomyelinase (SMase) is an enzyme that hydrolyzes sphingomyelin into ceramide and phosphocholine via the sphingomyelin hydrolysis pathway. Ceramide is a major lipid component of the stratum corneum (SC) and plays a crucial role in maintaining skin barrier integrity and epidermal homeostasis. Previous studies have demonstrated that SMase is produced by several bacterial species, including *Staphylococcus aureus* and *Staphylococcus epidermidis*. Unlike the cytotoxic β-toxin produced by *S. aureus*, SMase derived from *S. epidermidis* has been reported to enhance ceramide production and skin barrier homeostasis. This study, therefore, aimed to clone, express, and purify recombinant SMase encoded by the *SMase* gene of *S. epidermidis*. The *SMase* gene was amplified by polymerase chain reaction (PCR) and ligated into the pET-32a(+) expression vector at *BamHI* and *XhoI* restriction sites, and transformed into *Escherichia coli* TOP10 for recombinant plasmid amplification. Successful amplification of the *SMase* gene was confirmed by the presence of a DNA fragment of approximately 1,005 bp after restriction enzyme digestion. Recombinant protein was expressed in *E. coli* BL21 (DE3) and optimized using different IPTG concentrations and induction times at 16 °C, and sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) analysis revealed a protein band corresponding to the expected molecular weight of SMase (~56 kDa), with the highest expression observed following induction with 0.2 mM IPTG for 12 h. The recombinant SMase protein was purified by Ni-NTA affinity chromatography with stepwise imidazole gradient elution (30 mM-1 M), and the highest protein yield was obtained in the 200 mM imidazole fraction. These findings demonstrate the successful production of recombinant *S. epidermidis* SMase for future studies, including biochemical and functional characterizations.

Keywords: *Staphylococcus epidermidis*; Sphingomyelinase; Expression; Purification, pET-32a (+)

Optimizing Mycelium Pellet Morphology and Its Impact on Bioactive Compound Production via a Taguchi Image Analysis Framework

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ABSTRACT: Mycelial pellet morphology is a key determinant of transport phenomena and productivity in submerged fungal fermentations, yet quantitative frameworks for its control remain underdeveloped. This study presents an integrated framework combining Taguchi experimental design, automated image analysis in FIJI, and multivariate analysis to optimize mycelial pellet morphology in *Pleurotus* spp. and to evaluate its impact on polysaccharides and triterpenoids production. The Taguchi L_9 orthogonal array was employed to evaluate the effects of four key medium components (olive oil, $CaCO_3$, yeast extract, and Tween 80) at three levels each. Fiji-based image analysis enabled the extraction of quantitative descriptors, including pellet count, circularity, and Feret diameter. Analysis of signal-to-noise (S/N) ratios identified the optimal condition (4mL olive oil, 0.25g $CaCO_3$, 0.5g yeast extract, and 0.5mL Tween 80) with pellet morphology significantly higher circularity 0.84 ± 0.05, an increase in triterpenoid content of 1.38 ± 0.11 mg/dL, and polysaccharide yields of 1.96 ± 0.4 mg/dL. PCA explained 83% of total variance, with PC1 (44%) driven by productivity markers (circularity: 0.40; polysaccharides: 0.39; triterpenoids: 0.39) and negatively by pellet size (−0.36), while PC2 (30%) captured biomass-related traits (pellet count: 0.50; biomass: 0.46; circularity: 0.38). Circularity's strong positive loadings on both PCs (0.40 and 0.38) establish it as the most integrative morphological descriptor, positively correlates with all bioactive compounds, and inversely correlates with pellet size, thereby confirming that small, highly circular pellets optimize mass transfer and productivity. The findings establish a quantitative relationship between pellet morphology and fermentation performance in *Pleurotus* spp. and demonstrate that an integrated design-of-experiments approach with image-based analysis provides a reproducible, data-driven framework for morphological assessment and process optimization in submerged fungal fermentation.

