

GRUBER - SOEDIGDO



DIKTISAINTEK
BERDAMPAK

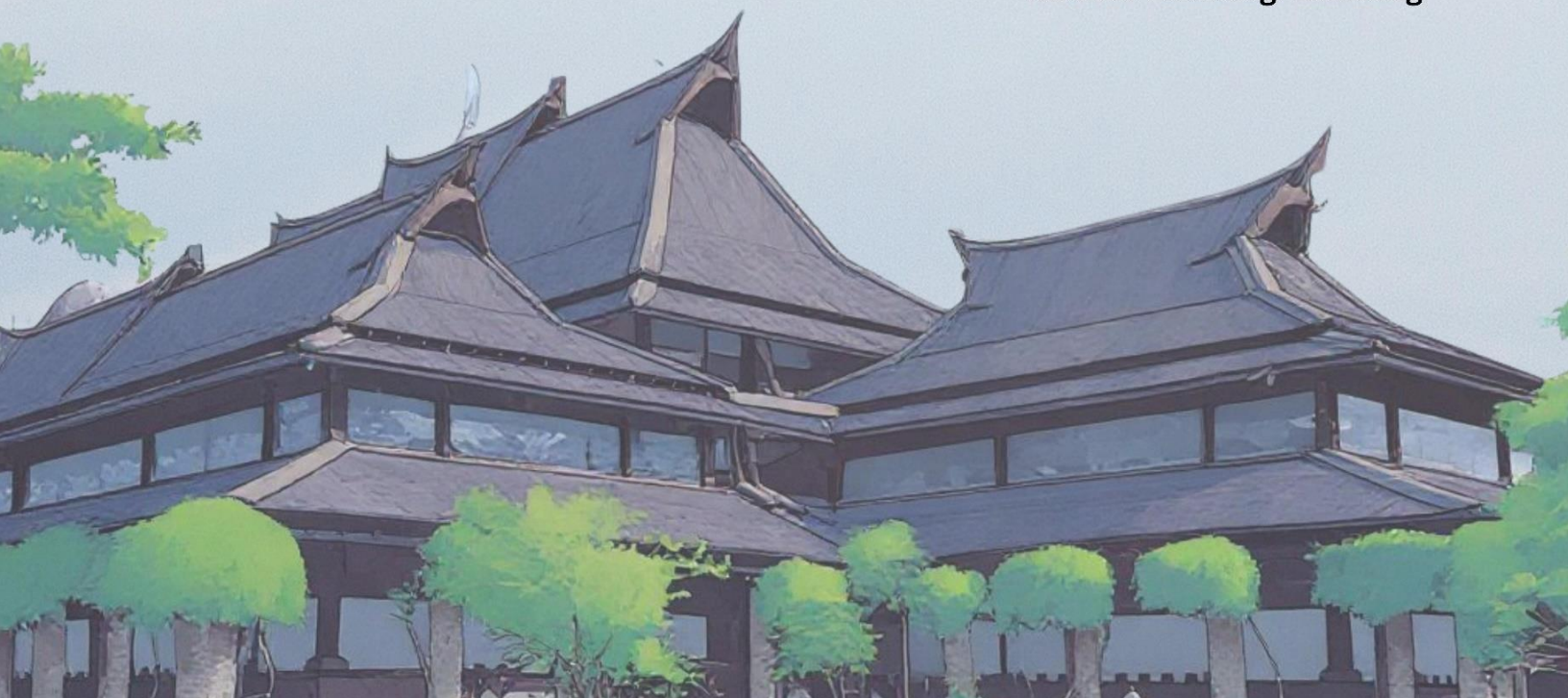
THE 8TH GRUBER-SOEDIGDO LECTURE (GSL) 2025

*"Biomaterial and Biomolecular Engineering
for Health, Environment, Food, and Bio-Based Industries"*

BOOK OF ABSTRACT

Thursday, October 30th 2025

CRCS Multipurpose Hall 3rd Floor, Ganesha Campus,
Institut Teknologi Bandung



BOOK OF ABSTRACT

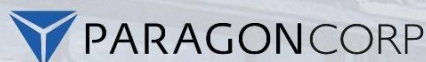
GRUBER - SOEDIGDO



THE 8TH GRUBER-SOEDIGDO LECTURE (GSL) 2025

*"Biomaterial and Biomolecular Engineering
for Health, Environment, Food, and Bio-Based Industries"*

SPONSORED BY



Established in 1994, PT. Kromtekindo Utama is the authorized distributor of Waters Corporation in Indonesia, a leading pioneer in Liquid Chromatography (LC) and Mass Spectrometry (MS).



Chromatography Systems (HPLC/UHPLC/UPLC)

Meet all your application requirements with Waters chromatography systems, including our Dependability line of HPLC Systems, Flexibility line of HPLC/UHPLC Systems, Performance line of UHPLC/UPLC Systems, Purification Systems, and Specialty Systems.

Mass Spectrometry (LC-MS/MS and LC-HRMS)

Waters mass spectrometry solutions provide you with the tools to confidently identify and quantify unknown compounds in complex samples, and confirm trace components at the lowest possible levels. Instrumentation that allows you to comprehensively catalog complex samples in a single analysis is now available.

With technologies like QuanTof (for a new dimension in high-resolution exact mass MS), StepWave (for confirmation of trace components), Triwave (for characterization of complex mixtures), and MSE (for exact-mass ion spectra from your samples), your possibilities are endless.



Chromatography Consumables and Supplies

Reach the highest level of chromatographic performance and ensure that methods you develop today will have the same repeatable result tomorrow with Waters chromatography consumables & supplies.



Sample Preparation Instrument Andrew+ Pipetting Robot

Andrew is a novel pipetting robot that enhances the reproducibility and efficiency of a laboratory by automating the use of standard manual pipettes. By providing scientists with a fully automated and unattended pipetting solution, scientific resources can now focus their efforts on important tasks without being slowed down by the pipetting process.



About PT Batuwaris Dinamika

Established since 1994, PT Batuwaris Dinamika is distributor for several brands such as, **JASCO**, **NEOSPECTRA SI-WARE**, **MIURA**, **DAICEL**, **SHODEX**, **OSAKA SODA**, **IMCHEM**, **CHROMANIK** and **SHINWA**. We focus on analytical instruments and analytical accessories for pharmaceutical, food, chemical, environmental, feed, even airport security companies.

Get to Know Our Product

• **JASCO** Spectroscopy



UV/Vis-NIR
Spectrophotometer



FTIR-4X



FTIR Microscopy



Spectrofluorometer



CD Spectrometer



Digital Polarimeter

Other Products:

Vibrational CD, Circularly Polarized Luminescence (CPL), FTIR, FTIR-Portable, Probe Raman, Raman Imaging Microscopy, UV Vis/NIR Microscopy, Spectrofluorometers, Dissolution Test er, Film Thickness, Near Field Scanning, Spectra Manager™ Suite.

• **JASCO** Chromatography



LC-4000 Series

Other Products:

HPLC, UHPLC, RHPLC, Single Quad LC-MS, Prep LC, Analytical SFC, Semi-Preparative SFC, Hybrid SFC, Fuel Analysis by SFC-FID, Prep SFC, Supercritical Fluid Extraction, Chromatography Software

• **NeoSpectra™** by Si-Ware **Handheld NIR Spectroscopy**



The NeoSpectra platform includes easy-to-use software and hardware products ready to provide instant results and analysis for most product types from anywhere



Rotator



Saucer



Liquid

Get to Know Our Product

- **Automated Sample Preparation**

Fully Automated Sample Preparation System for POPs analysis

Miura

GO-4EHT



NO. 1 CHOICE
For DIOXINS
& PCBs

GO-EHT systems resulting independent and efficient automated sample preparation for Dioxins and PCB as well as other persistent organic pollutants.

- **HPLC Solution**



DAICEL

Chiral Column
New Generation
Chiral Column



Shodex

Polymer Column
High-Quality Polymer-
based Column



OSAKA SODA

Capcell PAK Column
A Column that Best
Matches to Your Needs



inChem

Silica Column
One-stop Supply for
Chromatography Column



Core Shell

HPLC Column
Technology



Shinwa Chemical

**Chiral Separation
Chromatography**

One Stop
HPLC Solution

Demo Ready

- **Pharmaceutical Impurities & Labelled Standard**

A Wide Range of High-Quality Pharmaceutical Standards with High Purity

The presence of impurities in pharmaceutical products, even in trace amounts, may influence the efficacy and safety of pharmaceutical products. Identification and quantification of impurities (Impurity Profile Study) is a critical quality parameter and carefully reviewed by regulatory authorities.