Keywords: Circularity; FIJI; Principal component analysis; Submerged fermentation; Triterpenoids

Nucleotide Variations in the Middle Region of Melanocortin 4 Receptor Gene and Their Potential Association with Obesity Risk in the Thai Population

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ABSTRACT: At present, the analysis of specific gene variations can be used for the prognosis of obesity. The MC4 receptor protein, encoded by the *MC4R* gene, plays a key role in the leptin-melanocortin pathway, which regulates satiety and energy balance in humans. This research aimed to evaluate polymorphisms in the middle region of the *MC4R* gene and investigate the possible correlation between these gene variations and obesity in the Thai population. DNA was collected from 114 non-diabetic Thai volunteers, consisting of 60 normal-weight individuals (Body Mass Index [BMI] 18.5–22.9 kg/m²) and 54 obese individuals (BMI equal to or greater than 25.0 kg/m²). The middle region of the *MC4R* gene (positions 5,555–6,166) was amplified, producing a specific PCR product of 612 base pairs. Nucleotide sequence analysis of the 114 samples revealed two heterozygous SNPs exclusively in obese volunteers, identified as G5726A and T6100C. The G5726A mutation, also identified in previous study, results in a valine-to-isoleucine substitution at position 103 (V103I) in the MC4 receptor; however, as a conservative missense mutation, it is unlikely to significantly impact the chemical properties or the function of the protein. Conversely, the T6100C mutation is silent, causing no change to the amino acid sequence or protein function. Based on preliminary data from this study, it is recommended to increase the sample size in both groups and extend the analysis to encompass the entire *MC4R* gene. This approach will enhance the accuracy, reliability, and validity of assessing the potential of this gene for predicting obesity risk in the Thai population.

Keywords: Leptin - melanocortin pathway; *MC4R* gene; Nucleotide variations; Obesity; Thai population

Expression and Purification of Recombinant *Sp*Cas9-HF1-Plus Protein in *Escherichia coli LysY/I^q* for High Precision Gene Editing

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ABSTRACT: The high-fidelity Cas9 variant, *Sp*Cas9-HF1-plus, is a powerful tool for precise genome editing. It significantly reduces off-target effects compared to wild-type Cas9. However, the application of this technology in fungi via Cas9 ribonucleoprotein (RNP) complexes requires the production of high-purity recombinant proteins. This study focuses on the production, optimization, and purification of *Sp*Cas9-HF1-plus with 3× NLS (Nuclear Localization Sequence) in recombinant *Escherichia coli lysY/I^q*. The *Sp*Cas9-HF1-plus gene with 3× NLS was successfully cloned from pET-FLAG-*Sp*Cas9-HF1-plus by PCR and ligated with a pET28a vector. The resulting plasmid named pET28a-*Sp*Cas9-HF1-plus was introduced into an expression host, *E. coli lysY/I^q*. For expression of heterologous protein, the recombinant *E. coli* was induced with 0.4 mM IPTG, and results from these expression trials showed that the highest yield among the conditions tested was achieved at an induction temperature of 18 °C for 24 h. The recombinant protein was purified using Ni-NTA affinity chromatography, with the target protein effectively eluting at imidazole concentrations between 100–200 mM. SDS-PAGE analysis revealed a prominent band at approximately 170 kDa, matching the theoretical molecular weight. The purified protein was further confirmed by Western blot analysis using an anti-6× His tag antibody. In summary, this established production process provides a reliable platform for producing the Cas9 protein, serving as a crucial foundation for genome editing in fungi in the future.

Keywords: CRISPR/Cas9; *Sp*Cas9-HF1-plus; Protein purification

A Multipurpose Antibody Format for Flexible Assay Development Using Cell-Based and Cell-Free Production

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ABSTRACT: Antibody reagents used in diagnostics often require separate optimization for each assay format or detection reporter, which can limit rapid development and increase production burden. This study aimed to develop a multipurpose antibody format that can be produced by both *Escherichia coli*-based expression and cell-free protein synthesis (CFPS) and then applied across multiple assay platforms. The antibody format was designed to maintain antigen recognition while enabling flexible coupling with different detection modules. In the cell-based route, recombinant proteins were produced in *Escherichia coli*, recovered from inclusion bodies, refolded using an automated dialysis-based process developed in our group, and purified to obtain functional reagents at milligram scale. The purified antibodies retained antigen-binding activity and were successfully used in conventional enzyme-linked immunosorbent assay (ELISA) and simplified one-step ELISA which does not require secondary antibodies. In parallel, CFPS enabled rapid preparation of assay-ready antibody reagents directly from DNA templates. The cell-free products showed antigen-dependent signals in plate-based assays and were also applicable to fluorescence-based immunostaining after simple mixing with a reporter component. These results demonstrate that the proposed antibody format can bridge scalable production and rapid on-demand preparation while supporting reporter exchange and multiple analytical applications. The platform may contribute to flexible diagnostic reagent development, particularly when rapid customization and assay adaptability are required.

Keywords: Antibody engineering; Cell-free protein synthesis; Diagnostic assays; *Escherichia coli*; Multipurpose antibody

Thermo-Responsive Morphological Evolution and Rheological Behavior of Wax/Butter-Based Phase Change Microparticles

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ABSTRACT: Phase change materials (PCMs) are materials capable of storing and releasing thermal energy via reversible phase transitions, such as solid-liquid and liquid-gas transitions, over a specific temperature range. Owing to their thermal energy storage and release capacity, as well as their temperature-regulating properties, PCMs have been widely investigated in various industrial and scientific fields, including agriculture, cosmetics, biomedicine, and pharmaceutics. In particular, their ability to undergo changes in physical properties in response to subtle temperature variations demonstrates their potential as stimuli-responsive delivery systems for the precise control of active ingredient release. In this study, wax (W)/butter (B)-based PCM microparticles with sizes of approximately 1-2 μm were successfully fabricated. This study focused on investigating how temperature-dependent shape transformation is associated with the rheological and thermal properties of the material. At 30 °C, the PCM particles exhibited a distinct anisotropic morphology, whereas increasing the temperature to 50 °C resulted in a transformation into an isotropic spherical morphology. This morphological evolution is considered to arise from the complex interplay among viscosity, interfacial tension, and solidification kinetics during particle formation. In addition, the composition and thermal properties of the fabricated microparticles were analyzed, and their temperature-dependent viscoelastic behavior was further evaluated. Rheological analysis confirmed that the viscosity and viscoelastic moduli decreased with increasing temperature, which is consistent with the observed morphological transformation of the PCM particles. Overall, the developed W/B-based PCM microparticles exhibit thermo-responsive shape transformation and temperature-dependent rheological behavior, highlighting their potential as functional materials for thermally controlled delivery systems. Furthermore, their inherent biodegradability and sustainability make the PCM microparticles attractive eco-friendly materials for future cosmetic and pharmaceutical formulations.

Keywords: Phase Change Materials (PCMs); Wax-Based Microparticles; Temperature-Responsive Morphological Evolution; Viscoelasticity; Rheology

Skin-Adhesive Illite-Containing Amphiphilic Hydrogel Composite Patches for Wound Care

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ABSTRACT: Hydrogel-based wound dressings have attracted considerable attention owing to their high water content, biocompatibility, and ability to maintain a moist wound environment. Despite these advantages, achieving both robust mechanical properties and reliable skin adhesion remains a significant challenge for hydrogel wound dressings. In this study, skin-adhesive tough amphiphilic hydrogel composite patches containing illite, a natural clay mineral abundant in the Yeongdong region of Chungcheongbuk-do, South Korea, were developed for wound dressing applications. The N,N-dimethylacrylamide (DMAAm)-based amphiphilic hydrogel composite patches containing illite were synthesized by varying the contents of hydrophobic moieties and illite particles using UV radical polymerization. The resulting amphiphilic network, composed of hydrophilic and hydrophobic polymer phases and size-controlled illite particles, provided a balanced combination of hydration, mechanical flexibility, and skin-interfacial adhesion. In addition, the incorporation of illite particles enhanced network integrity and introduced additional functionalities into the composite structure, including antibacterial activity, adsorption capability toward wound-associated harmful substances, and UV protection. This inorganic–polymer hybrid design provides a simple, scalable fabrication strategy for functional hydrogel composite patches. The developed illite-containing amphiphilic hydrogel patches exhibited promising characteristics as skin-adhesive wound dressing materials, thereby providing a versatile platform for future biomedical applications.