DAICEL

- **Laboratory Equipment & Consumable**

Proven Laboratory Equipment technology for mixing, heating, distilling and crushing applications.

Pipette



GC Column



Imchem Vials



Magnetic Stirrer



Disperser



Viscometer



**BATUWARIS
DINAMIKA**

To learn more about Batuwaris Dinamika products please visit :



Main Office:

Jl. RCVeteran No. 9 Tanah Kusir Jakarta Selatan
DKI Jakarta - 12330

Support Office:

AMG Tower, room B03-B 8th floor Jl. Dukuh Menanggal 1-A
Surabaya Jawa Timur - 60234

0811 9690 9159

info@batuwaris.com

www.batuwaris.com

Welcome Speech

Chair of GSL Organizing Committee

It is with great pleasure and honor that I welcome all speakers, guests, and participants to The 8th Gruber–Soedigdo Lecture (GSL) 2025, organized by the Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences (FMIPA), Institut Teknologi Bandung (ITB), in collaboration with Himpunan Kimia Indonesia (HKI) – Divisi Kimia Biologi and Perhimpunan Biokimia dan Biologi Molekuler Indonesia (PBBMI) – Cabang Jawa Barat.

The Gruber–Soedigdo Lecture is a biennial scientific forum first established in 2006 as an academic tribute to Prof. Max Gruber (University of Groningen, The Netherlands) and Prof. Soedigdo Pringgoprawiro (Institut Teknologi Bandung, Indonesia), who together pioneered the establishment of the Biochemistry Division at ITB. Their vision, mentorship, and scientific leadership laid the foundation for biochemical education and research in Indonesia. Their legacy continues to inspire generations of scientists and educators to advance knowledge, innovation, and collaboration in the biochemical sciences.

Since its inception, the GSL has served as a vital platform for scholarly exchange, uniting academics, researchers, and practitioners from both national and international institutions. Each lecture series reflects the evolving frontiers of biochemical and biomolecular research and embodies the commitment of ITB’s scientific community to collaboration, innovation, and excellence.

The inaugural GSL 2006, focused on carbohydrases, enzymes fundamental to carbohydrate transformation and industrial biotechnology. The second GSL (2008) explored protein folding and dynamics in disease, while the third (2010) addressed molecular biotechnology in health and bioindustry. The fourth GSL (2012) advanced the theme of carbohydrate and lipid bioengineering, and the fifth (2015) centered on biocatalysts for food, energy, and medical applications. The sixth GSL (2019) highlighted advances in health and biomaterials, and the seventh (2023) expanded its focus to biochemistry in medical and environmental applications.

Over nearly two decades, the Gruber–Soedigdo Lecture has consistently featured distinguished scientists as keynote speakers, alongside oral and poster presentations and technical workshops that strengthen the capacity and connectivity of Indonesia’s biochemical community.

This year’s symposium continues that legacy under the theme “Biomaterial and Biomolecular Engineering for Health, Environment, Food, and Bio-Based Industries.” The theme reflects our shared commitment to integrating molecular science and biomaterial engineering in pursuit of sustainable innovation for human and environmental well-being. We are delighted to welcome around one hundred participants representing universities and research institutions from across Indonesia, including Institut Teknologi Bandung, Universitas Muhammadiyah Purwokerto, Universitas Pendidikan Indonesia Bandung, Universitas Jember East Java, Universitas Airlangga Surabaya East Java, Universitas Padjadjaran Bandung, Universitas Gadjah Mada Yogyakarta Central Java, Universitas Pertamina Jakarta, Universitas Negeri Jakarta, Universitas Jenderal Soedirman Central Java, Universitas Lambung Mangkurat South Kalimantan, Universitas Pattimura Maluku, Universitas Islam Negeri Ar-Raniry Banda Aceh, Universitas Lampung, UIN Sunan Gunung Djati Bandung, I3L University Jakarta, Universitas Riau, Politeknik Kesehatan Kementerian kesehatan Bandung, Universitas Bhakti Kencana Bandung, and the National Research and Innovation Agency (BRIN). This diverse participation—comprising faculty members, researchers, and students—reflects the collaborative and inclusive spirit of the Gruber–Soedigdo Lecture, which continues to unite the biochemical and biomolecular research community across Indonesia.

This year's distinguished speakers are:

1. Prof. Katja Loos (Zernike Institute for Advanced Materials, University of Groningen, The Netherlands)
2. Prof. Keiji Numata (Kyoto University, Japan)
3. Prof. Dessy Natalia (Institut Teknologi Bandung)
4. Prof. Dede Heri Yulianto (National Research and Innovation Agency – BRIN)
5. Dr. Rindia Maharani Putri (Institut Teknologi Bandung)
6. Dr. Lia Amelia Tresna Wulan Asri, PhD (Institut Teknologi Bandung)

Together, they represent the broad and interdisciplinary spirit of modern biomolecular science — spanning biomaterial chemistry, enzyme engineering, molecular design, and sustainable biotechnology. In addition to the symposium, GSL 2025 features two specialized workshops designed to strengthen technical expertise and promote collaboration among young scientists and postgraduate researchers:

1. Proteomics: Techniques, Applications, and Data Analysis — *sponsored by PT Kromtekindo Utama and WATERS™*, and
2. Genomic Mining for Enzyme Discovery — *sponsored by PT Indolab Utama*.

Held on 31 October and 1 November 2025, these workshops attracted participants from a wide range of institutions, including Institut Teknologi Bandung, Universitas Padjadjaran, Universitas Jember, Universitas Riau, UIN Sunan Kalijaga Yogyakarta, Universitas Jenderal Achmad Yani (Unjani), STIFAR Riau, and the Faculty of Medicine. Participation also came from Prodia, Labiovak, and PT Pakar Biomedika Indonesia, representing strong collaboration between academia, healthcare, and the biotechnology industry. Their active engagement demonstrates the growing national interest in advanced molecular and analytical techniques that drive today's biochemical and biotechnological discoveries.

We extend our deepest gratitude to all our sponsors for their invaluable partnership and generous support of The 8th Gruber–Soedigdo Lecture 2025: PT Kromtekindo Utama, WATERS™, PT Batuwaris Dinamika, PT DYNATECH, PT Indolab Utama, PT Bangun Rasaguna Lestari (WINCHEEZ), IRSI, LABQUIP, GENE CRAFT LABS, PARAGON CORP, PT Genetika Science, PT Nutrilab Pratama, and PT Sartonet Filtrasi Indonesia. Your continued collaboration and commitment play an essential role in supporting scientific excellence and education in Indonesia.

On behalf of the organizing committee, I would also like to express my sincere appreciation to our Advisory Board, committee members, and student organizers for their dedication and teamwork in realizing this event. I would especially like to recognize my fellow lecturers in the Division of Biochemistry and Biomolecular Engineering, who, despite their busy schedules in teaching and research, have devoted their time, creativity, and leadership to organizing and delivering this year's program with great dedication and care.

To all participants, I hope that The 8th Gruber–Soedigdo Lecture 2025 will inspire meaningful dialogue, new collaborations, and a renewed sense of purpose in advancing biochemical and biomolecular research.

Once again, welcome to The 8th Gruber–Soedigdo Lecture 2025.

Let us celebrate science, collaboration, and the enduring legacy of Prof. Soedigdo and Prof. Max Gruber, whose vision continues to guide and inspire us toward innovation and excellence.

Thank you, and I wish you all an inspiring and productive meeting.

Alfredo Kono, Ph.D

Chair, Organizing Committee

The 8th Gruber–Soedigdo Lecture 2025

Biochemistry and Biomolecular Engineering Research Division

Faculty of Mathematics and Natural Sciences

Institut Teknologi Bandung

Welcome Speech

Dean of Faculty of Mathematics and Natural Sciences

Assalamualaikum warahmatullahi wabarakaatuh

Dear Esteemed Speakers, Presenters, Sponsors, and Honorable Guests,

Dear Participants and Students,

It is with great honor and joy that I welcome all distinguished guests, esteemed speakers, and participants to the 8th Gruber-Soedigdo Lecture (GSL) 2025, hosted by the Biochemistry and Biomolecular Engineering Research Division, the Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung. This prestigious lecture series not only commemorates the legacy of Prof. Gruber and Prof. Soedigdo and their contribution to the Biochemistry field, but also continues their vision of advancing scientific knowledge for the benefit of society and humanity.

The theme of this year's event, "Biomaterial and Biomolecular Engineering for Health, Environment, Food, and Bio-Based Industries," reflects the pivotal role of biochemistry and biomolecular sciences in addressing global challenges. Biochemistry touches nearly every aspect of our lives, from disease diagnosis, drug formulation, food technology, to energy, industry, and environmental sustainability. By unraveling the intricate chemical processes that underlie life, biochemistry provides the foundation for innovations that improve human welfare, protect our planet, and shape the future of industries.

Universities and institutes, including ITB, play a crucial role in preparing the next generation of scientists, engineers, and leaders capable of navigating disruption, fostering prosperity, and contributing to peace and sustainable development. At FMIPA ITB, we realize that science and mathematics remain indispensable tools for equipping our youth with the skills necessary to thrive in global competition.

Thus, the Gruber-Soedigdo Lecture serves as a vital platform for knowledge exchange, collaboration, and inspiration. It brings together world-renowned scholars, national leaders in research, and young scientists to share cutting-edge discoveries, explore transformative applications, and forge new partnerships. The accompanying Biochemistry Workshops on Advances in Proteomics and Genomic Mining for Enzyme Discovery will further enrich this forum, enabling participants to gain practical insights and expand their research horizons.

On behalf of FMIPA ITB, I express my deepest appreciation to our distinguished speakers, dedicated organizing committee, and valued sponsors for making this event possible. May this year's Gruber-Soedigdo Lecture not only advance our scientific frontiers, but also inspire us all to work together toward a healthier, more sustainable, and more prosperous future.

I wish you a fruitful and memorable experience at the 8th Gruber-Soedigdo Lecture 2025.

Wassalamualaikum warahmatullahi wabarakaatuh,

Dr. Aep Patah

Dean of the Faculty of Mathematics and Natural Sciences

Institut Teknologi Bandung

Organizing Committee

Advisory Committee:

Prof. Dessy Natalia, Ph.D
Prof. Akhmaloka, Ph.D
Prof. Fida Madayanti W., Ph.D
Prof. Enny Ratnaningsih, Ph.D
Prof. Dr. Rukman Hertadi
Prof. Zeily Nurachman, D.Sc

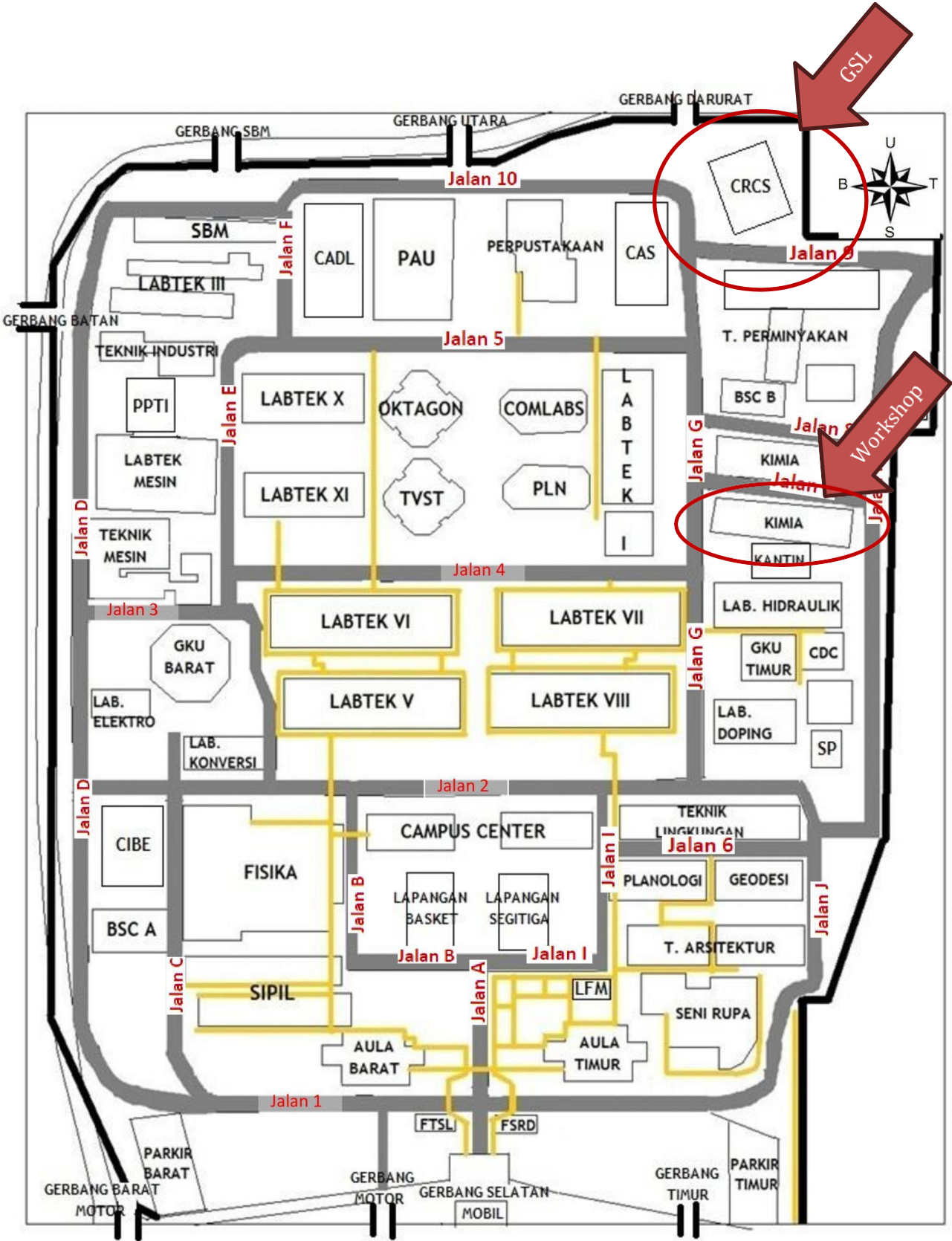
Committee:

Alfredo Kono, Ph.D
Rindia Maharani Putri, Ph.D
Dr. rer. nat. Fifi Fitriyah Masduki
Dr. Made Puspasari W.
Dr. Yanti Rachmayanti
Dr. Ihsanawati
Dr. Reza Aditama
Dr. Wiwit Nurhidayah

Students and Supporting Staff:

Abdur Rahman Arif	Khansa Luthfiyah
Aisyah Meichika Tazkia	Khansa Taqy
Alma Tyara Simbara	Lewi Axel Badia Sitorus
Angela Dwi Puspiturasia	Luthfanada Adrini
Anhar Rahmawan	Luxy Grebers
Baiq Repika Nurul	M. Fauzan Al-Amin
Bella Yashinta	M. Fauzan Azima
Behzad Farhan	Marsaa Syafaqah A.
Dadan Gunawan	Murni Fitria
Deviyanthi N. A.	Nadia Tuada Afnan
Desak Gede Tirta Andini	Najma Salsabila
Diah Hardianti	Naomi Azalia
Diajeng Kesuma Dinda	Novan Rois
Dwindi Agryanti	Nur Shabrina Rufaidah
Fadila Tsania	Putri Ayunita Azahra
Fatimah Qurrota Ayun	Puspa Sari Dewi
Fera Faridatul	Rachma Ayu Widiasanti
Gerald Arya Dewangga	Rizarullah
Gita Ostensia	Risma Septi Insani
Intan Khoerunnisa	Satria Widiatmoko
Jesa Eranda Ramadhani	Wiwit Ridhani Rahmaniyah
Khala Iva Khiyarudami	Zeini Alkarina

Map of ITB



Lectures Schedule

Timetable (WIB)	Program
08.00 – 08.30	Open gate and registration For poster presenters, please submit your A1-sized poster at the registration desk
08.30 – 08.40	Opening by Master of Ceremony (MC)
08.40 – 09.00	Welcome speech
09.00 – 09.10	Photo session
09.10 – 09.50	Lecture by Prof. Dr. Katja Loos University of Groningen, The Netherlands
09.50 – 10.20	Lecture by Prof. Dessy Natalia, PhD Institut Teknologi Bandung
10.20 – 10.30	Panel discussion
10.30 – 10.50	Sponsor Showcase by PT Batuwaris Dinamika and PT Kromtekindo Utama
10.50 – 11.00	Coffee break, move to parallel sessions at CRCS 2 nd floor
11.00 – onwards	Parallel session (Q & A by the end of the session) For oral presenters, please prepare a 7-min presentation deck
until 13.00	Lunch and prayer break Lunch will be provided on the 3 rd floor Prayer room (musholla) is available on the 2 nd floor
13.00 – 13.40	Lecture by Prof. Dr. Keiji Numata Kyoto University, Japan
13.40 – 14.10	Lecture by Prof. Dede Heri Yuli Yanto, PhD National Research and Inovation Agency (BRIN)
14.10 – 14.30	Lecture by Rindia Maharani Putri, PhD Institut Teknologi Bandung
14.30 – 14.50	Lecture by Lia Amelia Tresna Wulan Asri, PhD Institut Teknologi Bandung
14.50 – 15.05	Panel discussion
15.05 – 16.00	Poster session and coffee break
16.00 – 16.15	Closing ceremony