Keywords: Amphiphilic hydrogel Composites; Illite; Skin-Adhesion; Wound Dressings; UV Radical Polymerization

Investigating the Role of *Fusobacterium nucleatum* in Colorectal Cancer and the Inhibitory Effect of *Dendranthema morifolium* as a Natural Antibacterial Agent

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ABSTRACT: *Fusobacterium nucleatum* is a gram-negative anaerobic bacterium that is commonly found in periodontal disease and is also linked to several systemic diseases. This study looks at the relationship between *F. nucleatum* and colorectal cancer and also studies whether *Dendranthema morifolium* may help inhibit this bacterium as a natural antibacterial agent. The antibacterial activity of *Dendranthema morifolium* extract against *F. nucleatum* was tested using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) analysis through the ten-fold serial dilution method, ranging from 10^{-1} to 10^{-6} concentrations. It explains how *F. nucleatum* may affect the human body and how it may be involved in disease development, especially colorectal cancer. This study also discusses important compounds found in *Dendranthema morifolium* and how *F. nucleatum* responds to antibiotics. The results from MIC and MBC analysis showed that higher concentrations of *Dendranthema morifolium* extract demonstrated stronger antibacterial activity against *F. nucleatum*. The findings may be useful for future study in the medical and pharmaceutical fields and may support the use of natural substances as alternative antibacterial agents. However, further studies are still needed to better understand its effects and evaluate its safety for future medical use.

Keywords: Antibacterial activity, Colorectal cancer, *Dendranthema morifolium*, *Fusobacterium nucleatum*, MIC and MBC

AI-Based Oral Lesion Detection System with Integrated Online Chatbot

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ABSTRACT: Many individuals struggle to correctly identify oral ulcers, often leading to incorrect self-treatment that can worsen their condition. To address this issue, this study introduces an accessible AI-driven LINE Official Account chatbot, Smile Bot, designed to provide instant and user-friendly oral lesion screening. The system classifies oral conditions into five primary categories: Canker Sores, Oral Thrush, Herpes, Oral Cancer, and Normal tissue, allowing users to seek the correct medical treatment. To develop the core classification engine, a dataset comprising 409 training images, 113 validation images, and 109 testing images was utilized. The study evaluated and compared four pretrained convolutional neural network architectures: VGG16, ResNet50, Xception, and EfficientNetB0. For each architecture, the pretrained convolutional layers were frozen, and a new classifier was trained on the custom dataset. Among the tested networks, EfficientNetB0 demonstrated the best performance, achieving the highest overall accuracy of 70.64%, with a precision of 0.6948, a recall of 0.6950, and an F1 score of 0.6929. The model's supremacy was further supported by a confusion matrix showing high values along the main diagonal. Google Colab was used for code development, and the model was successfully integrated with the LINE application using Ngrok, a channel secret, and a channel access token. To use the tool, users simply upload a photo of their oral ulcer to the Smile Bot chat. The bot immediately replies with the predicted lesion type, a classification, confidence percentage, and a Grad-CAM visualization map showing exactly which part of the image the AI analyzed. Future work will focus on gathering more data to improve accuracy, preventing overfitting, expanding the system to detect a wider variety of oral diseases, and providing causes and treatment advice within the chat. To reach users without social media, plans also include expanding the platform to web-based and application-based interfaces.

Keywords: AI; Chatbot; Convolutional Neural Networ; Detection for Oral Diseases; EfficientNetB0

Deciphering the Tissue-Specific Molecular Imprint of Oral Mesenchymal Stem Cells: A Comparative RNA-Seq Analysis

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ABSTRACT: Owing to their multilineage differentiation capabilities, mesenchymal stem cells (MSCs) serve as a cornerstone in regenerative medicine. However, the tissue origin fundamentally dictates their functional traits. This present study explores to decipher the transcriptomic heterogeneity between stem cells from human exfoliated deciduous teeth (SHED) and alveolar bone mesenchymal stem cells (ABMSCs) to establish precise cell-selection criteria for oral tissue engineering. High-throughput RNA sequencing was performed on biological replicates (n = 3 per group) obtained from independent human tissue donors, allowing biological variation between donors to be captured and improving the robustness and reproducibility of the findings. Differentially expressed genes (DEGs) were identified ($\log_2FC \geq 2$, $p < 0.05$) and analyzed via DAVID and STRING bioinformatics tools. Transcriptomic analysis identified 477 upregulated and 220 downregulated transcripts in ABMSCs relative to SHED. ABMSCs exhibited elevated genes involved in immunomodulatory responses and cytokine-mediated signaling, whereas suppressed genes (upregulated in SHED) were enriched in neurogenic pathways. Importantly, STRING analysis revealed distinct topological structures and hub proteins between groups, confirming that ABMSCs and SHED operate via fundamentally different molecular machinery. Collectively, our data demonstrates that the tissue origin of oral MSCs establishes distinct molecular signatures that shape their biological properties and therapeutic potential. The identification of clearly divergent regulatory networks provides important insights into the functional characteristics of MSCs derived from different tissue sources and serves as a critical foundation for developing targeted and highly specific regenerative therapies for oral and maxillofacial tissues.

Keywords: Alveolar bone; Mesenchymal Stem Cells, RNA sequencing, Regenerative tissue, SHED

Transcriptomic Effects of Propylene Glycol on Oral Mucosal Barrier Integrity

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ABSTRACT: Despite its established status as a safe compound for systemic consumption, the localized cellular effects of propylene glycol (PG) on the oral cavity are not yet fully understood, a critical knowledge gap given its pervasive use in oral care products, cosmetics, and vaping devices. To address this, the present study utilized RNA sequencing to map the comprehensive transcriptomic profile of oral epithelial cells subjected to PG exposure. Following a 72-hour treatment with 100 µM PG, high-throughput transcriptomic analysis of 13,620 annotated genes revealed 65 significantly altered transcripts, consisting of 43 up-regulated and 22 down-regulated genes. Bioinformatic enrichment unveiled a coordinated, two-pronged cellular response to the compound. The up-regulated gene cohort primarily clustered around immunomodulatory and stress pathways, notably interferon (IFN) signaling and cytokine-mediated antiviral defenses. Conversely, genes vital to mucosal barrier maintenance, including those regulating keratinocyte differentiation, cornified envelope assembly, and tissue keratinization, were systematically suppressed. These data suggest that non-lethal PG exposure forces a homeostatic reallocation in oral keratinocytes, driving immune-stress reactivity while actively undermining the structural maturation necessary for physical defense. Ultimately, this PG-mediated dampening of barrier-associated gene networks could leave the oral mucosa more susceptible to external toxins or pathogenic invasion.

Keyword: Epithelial cells, Gene expression, Propylene glycol, RNA sequencing, Transcriptomics

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ABSTRACT: Surgical site infections (SSIs) represent a major global health challenge, contributing to increased patient morbidity, prolonged hospital stays, and rising healthcare costs worldwide. Current post-operative monitoring relies primarily on visual clinical inspection, which is inherently subjective and cannot detect biochemical changes before symptoms become clinically apparent. This study proposes the development and bench-scale evaluation of a proof-of-concept smart suture intended to support early detection of SSIs through continuous electrical monitoring of wound-fluid pH. A polyaniline (PANI) emeraldine salt coating will be synthesised by chemical oxidative polymerisation of aniline monomer using ammonium persulfate as oxidant in hydrochloric acid, and applied to a USP-certified, medical-grade suture thread through repeated dip-coating cycles to render it conductive. The sensing mechanism exploits the protonation-dependent conductivity of PANI, which undergoes measurable resistance changes as fluid pH rises from a healthy baseline of approximately 7.4 toward the mildly alkaline range of 8.0–9.0 reported in some infected wounds. Wound pH is treated here as a non-specific indicator: alkalinisation has been associated with bacterial ammonia production and proteolytic enzyme activity, but it is also influenced by tissue perfusion, exudate composition, dressing materials, and normal healing dynamics, so the device is positioned as a screening aid rather than a diagnostic test. The coated suture will be incorporated into a dual-channel voltage-divider circuit alongside a silver/silver chloride (Ag/AgCl) reference electrode, connected to an ESP32 microcontroller with 12-bit analogue-to-digital conversion; calibrated pH readings will be transmitted in real time via Bluetooth Low Energy to a smartphone application. Initial validation will be performed in abiotic agar gel tissue simulants at depths of 1–2 cm to demonstrate subsurface sensing without direct surface access to the fibre, and a calibration curve will be established across pH 7.4–8.6 with a minimum of ten repeated trials per condition. Anticipated results: the PANI-coated suture is expected to produce a consistent, repeatable resistance response varying monotonically with pH across this range, with trial-to-trial variation small enough to resolve a shift on the order of 0.3 pH units. These outcomes are anticipated rather than experimentally confirmed; validation in bacterial infection models and biological wound fluid, alongside assessment of biocompatibility, coating stability, and protein fouling, is required before any performance claims can be made. If realised, the approach would support a low-cost, passive sensing platform for early SSI screening in resource-limited clinical settings.