Contents

Welcome Speech Chair of GSL Organizing Committee6

Welcome Speech Dean of Faculty of Mathematics and Natural Sciences8

Organizing Committee9

Map of ITB..... 10

Lectures Schedule..... 11

Contents 12

SPEAKER ABSTRACTS..... 15

 [S-1] Unleashing the Potential of Enzymes for Green Furan-based Polymer Synthesis.... 15

 [S-2] Diversity and Adaptation of α -Amylases: Unlocking the Potential of Starch-Degrading Enzymes for a Sustainable Future 16

 [S-3] Natural and Artificial Spider Silk..... 17

 [S-4] The Role of Laccase in Environmental Bioremediation, Cosmetics, and Health Applications 18

 [S-5] Harnessing Nano-Architectures from the Sea: Multifaceted Strategies for Transforming Diatoms into Functional Materials..... 19

 [S-6] Valorising Keratin and Sericin Proteins from Biomass Residues into Functional Hydrogel Biomaterials 20

RESEARCH ABSTRACTS 21

Bio-based Industries 21

 [BI-1] Immobilization of *Candida rugosa* Lipase on polyhydroxybutyrate Biopolymer as a Supporting Material in Biodiesel Synthesis 21

 [BI-2] Effect of Single Point Mutation in *BaqA4C α -Amylase* to Enhance Activity, Thermostability, and Product Specificity 22

 [BI-3] Preparation and Characterizations of Starch-(Polyethylene-b-Poly(ethylene glycol)) Complexes as Naturally Degradable Plastic Materials 23

 [BI-4] Development of Nutrient-Rich Biostimulants using Seaweed, Fish Paste, and Banana Peel Derivatives 24

 [BI-5] Valorization of Fruit Peels for the Production of Valuable Organic Chemicals Using Metabolically Engineered *Komagataella phaffii* (*Pichia pastoris*) 25

 [BI-6] Genomic Sequencing Analysis of a Unique PLS47 Isolated from Deep Sea Vent..... 26

Environmental Biochemistry 27

 [EB-1] Laccase Production by *Mycorrhizal* Isolates from a Central Kalimantan National Peat Swamp Forest: Screening and Challenges in Quantitative Assesment 27

 [EB-2] Identification and Growth Optimization of Indigenous Thermoacidophilic *Galdieria sulphuraria* from Indonesia for Enhanced CO₂- Sequestration..... 28

 [EB-3] Indonesian Tropical Marine Diatom *Navicula salinicola* NLA: Morphology, Genetic Identification, and Lipid Content..... 29

 [EB-4] A Self-Assembled Erythrocyte Biomatrix as a Superior Biocatalyst for Carbon Capture..... 30

 [EB-5] *Pumiliosphaera acidophila* as Carbon Dioxide Capture in Partial Simulating Flue Gas..... 31

 [EB-6] DNA Barcoding and Antibacterial Activity of *Cryptocarya pulchrinervia* Indigenous Indonesia..... 32

[EB-7] Isolation, Identification and Draft Genome Library Construction of Acidophilic Microalgae from Indonesian Hot Springs	33
[EB-8] Analysis of Growth and Photosynthetic Capacity of Local Green Microalgae Isolate <i>Chlorella sp.</i> ITB2 A in a Semi-Open Phototank System.....	34
Food Biochemistry	35
[FB-1] Synergistic Enhancement of Antimicrobial Activity in <i>Lactococcus lactis</i> ATCC 11454 through CRISPR/Cas9-Mediated <i>ldh</i> Deletion and <i>nisRK</i> Overexpression.....	35
[FB-2] Variation of IPTG Inducer Substitution on the Expression of the <i>xynBTN63D</i> Gene Encoding the Endo- β -1,4-D-Xylanase in <i>Escherichia coli</i> BL21 (DE3)	36
[FB-3] Response Surface Optimization of Black and Green Tea Kombucha Fermentation and Its Impact on Bioactivity, Chemistry, and Sensory Quality	37
Health	38
[H-1] Molecular Insights into Novel IDS Mutations: Protein Structural and Biomarker Correlations in Indonesian Patients with Hunter Syndrome	38
[H-2] Efficacy Test of Master Diagnostic Kit for <i>Salmonella typhi</i> Targeting the <i>sifA</i> Gene in Chicken Samples	39
[H-3] Rational Design and In Silico Validation of a Potent Multi-Epitope Vaccine Candidate Against Dengue Virus	40
[H-4] Metabolomic Analysis to Evaluate the Effect of Fermentation Agitation and Type of Extraction Solvent on Co-Culture of <i>Penicillium sp.</i> LBKURCC34 and <i>Staphylococcus aureus</i>	41
[H-5] Polyvinyl Alcohol Hydrogel Incorporated Keratin and Sericin for Elastic Implants Technology.....	42
[H-6] Comparative Genomics and Genome Mining of Novel Antimicrobials from Gili Meno Lake, Indonesia (Dry Season)	43
[H-7] Development and Experimental Validation of an Optimized mRNA-Based Multi-Epitope Therapeutic Vaccine Candidate for Chronic Hepatitis B	44
[H-8] Efficacy Test of Master Diagnostic <i>Vibrio parahaemolyticus</i> with <i>toxS</i> Gene Target in Food Sample.....	45
[H-9] Potential of <i>ebpS</i> Gene as a Target Detection for <i>Staphylococcus aureus</i> using real-time Polymerase Chain Reaction	46
[H-10] Efficacy Test of the Master Diagnostik <i>Cronobacter sakazakii</i> with <i>grxB</i> Gene Target in Infant Formula Milk Samples.....	47
[H-11] Efficacy Test of the Master Diagnostic <i>Escherichia coli</i> Targeting the <i>acrF</i> Gene in Food Samples.....	48
[H-12] Efficacy Test of Master Diagnostic <i>Shigella flexneri</i> with <i>sfmD</i> Gene Target on Chicken Samples.....	49
[H-13] Stability Assessment of a Prototype Master Diagnostic Kit for Detecting <i>Salmonella typhi</i> , <i>Shigella flexneri</i> , and <i>Escherichia coli</i>	50
[H-14] Expression, Purification, and Characterization of Hepatitis B VLP using LEGO Vaccine Concept.....	51
[H-15] Tuning the Structure and Bioperformance of Doped Biphasic Calcium Phosphate Biomaterial Toward Next Generation Bone Tissue Engineering	52
[H-16] Chemical Modification of Inulin via Acetylation: Optimization, Physicochemical Characterization and Antibacterial Evaluation	53

[H-17] Carotenoids Profile of Seaweed <i>Halimeda sp.</i> Harvested In Two Different Seasons	54
[H-18] The Study of Campesterol as a Therapeutic Agent Candidate	55
[H-19] Development of Multimeric Bann-Rbd Fusion Protein as A Covid-19 Vaccine Candidate	56
[H-20] PHB-Ectoine Microparticles (MPs) with Rhamnolipid Formulation: A Triple-Action System for Skin Protection.....	57
[H-21] The Effect of N331Q Mutation on the Multimer Formation of COVID-19 Vaccine Candidate Bann-RBD.....	58
[H-22] Genome Mining-Based Exploration of Novel Antimicrobial Compounds from Gili Meno Lake Bacterial Isolates During the Rainy Season	59
[H-23] Cloning and Expression of the Gene Encoding Protease from the Marine Bacterium <i>Bacillus amyloliquefaciens</i> ABBD	60
[H-24] CRISPR-Cas9-Based Electrochemical Biosensor for the Detection of Katg Gene Mutation in Isoniazid-Resistant Tuberculosis	61
Others	62
[O-1] Expression of Serine Hydroxymethyltransferase (SHMT) through Metagenomic Approach	62
[O-2] Expression and Characterization of Recombinant Major Ampullate Spidroin Subtype-2 (MaSp2) in <i>Pichia pastoris</i>	63
[O-3] Identification of Pitcher Plant (<i>Nepenthes sp.</i>) Types using Deep Learning-Based Models	64
[O-4] In Silico Multiligand Analysis of <i>Spirulina platensis</i> Bioactive Compounds Targeting IL-6, EGFR, FGFR1, and MMP9 for Wound Healing	65
[O-5] Evaluation of α -amylase Inhibitory Potential of <i>Carica papaya</i> Seed Extracts.....	66
[O-6] Water-Based Extraction and Characterization of κ -carrageenan from <i>Eucheuma spinosum</i> for Future Biomedical Applications.....	67
[O-7] Isolation and Characterization of Growth and Photosynthetic Activity of the Green Microalgae <i>Chlorella sp.</i> ITB1	68

SPEAKER ABSTRACTS

[S-1]

Unleashing the Potential of Enzymes for Green Furan-based Polymer Synthesis

Katja Loos

Macromolecular Chemistry and New Polymeric Materials
Zernike Institute for Advanced Materials, University of Groningen
Nijenborgh 3, 9747 AG Groningen, The Netherlands

e-mail: k.u.loos@rug.nl

Abstract

The enzymatic synthesis of polymers via non-metabolic pathways has a long history but was overshadowed by petroleum-based methods. However, due to the depletion of petroleum resources and rising costs, enzymatic polymerizations are experiencing a resurgence. By combining biobased monomers and enzymatic polymerizations, both the field of enzymatic polymerization and the use of renewable resources can be accelerated, contributing to sustainability in the polymer and coatings industry. Furan derivatives and furan chemistry offer a biobased alternative to phenyl-based polymers, with 2,5-Furandicarboxylic acid (FDCA) being a promising biobased furan monomer. However, its potential is limited by the occurrence of decarboxylation during polymerization. To overcome this challenge, alternative synthesis routes are needed. Enzymatic polycondensation of biobased furan monomers with aliphatic comonomers has successfully produced furan-based polyesters, polyamides, and polyesteramides, offering a green and robust solution for sustainable polymer production.

Keywords: enzymatic polymerization, furan-based polymers, biobased monomers, FDCA, green chemistry, renewable resources, sustainable materials.

[S-2]

Diversity and Adaptation of α -Amylases: Unlocking the Potential of Starch-Degrading Enzymes for a Sustainable Future

Dessy Natalia

Biochemistry and Biomolecular Engineering Research Group,
Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung,
Jl. Ganesha 10, Bandung

e-mail: dessynatalia@itb.ac.id

Abstract

Starch is one of the most common natural carbohydrates and acts as a main source of stored energy in plants. As a versatile and biodegradable biopolymer, starch holds enormous potential as a sustainable raw material for the food, feed, pharmaceutical, and bioenergy industries. Among the enzymes that drive starch biotransformation, α -amylases play a central role by catalysing the hydrolysis of α -1,4-glycosidic linkages. According to the Carbohydrate-Active Enzyme (CAZy) database, α -amylases are classified under the Glycoside Hydrolase family 13 (GH13), a group remarkable for its evolutionary diversity in sequence, structure, and function. Our recent studies have focused on two α -amylases within the GH13_45 subfamily—BaqA from *Bacillus aquimaris* MKSC6.2 and BmaN1 from *Bacillus megaterium* NL3—which exhibit distinctive adaptive features reflecting their ecological origins. BaqA demonstrates halotolerance and enhanced raw starch binding mediated by tandem tryptophan residues and an aromatic-rich C-terminal region, while BmaN1 harbours an atypical catalytic triad (Asp203–Glu231–His294). Through truncation and site-directed mutagenesis, complemented by molecular dynamics simulations, we have uncovered how variations in C-terminal architecture and catalytic configuration fine-tune the trade-off between structural stability and substrate affinity. These findings reveal the evolutionary flexibility of GH13_45 α -amylases and highlight their potential as biocatalysts for sustainable starch processing.

Keywords: α -amylases, BaqA, BmaN1, C-terminal region, catalytic triad.

[S-3]
Natural and Artificial Spider Silk

Keiji Numata^{1,2,3}

¹Department of Material Chemistry, Kyoto University, Kyoto, Japan

²RIKEN Center for Sustainable Resource Science, Saitama, Japan

³Institute for Advanced Biosciences, Keio University, Tsuruoka, Japan

e-mail: numata.keiji.3n@kyoto-u.ac.jp / keiji.numata@riken.jp

Abstract

Structural protein such as silk, collagen, and keratin, is one of the key molecules to realize the unique properties and functions of natural tissues and organisms. Spider silks are among the toughest known materials and thus provide models for renewable, biodegradable, and sustainable biopolymers. However, the entirety of their diversity still remains elusive, and silks that exceed the performance limits of industrial fibers are constantly being found. We obtained transcriptome assemblies from 1098 species of spiders to comprehensively catalog silk gene sequences and measured the mechanical, thermal, structural, and hydration properties of the dragline silks of 446 species. The combination of these silk protein genotype-phenotype data revealed essential contributions of multicomponent structures with major ampullate spidroin 1 to 3 paralogs in high-performance dragline silks and numerous amino acid motifs contributing to each of the measured properties. Our global sampling, comprehensive testing, integrated analysis, and open data will provide a solid starting point for future biomaterial designs. Our research group also reported the new finding in spider silk spinning, which is essential to clear the hierarchical structure of spider silk. The scalable and sustainable synthesis method along the clarified structure-function relationship of natural proteins provides a new insight for structural and functional material design of amino acids-based polymers. Further, my research group is interested in photosynthetic production of biopolymers to reduce production costs and to contribute sustainable society. My research group studies on the photosynthetic bacteria and plant cells to produce spider silk-like polymers. To establish the fundamental platforms for photosynthetic technology, we are currently developing peptide-mediated transformation and protein introduction methods for alga, photosynthetic bacteria, and plants. These new methodologies will be able to support the high-throughput characterizations for biopolymer productions.

Keywords: spider silk, spidroin, biopolymer design, structural proteins, photosynthetic production, sustainable materials, genotype-phenotype relationship.

[S-4]

The Role of Laccase in Environmental Bioremediation, Cosmetics, and Health Applications

Dede Heri Yuli Yanto^{1,2}

¹Research Center for Applied Microbiology, Research Organization of Life Science and Environment, National Research and Innovation Agency (BRIN)

²Soekarno Science and Technology Park, Cibinong Science Center, Jl. Raya Bogor Km. 46, Cibinong, Bogor 16911, Indonesia

e-mail: dede.heri.yuli.yanto@brin.go.id

Abstract

Laccase, a multi-copper oxidase enzyme, is distinguished by its capacity to catalyze the oxidation of a diverse array of substrates, rendering it valuable in various domains such as environmental bioremediation, cosmetics, and health. In environmental bioremediation, laccases facilitate the breakdown of complex pollutants into less toxic forms. This process is accomplished by converting phenolic and non-phenolic compounds into reactive radicals, promoting the degradation of hazardous materials such as dyes and endocrine disruptors, and detoxifying contaminated environments. In the cosmetics industry, laccases contribute to safer formulations by degrading potentially harmful xenobiotic compounds, thereby reducing the risk of allergic reactions and enhancing the stability and efficacy of skincare products. This is achieved through an oxidative mechanism that modifies the molecular structure of allergens and other reactive components. Laccase shows anti-bacterial activity, which is promising for personal care products. In health applications, particularly in cancer therapy, laccase-induced oxidative stress can be utilized to modulate redox signaling pathways, promote apoptosis in cancer cells, and potentially enhance the therapeutic efficacy of treatments through the generation of reactive oxygen species (ROS). This multifunctionality of laccase underscores its potential impact on sustainable industrial applications and promises more efficient and eco-friendly solutions.

Keywords: laccase, environmental bioremediation, anti-bacterial activity, cancer therapy, cosmetics, health.