Keywords: Surgical site infection (SSI); polyaniline (PANI); protonation; bacterial ammonia production; proteolytic enzyme activity; Ag/AgCl reference electrode; ESP32; wound pH sensing

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Development of a Graphene-Modified Quartz Crystal Microbalance Biosensor for Non-Invasive Prostate Cancer Detection

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ABSTRACT: Prostate cancer is one of the most common cancers among men worldwide, and early diagnosis is essential for improved treatment outcomes and survival rates. This preliminary study presents a graphene oxide-coated quartz crystal microbalance (GO-QCM) biosensor for label-free detection of distal-less homeobox-1 (DLX1), a biomarker associated with prostate cancer progression. The objective of this work was to investigate the feasibility of a graphene-modified QCM platform for sensitive and reusable DLX1 detection. Gold-coated QCM sensors were modified with graphene oxide to improve surface area and biomolecular interaction. DLX1 single-stranded DNA probes were immobilized onto the GO-QCM surface through EDC/NHS coupling chemistry. Biosensor performance was evaluated using DLX1 target concentrations ranging from 1 nM to 10 μM by monitoring resonance frequency changes during hybridization. The results confirmed an immobilization of the DLX1 probe through resonance frequency reduction caused by mass loading on the sensor surface. Concentrations from 10 nM to 10 μM produced negative frequency shifts that confirmed successful probe-target hybridization, whereas weak hybridization behavior was observed at a concentration of 1 nM. The strongest response was observed at a concentration of 1 μM. In addition, the biosensor demonstrated regeneration capability following NaOH treatment, which indicated potential reusability for repeated detection cycles.

Keywords: DLX1 biomarker; DNA biosensor; Graphene oxide; Prostate cancer; Quartz crystal microbalance

mecA and *dnaG* Gene Knockout in *Staphylococcus aureus* via CRISPR-Cas9 System as a Model for *Methicillin-resistant Staphylococcus aureus* Inhibition

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ABSTRACT: The rapid rise of antibiotic-resistant *Staphylococcus aureus* (*S. aureus*) poses a significant global public health challenge. Although *S. aureus* commonly colonizes the skin and respiratory tract of approximately 30% of healthy individuals without causing disease, it can cause infections ranging from mild skin and soft tissue infections to severe, life-threatening illnesses when it enters the body through wounds or other breaches in host defenses. Conventional antibiotics often lack specificity, resulting in disruption of beneficial microbiota and contributing to the spread of antimicrobial resistance. This study explores the potential of CRISPR-Cas9 as a programmable antimicrobial strategy by targeting two genes in *S. aureus*: mecA, which confers methicillin resistance in methicillin-resistant *S. aureus* (MRSA), and dnaG, which encodes a DNA primase essential for bacterial DNA replication. Following CRISPR-Cas9 treatment, PCR amplification and gel electrophoresis were used to assess the targeted genomic regions for evidence of editing. The observed PCR results were consistent with successful modification of the target loci, supporting the feasibility of CRISPR-Cas9-mediated gene targeting in *S. aureus*. These findings demonstrate the potential of CRISPR-Cas9 as a targeted antimicrobial platform against antibiotic-resistant *S. aureus*. Additional validation, including DNA sequencing and functional assays, will be necessary to confirm gene disruption and evaluate treatment specificity and its effects on non-target microbial communities.