[S-5]

Harnessing Nano-Architectures from the Sea: Multifaceted Strategies for Transforming Diatoms into Functional Materials

Rindia M. Putri^{1,2}

¹Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Indonesia

²Research Center for Nanoscience and Nanotechnology, Institut Teknologi Bandung, Indonesia

e-mail: rindia.m.putri@itb.ac.id

Abstract

The diatoms, a class of microalgae encased in intricately patterned silica shells, represent one of the most remarkable examples of biological nano-architectures. These naturally occurring biosilica frameworks offer hierarchical porosity, high surface area, and unique optical features. Our group at ITB harnesses multifaceted strategies to repurpose and engineer marine diatom biosilica, such as *Navicula salinicola* NLA and *Cyclotella striata* TBI into functional materials for applications spanning biomaterial formulation, biogenic catalysis, and fine chemical synthesis. Our recent study explored the potential of biosilica as blood-contacting biomaterials by examining how diatom biosilica interacts with human plasma proteins. Using both model albumin and whole plasma, we demonstrated that diatom surfaces rapidly form a distinct “protein corona,” with adsorption kinetics following pseudo-first-order behaviour and selective enrichment of immunoglobulins, apolipoproteins, and coagulation factors. Interestingly, elongated biosilica from *Navicula salinicola* NLA exhibited higher protein adsorption capacity than centric biosilica from *Cyclotella striata* TBI, underscoring the importance of morphology and porosity in defining (bio)nano-interfaces. Proteomic profiling revealed that biosilica preferentially interacted with positively charged and hydrophilic proteins, many of which play key roles in biological processes such as immune modulation, complement activation, and wound healing. Furthermore, by controlled chemical transformation, diatom frustules can be converted into aluminosilicate catalysts with tunable acid sites, enabling selective reactions such as etherification, or as photocatalytic systems. Together, these approaches highlight the potential of nanostructured biosilica from marine resources as a sustainable platform for functional materials.

Keywords: diatoms, microalgae, biosilica, biomaterials, proteomics.

[S-6]

Valorising Keratin and Sericin Proteins from Biomass Residues into Functional Hydrogel Biomaterials

Lia A.T.W. Asri

Materials Science and Engineering Research Group, Faculty of Mechanical and Aerospace Engineering, Institut Teknologi Bandung, Jl. Ganesa 10 Bandung, Indonesia

e-mail: lia.asri@itb.ac.id

Abstract

Protein-rich waste valorization provides a sustainable strategy to recover bioresources and reduce environmental impact. In this study, keratin and sericin derived from biomass residues were utilized as precursors for functional biomaterials. Keratin was extracted from chicken feathers, hair, and wool via a reduction process, while sericin was obtained from silk cocoons through degumming. Keratin and sericin were converted into hydrogels, three-dimensional polymeric networks with potential applications in tissue engineering and wound dressings. To enhance mechanical strength and stability, cellulose nanofibers were incorporated, followed by crosslinking with glutaraldehyde or genipin. The resulting hydrogels exhibited improved mechanical performance, controlled degradation, and biocompatibility comparable to gelatin methacrylate, with 70–80% cell viability. Furthermore, thiol functionalities in keratin were exploited to design injectable, self-healing hydrogels via dynamic disulfide crosslinking. Thiol groups were generated through the reduction of native keratin using 2-mercaptoethanol or sodium metabisulfite, and gel formation was achieved by pH modulation. The resulting hydrogels demonstrated tunable mechanical and degradation properties, underscoring the potential of keratin–sericin-based systems as sustainable and versatile biomaterials for biomedical applications.

Keywords: keratin, sericin, hydrogel, biomaterials, biomass.

RESEARCH ABSTRACTS

Bio-based Industries

[BI-1]

Immobilization of *Candida rugosa* Lipase on polyhydroxybutyrate Biopolymer as a Supporting Material in Biodiesel Synthesis

Irgi Henesta, Rukman Hertadi

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Indonesia

e-mail: rhertadi@itb.ac.id

Abstract

The need for reliable and sustainable energy sources is a critical concern at both regional and global levels. Biodiesel represents a renewable and environmentally friendly alternative to conventional fossil fuels. As the world's largest producer of palm oil, Indonesia possesses significant potential to become a major producer and developer of biodiesel energy. This study aims to synthesize biodiesel using immobilized *Candida rugosa* lipase as a catalyst on a biopolymer-based material, polyhydroxybutyrate (PHB). The immobilization process is intended to enhance the enzyme's stability as a catalytic agent, which is advantageous for industrial applications. Immobilization was performed by incubating the enzyme with PHB at 6°C for 45 minutes. The concentration of the free enzyme was determined using the Bradford method. The activities of both free and immobilized enzymes were assessed by incubating oleic acid and methanol substrates with the lipase enzyme. Enzyme activity was measured based on the difference in titration volume between sample and control solutions, representing the reduction of oleic acid substrate per minute of reaction per milligram of enzyme used. The immobilization procedure was successful, achieving 56.2% immobilization of *Candida rugosa* lipase by PHB at saturation. The optimal activities of free and immobilized lipase were 0.068 pm-0.002 U/mg and 0.568 pm-0.026 U/mg, respectively. These results indicate that the immobilization process significantly enhances enzyme activity. Furthermore, the immobilized lipase exhibited improved stability at elevated temperatures compared to the free enzyme.

Keywords: immobilization, lipase, biodiesel, *Candida rugosa*, polyhydroxybutyrate.

[BI-2]

Effect of Single Point Mutation in *BaqAΔC* α -Amylase to Enhance Activity, Thermostability, and Product Specificity

Muhammad Aqib Hanif, Ihsanawati, Fernita Puspasari, Reza Aditama, Dessy Natalia

Biochemistry and Biomolecular Engineering Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesha No. 10, Bandung, Indonesia

e-mail: dessynatalia@itb.ac.id

Abstract

BaqA, an α -amylase from *Bacillus aquimaris* MKSC 6.2, isolated from soft coral-associated marine bacteria in Merak Kecil, Indonesia, has the unique ability to hydrolyze raw starch. This study focuses on the role of a specific residue present in domain B, which is believed to affect enzyme stability, structure, and substrate binding. A Gln174→Glu174 substitution was introduced in BaqAΔC using site-directed mutagenesis and successfully expressed in *Escherichia coli* ArcticExpress (DE3). SDS-PAGE analysis confirmed a protein band of ~58 kDa. BaqAΔCQ174E exhibited a specific activity of 6.65 ± 0.8 U/mg, slightly higher than BaqAΔC (5.8 ± 0.4 U/mg). Both BaqAΔC and BaqAΔCQ174E worked optimally at 50°C, at an optimum pH 6.5 and 5.5 respectively. Remarkably, BaqAΔCQ174E showed a half-life of 10 hours, which is 2.5 times higher than BaqAΔC leading to distinguished maltose formation. Furthermore, the relative activity of BaqAΔCQ174E enhanced significantly upon the addition of 10 mM $[\text{Ca}^{2+}]$. BaqAΔCQ174E revealed a k_{cat} value of 142.1 ± 3.8 s⁻¹, with a catalytic efficiency (k_{cat}/K_m) of 39.1 ± 4.9 mL mg⁻¹ s⁻¹, which is quite higher than BaqAΔC (with catalytic efficiency (k_{cat}/K_m) of 5.65 ± 0.5 mL mg⁻¹ s⁻¹). Surprisingly, BaqAΔCQ174E produced 3 times more amount of maltose than that of BaqAΔC. Additionally, molecular dynamics simulation discovered variations in the catalytic pocket of BaqAΔCQ174E. This research highlights the significant impact of the Q174E mutation in enhancing the stability and catalytic efficiency of BaqAΔC, offering promising applications in industrial processes requiring robust enzymes.

Keywords: α -amylase, BaqA, calcium, site-directed mutagenesis, thermostability.

[BI-3]
Preparation and Characterizations of Starch-(Polyethylene-b-Poly(ethylene glycol)) Complexes as Naturally Degradable Plastic Materials

Hana Salsabila, Rachmawati

Division of Inorganic and Physical Chemistry, Faculty of Mathematics and Natural Sciences,
Institut Teknologi Bandung, Jalan Ganesha 10, Bandung 40132, Indonesia

e-mail: rachmawati@itb.ac.id

Abstract

Due to high usage of polyethylene (PE) and its difficulty to degrade naturally, accumulation of plastic waste is inevitable. A lot of researches have been reported to reduce the usage of PE and to increase the degradability of PE-based products. For example, starch, an easily degradable biopolymer, is often incorporated in blends with PE. However, due to different characteristic of those two polymers, composites of PE and starch are hard to mix homogeneously. This research aimed to explore alternative homogenization method, which is by forming starch inclusion complex, where hydrophobic molecules (PE in this research) reside inside amylose helix cavities. In this research, starch-(polyethylene-b-poly(ethylene glycol)) (starch-(PE-b-PEG)) was prepared and characterized for its potential as naturally easily degraded plastic material. The inclusion complex based plastic films were prepared by dispersing starch in hot water until gelatinized, followed by addition of varied amount of PE-b-PEG, and mixing with plasticizer (glycerol). The mechanical properties of this film was found to be better than starch film without PE-b-PEG, with elongation increased by 2.5-8 times. The soil burial test was conducted to test the degradability of the film in the nature, and it was found that starch-(PE-b-PEG)-based plastic films lost 42,48%-48,82% of its mass in 14 days. These data shows that starch-(PE-b-PEG)-based plastic films had a potential as naturally degradable materials.

Keywords: biopolymer, inclusion complex, natural degradation, PE-b-PEG, starch.

[BI-4]
Development of Nutrient-Rich Biostimulants using Seaweed, Fish
Paste, and Banana Peel Derivatives

Desak Gede Tirta Andini, Rukman Hertadi

Biochemistry and Biomolecular Engineering Division, Faculty of Mathematics and Natural
Sciences, Institut Teknologi Bandung, Jl. Ganesha No. 10, Bandung, Indonesia

e-mail: rhertadi@itb.ac.id

Abstract

In recent years, Indonesia has been facing various challenges that threaten food security and the sustainability of its agricultural sector. The three main issues include: unhealthy soil conditions caused by the excessive use of synthetic fertilizers and pesticides that damage soil structure and fertility, low crop productivity across various commodities, and plant pest and disease disturbances (OPT) that result in substantial yield losses. To overcome these challenges, innovative and sustainable solutions are needed. Biostimulants offer a promising approach due to their ability to improve soil health, enhance nutrient uptake efficiency, promote plant growth and development, and strengthen plants' natural defense mechanisms against both abiotic and biotic stresses, such as pest and disease attacks. In line with the principles of sustainable agriculture and the circular economy, there is great potential for developing biostimulants from local resources and organic waste. Seaweed extract, fish paste, and banana peels are raw materials rich in bioactive compounds, amino acids, growth hormones, and micronutrients, making them ideal substrates for biostimulant formulation. In our research, it was found that the application of biostimulants could enhance the growth and resilience of curly chili plants against extreme weather conditions and pest disturbances. The use of these organic-based biostimulants is expected to restore soil quality, significantly boost productivity, and mitigate the adverse effects of pest and disease disruptions, while also adding value to agricultural waste-thereby contributing to more resilient and sustainable agriculture in Indonesia.

Keywords: biostimulant, macronutrient, micronutrient, phytohormone, seaweed extract.

[BI-5]
Valorization of Fruit Peels for the Production of Valuable Organic
Chemicals Using Metabolically Engineered *Komagataella phaffii*
(*Pichia pastoris*)

Yoshua Donny Rudinatha, Eleonora valentia Sode Muda, Dina Hermawaty

i3L University, Jl. Pulomas Barat Kav. 88, Jakarta Timur, DKI Jakarta

Abstract

Indonesia is one of the biggest producers of food waste in the world. There are two types of food waste: edible food waste and inedible food waste. Edible food waste is an avoidable food waste, however inedible food waste is unavoidable. Inedible food waste contains a lot of organic compounds that can still be used as resource for valorization purposes. With increasing global emphasis on sustainability and climate change mitigation, conversion of food waste into valuable biochemicals represents a promising research direction. This study focuses on the valorization of fruit peels to extract fermentable sugars that can serve as substrates for microbial conversion. One of the main challenges in fruit peel valorization is the presence of natural antimicrobial compounds that can inhibit bacterial growth. Yeast might be the more suitable options as yeast has higher tolerance towards these inhibitory compounds. Among them, *Komagataella phaffii* (*Pichia pastoris*) is a well-established host organism traditionally for recombinant protein production. However, in recent years, it has been shown that *K. phaffii* also has a huge potential for producing valuable non protein compounds. Using CRISPR/Cas9, *K. phaffii* can be modified to efficiently convert sugars derived from fruit peels hydrolysates into valuable organic chemicals. This approach aims to integrate food waste valorization with synthetic biology to develop a sustainable bioprocess.

Keywords: valorization, fruit peels, *Komagataella phaffii*, metabolic engineering, CRISPR/Cas9.

[BI-6]
Genomic Sequencing Analysis of a Unique PLS47 Isolated from Deep
Sea Vent

Baiq Repika Nurul Furqan¹, Made Puspasari Widhiastuty¹, Febriani², Akhmaloka¹

¹Biochemistry and Biomolecule Engineering Research Group, Faculty of Mathematics and Sciences, Institut Teknologi Bandung, Jl. Ganesha, no.10 Bandung 40132, Indonesia

²Biomolecules Application Research Group, Chemistry Department, Faculty of Mathematics and Natural Sciences, Syiah Kuala University, Banda Aceh, Indonesia

Abstract

Here we report the isolation and complete genome sequence of the uniq PLS47. The strain was isolated from deep-sea vent at Pria Laot Sabang hydrothermal Vent Site, was studied through whole-genome sequencing and annotation to explore gene functions and thermostable enzyme production. Its genome consists of a 3,772,236 bp chromosome with a GC content of 52.02%, along with 56,806 bp of plasmid DNA with a GC content of 41.06%. A total of 3,708 coding sequences (CDSs) were identified, 6 RNA (5S, 16S, and 23S), 27 rRNA, 88 tRNA genes, and 17 Pseudogenes. A comparison of the genome to data based on Average Nucleotide Identity from Dfast-qc shows that the genome is closely related to *Geobacillus thermocatenulatus*. Functional analysis revealed numerous enzyme-coding genes, including proteases, peroxidases hydrolases, esterases, dehydrogenase, hydratases, and lipases. In addition, the genome exhibits a number of stress-tolerant genes. Detailed analysis of the hydrolase genes, especially for lipolytic enzymes such as esterase and lipase, showed that the genome exhibits true lipase like putative lipase, monoacyl glycerol lipase (MAGL motif) and other lipase like GDSL-type esterase/lipase motif. The genomic information provides an understanding of thermophilic genomes and their relevance to stress-tolerant adaptation and explores potential genes, especially for industrial applications.

Keywords: deep-sea Vent, PLS47, *Geobacillus thermocatenulatus*, genome.

Environmental Biochemistry

[EB-1]

Laccase Production by *Mycorrhizal* Isolates from a Central Kalimantan National Peat Swamp Forest: Screening and Challenges in Quantitative Assessment

Titania Tjandrawati Nugroho^{1*}, Selfi Yanti Safitri¹, Andi Dahliaty¹, Septiani Risdarenuadie¹, Khalid Hafazallah^{2,3}, Valeria Veronne³, Sanjay Swarup^{3,4}

¹Dept. of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Riau, Pekanbaru 28293, Indonesia

²Generasi Biologi Indonesia Foundation, Gresik, Indonesia

³Mycosilviculture Project, National University of Singapore-Environmental Research Institute

⁴National University of Singapore-Environmental Research Institute

e-mail: titania.nugroho@lecturer.unri.ac.id

Abstract

Laccases are multicopper oxidoreductase enzymes (EC 1.10.3.2). Due to their promiscuous substrate specificity, the laccases are currently used in various biotechnology applications, including bioremediation and fine chemical synthesis. Fungal laccases have higher redox potential than bacterial laccases, hence they have broader ranges of substrates, and are known to be able to oxidize both phenolic and non-phenolic compounds. Isolation of new fungal strains producing laccase continue to be important, to add to the understanding of structure function relationship of the enzyme, and inventory of fungal laccases to choose from for a certain application. Screening for extracellular laccase production by eight ectomycorrhizal fungi isolated from Pungu Alas Sebangau National Park was conducted using agar and liquid fermentation systems. The fermentation systems were supplemented with either guaiacol or 2,2'-azino-di-3-ethylbenzotiazol-6-sulfonate (ABTS), with and without CuSO₄. Five isolates gave positive results. Of the 5 isolates, one indicated constitutive production of laccase, while the 4 other isolates indicated inductive production. One of these 4 isolates, *Calostoma insignne* M.6. was chosen as a model system to study further the production of inductive extracellular laccase. We discuss here the challenges of the quantitative assessment of laccase production by *C. insignne* M.6. These comprise production optimisation (time, nutrition, type and quantity of inducer, static vs shaking), fermentation system (solid state or submerged), and choice of substrate.

Keywords: laccase, *C. insignne* M.6., Pungu Alas Sebangau National Park, guaiacol, 2,2'-azino-di-3-ethylbenzotiazol-6-sulfonate.