Keywords: Antibiotic resistance; CRISPR Cas-9; *S. aureus*; Knockout; Gene editing

An AI-Based System for Facial Expression Classification: A Comparative Study of Model Training Across Various Emotions

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ABSTRACT: This study addresses the diagnostic challenges of monitoring depression, a major mental health disorder affecting millions worldwide, by developing a facial emotion recognition system designed to track emotional changes across therapy sessions. Current therapy outcome assessments heavily rely on subjective clinical interviews and self-report questionnaires, which are time-consuming and heavily strain limited psychiatric resources, particularly in countries like Thailand. To provide mental health professionals with objective, quantitative metrics, this research evaluated an AI framework to classify seven distinct emotions. Utilizing a dataset of 2,800 images partitioned into training (60%), validation (20%), and testing (20%) subsets, deep learning architectures, including VGG16, ResNet, EfficientNetB0, and Xception, were trained for 16 epochs, with Xception serving as the core model. The models demonstrated excellent stability with no signs of overfitting or underfitting, achieving an overall average accuracy of approximately 90% and average F1 scores ranging between 0.85 and 0.89. Explainable AI heatmaps successfully verified that the models focused accurately on key facial regions relevant to emotion detection. Among the categories, happiness was classified with the highest precision, while disgust yielded the lowest performance. By converting qualitative facial expressions into quantifiable data, this system reduces clinical workloads, supports psychiatrists with objective evaluation tools, and enhances the overall accessibility of mental health monitoring. Future work will focus on integrating real-time, frame-by-frame processing to continuously analyze emotional states within clinical, hospital, and psychiatric treatment environments, offering medical professionals comprehensive longitudinal insights for optimized patient care.

Keywords: Depression; Deep Learning; Emotion Recognition; Explainable AI; Xception

Development of an AI-Based LINE Chatbot for Preliminary Classification of Common Pediatric Skin Conditions

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ABSTRACT: This study addresses the diagnostic challenges posed by overlapping symptoms among common pediatric skin conditions, including Heat Rash, Molluscum Contagiosum, Ringworm, Seborrheic Dermatitis, Urticaria, and Normal Skin, by developing an artificial intelligence (AI)-based framework for preliminary classification. A dataset of 655 images was divided into training (398), validation (162), and testing (95) subsets. Four pre-trained convolutional neural network architectures (VGG16, Xception, EfficientNetB0, and ResNet50) were evaluated using transfer learning over 25 epochs. ResNet50 demonstrated the best overall performance, achieving a test accuracy of 82.22%, a precision of 0.8225, a recall of 0.8222, and an F1-score of 0.8188. The model achieved strong classification performance for Molluscum Contagiosum and Normal Skin, with F1-scores of 0.88 and 0.87, respectively. In contrast, Heat Rash remained the most challenging class (F1-score = 0.64) because of its visual similarity to other inflammatory skin conditions, highlighting the need for targeted class-weighting strategies and focal loss to improve classification performance for visually similar classes in future work. Training curves indicated slight overfitting, with validation accuracy stabilizing at approximately 80–86%. To translate the model into an accessible screening tool, the ResNet50 model was integrated into a LINE Chatbot. By uploading an image of the affected skin, users receive an immediate preliminary prediction, a confidence score indicating the estimated probability of the predicted class, an explainable AI heatmap highlighting the image regions influencing the prediction, and basic care recommendations. The chatbot clearly communicates that its predictions are intended solely for preliminary screening and should not be considered a substitute for professional medical diagnosis. Future work will expand the dataset to include more diverse skin tones and implement k-fold cross-validation to provide a more statistically robust model evaluation, thereby improving model robustness, generalizability, and clinical reliability.

Keywords: Image classification; LINE Chatbot; Pediatric skin conditions; ResNet50; Transfer learning

Computational Evaluation of Understudied Second-Shell Residues Surrounding the Catalytic Triad of PETase

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ABSTRACT: Polyethylene terephthalate (PET) pollution is a growing environmental challenge due to the persistence of plastic waste in natural ecosystems. With over 380 million tonnes of plastic produced annually and enzymatic degradation offers a promising low-energy recycling strategy, improving the thermostability of poly(ethylene terephthalate) hydrolase (PETase) is essential for industrial applications, particularly in tropical regions such as Southeast Asia. While previous engineering efforts have focused on active-site residues and known thermostability hotspots, the role of second-shell residues surrounding the catalytic triad remains poorly understood. This study aimed to identify and evaluate understudied second-shell residues as potential engineering targets in PETase. The crystal structure of PETase (PDB: 5XJH) was analyzed using PyMOL to identify residues surrounding the catalytic triad (Ser160, Asp206, and His237). Candidate residues were selected based on spatial proximity, secondary structure, and literature screening. Nine understudied residues were subjected to computational mutagenesis using DynaMut2 to predict changes in protein stability (ΔΔG). Among the single mutations evaluated, the least destabilizing effects were observed for A89P (-0.29 kcal/mol) and A202P (-0.32 kcal/mol). Five rationally selected double-mutant combinations were additionally assessed, all of which were predicted to further reduce stability, with ΔΔG values ranging from -0.26 to -1.30 kcal/mol. These results suggest that the second-shell environment surrounding the PETase catalytic triad is structurally constrained and sensitive to amino-acid substitutions. Most single and double mutations decreased predicted stability, indicating that these residues contribute to maintaining enzyme structure. This study establishes a computational elimination framework that narrows the mutational search space by identifying second-shell positions with limited tolerance to substitution, thereby supporting more targeted strategies for future PETase engineering and sustainable plastic biodegradation.

Keywords: Computational mutagenesis; Plastic biodegradation; Poly(ethylene terephthalate) hydrolase (PETase); Protein stability; Second-shell residues

Deep Learning-Based Classification of Oral Diseases

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ABSTRACT: Oral lesions, including fibroma, hand, foot, and mouth disease (HFMD), mouth ulcers, mucoceles, and oral cancer, are common health conditions that affect the mouth and can cause pain, discomfort, and difficulty eating or speaking. While some lesions are harmless, others may indicate serious diseases such as oral cancer, making early detection and accurate diagnosis important for maintaining oral health and improving patient outcomes. Currently, oral lesions are primarily diagnosed through visual examination by healthcare professionals, which can be challenging and time-consuming due to the similar visual appearances of different lesions, potentially leading to delayed diagnosis and treatment. Therefore, this study investigates the effectiveness of various pretrained models to identify the best-performing model for further development. The dataset consisted of 1,270 images, which were divided into 972 training images, 148 validation images, and 150 test images. Four pre-trained models: EfficientNetB0, ResNet50, VGG16, Xception, were compared for oral lesion classification. Each model was trained for 35 epochs using the same training, validation, and test sets. Their performances were evaluated and compared based on accuracy, F1 score, confusion matrix analysis, and training quality. ResNet50 achieved the best overall performance, with an accuracy of 83.33% and an F1 score of 0.8344, while EfficientNetB0 achieved an accuracy of 78.21% and an F1 score of 0.7439. Xception achieved an accuracy of 78.00% and an F1 score of 0.7870, whereas VGG16 achieved an accuracy of 60.66% and an F1 score of 0.600. For the oral cancer class, the selected ResNet50 model achieved a sensitivity (recall) of 84.0%, specificity of 96.8%, showing promising performance for oral cancer screening while maintaining a low false-positive rate. Heatmaps verified that the models focused on relevant oral lesion areas, though some confusion occurred between mouth ulcers and mucoceles due to their similar visual characteristics. Nevertheless, the model is intended as a screening support tool rather than a definitive diagnosis system, and its predictions should be interpreted in conjunction with clinical examination and confirmed by qualified healthcare professionals.

Keywords: Artificial intelligence; Deep learning; Oral disease; Image classification

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