[EB-2]
Identification and Growth Optimization of Indigenous
Thermoacidophilic *Galdieria sulphuraria* from Indonesia for
Enhanced CO₂- Sequestration

Bahzad Ahmad Farhan¹, Gita Ostensia¹, Dessy Natalia¹, Alfredo Kono¹, Zeily Nurachman^{1*}

¹Biochemistry & Biomolecular Engineering Division Faculty of Mathematics & Natural
Sciences, Institut Teknologi Bandung, Indonesia

e-mail: zeily@itb.ac.id

Abstract

Rising atmospheric CO₂ levels remain a major driver of global climate change, that emphasis the urgency for innovative and sustainable carbon mitigation strategies. Microalgae have appeared as promising biological agents for CO₂ capture and biomass production. This study investigates an indigenous strain of *Galdieria sulphuraria* from Tangkuban Perahu, West Java, Indonesia. Sample was collected from Kawah Domas hot springs, an environment characterized by high temperature and low pH (1.5-2). Isolation and purification were achieved through sequential liquid (Allen pH 1.8) and solid culture (Allen agar pH 4) techniques to obtain unialgal strain. Molecular identification was performed using 18s rRNA and *rbcl* gene sequencing with specific primers. The confirmed strain was subsequently cultivated under autotrophic and mixotrophic conditions employing both inorganic and organic carbon sources. Growth rate, biomass productivity, chlorophyll content, and CO₂ fixation efficiency will be assessed under varying CO₂ concentrations to determine the strain's optimal physiological conditions. Molecular characterization confirmed the isolate as *Galdieria sulphuraria* with >95% and >99% sequence similarity with 18s rRNA and *rbcl*, respectively. Distinct metabolic responses under autotrophic with different acids as buffers and mixotrophic regimes with different organic Carbon (C) sources revealed remarkable change in growth rate and C utilization mechanisms. Cell density and biomass production results shows ≈ 10 folds higher growth rate as compare with autotrophic growth because of dual system of C utilization (photosynthesis and respiration) in mixotrophic conditions that enhance the productivity of biomass. The indigenous *G. sulphuraria* strain from Tangkuban Perahu demonstrates exceptional tolerance to extreme environments and higher growth and biomass productivity, highlighting its potential for large-scale microalgae-based carbon capture and sustainable bioproduct development.

Keywords: *Galdieria sulphuraria*, CO₂ capture, indigenous strain (Indonesia), thermoacidophilic microalgae, biochemical profiling.

[EB-3]

Indonesian Tropical Marine Diatom *Navicula salinicola* NLA: Morphology, Genetic Identification, and Lipid Content

Yanti Rachmayanti^{1*}, Nurfarida Ulfah², Elva Stiawan³, Trisha Audria¹, Risma Septi Insani¹,
Sari Dewi Kurniasih Indrawan¹, Alfredo Kono¹, and Zeily Nurachman¹

¹Biochemistry Division, Departement of Chemistry, Faculty of Mathematic and Natural
Sciences, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung 40132, Indonesia

²Departement of Medical Laboratory Technology, Poltekkes Kemenkes Bandung, Jl. Babakan
Loa No. 10A, Cimahi 40514, Indonesia

³Departement of Chemistry, Universitas Pertahanan, Kawasan IPSC Sentul, Bogor 16810,
Indonesia

e-mail: rachmayanti@itb.ac.id

Abstract

Indonesian marine waters are rich in biodiversity, including tropical marine diatoms, which have significant potential for industrial applications such as biofuel. Diatom lipids can be converted into fatty acids for biodiesel production, with lipid accumulation reaching up to 40% of their dry weight. However, the exploration of various diatom species as lipid sources remains limited. Diatoms are generally identified based on cell morphological characteristics, but this method has low accuracy. Advanced technologies such as DNA barcoding offer a more precise approach, although no consensus has been established regarding specific genetic markers for diatom isolates. This study aims to identify a diatom strain isolated from the waters of Ambon Island based on cell morphology and genetic analysis using the marker genes *rbcl*-3P, LSU D2/D3, and 18S rDNA (V4 region), as well as to determine its lipid content. The research methods include diatom cell isolation and characterization using light microscopy and scanning electron microscopy (SEM), genetic marker amplification using PCR, phylogenetic analysis, and lipid quantification. The NLA strain diatom exhibits a yellowish-brown coloration with an elongated shape (22-23 μm in length, 6-8 μm in width), two chloroplasts along the cell sides, and two oil droplets in the center. Morphological analysis could only identify the genus level, but SEM imaging revealed distinct shell structures that enabled identification as *Navicula* sp. Phylogenetic tree analysis of the three marker genes showed a high similarity to *N. salinicola* (*rbcl*-3P 98%- LSU D2/D3 98%- 18S rDNA V4 99%), which was further confirmed by BOLD SYSTEM, indicating 98.4% similarity. Meanwhile, the lipid content of *N. salinicola* from the NLA strain reached 41.12% per 1 gram of dry biomass. In conclusion, the NLA strain isolated from Ambon Island was identified as *Navicula salinicola* based on both morphological and genetic analyses. *Navicula salinicola* NLA has great potential as a raw material for biodiesel production.

Keywords: tropical marine diatoms, NLA strain, morphology, genetic markers, *Navicula salinicola*, lipid accumulation.

[EB-4]
A Self-Assembled Erythrocyte Biomatrix as a Superior Biocatalyst
for Carbon Capture

*Muhamad Novan Agandra Rois, Rahel Marturia Aritonang, Diah Hardianti, Bella Yashinta,
Yanti Rachmayanti, Rindia Maharani Putri, Alfredo Kono, Zeily Nurachman*

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and
Natural Sciences, Institut Teknologi Bandung, Bandung, West Java, Indonesia

e-mail: zeily@itb.ac.id

Abstract

Rising atmospheric CO₂ necessitates novel carbon capture technologies. Human red blood cells (RBCs) offer a model, efficiently managing CO₂ via the synergistic action of Aquaporin-1 (AQP1), Carbonic Anhydrase (CA), and Band 3 (B3) proteins. This research reports the fabrication and characterization of a liposome-based biomatrix mimicking this functional architecture. RBC membrane fractions (containing AQP1 and B3) were isolated, reconstituted into liposomes, and then encapsulated with purified CA. Physicochemical characterization (DLS, Zeta potential), biochemical analysis (SDS-PAGE, Western Blot), and Cryo-TEM imaging confirmed the successful integration of all functional components. The process yielded uniform, CA-filled nanovesicles (~244 nm) that preserved the essential quaternary structures of the transmembrane proteins and possessed high membrane plasticity. Functional assays demonstrated exceptionally high CO₂ hydration activity. Inhibition studies supported a novel 'dual-location' model, with CA active both within the lumen (fed by AQP1) and adsorbed on the exterior surface. This biomimetic platform represents a promising new approach for efficient carbon capture and utilization.

Keywords: nanovesicle, biomatrix, carbon capture, red blood cell, liposome.

[EB-5]
Pumilosphaera acidophila as Carbon Dioxide Capture in Partial
Simulating Flue Gas

Murni Fitria^{1,3}, Zeily Nurachman², Alfredo Kono²

¹Chemistry Doctoral Student, Faculty of Mathematics and Natural Sciences, Institut
Teknologi Bandung

²Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics
and Natural Sciences, Institut Teknologi Bandung, Bandung, West Java, Indonesia

³Department of Applied Chemistry, Politeknik Negeri Lampung, Lampung, Indonesia

e-mail: zeily@itb.ac.id

Abstract

The continuous increase in anthropogenic carbon dioxide (CO₂) emissions, now exceeding 420 ppm, has become a major driver of global climate change, calling for efficient and sustainable mitigation strategies. Microalgae offer significant potential for CO₂ sequestration due to their photosynthetic efficiency, which is 10-50 times higher than that of terrestrial plants, and their ability to grow in diverse media. However, most conventional microalgae cannot survive under extreme conditions such as low pH, high temperature, and exposure to toxic flue gases (SO₂, NO_x). The polyextremophilic microalga *Pumilosphaera acidophila*, isolated from the Kamojang volcanic area (pH about 1.3, temperature up to 95 °C), exhibits remarkable tolerance to such extreme environments. Theoretically, this green microalga is capable of adapting to CO₂ concentrations up to 25%, while maintaining growth under highly acidic and high-temperature conditions. These traits make *P. acidophila* a strong candidate as a next-generation biological CO₂ capturing agent capable of functioning in environments where conventional microalgae fail to grow. In addition to its carbon mitigation potential, *P. acidophila* may also serve as a source of high-nutritional-value biomass, as extremophilic microalgae are typically rich in proteins (up to 68%), lipids (up to 39%), and essential amino acids such as methionine and cysteine. Nevertheless, experimental data on its CO₂ uptake efficiency, tolerance to flue gases, and biomass composition remain limited. Further studies are therefore required to evaluate its tolerance to acidic pH, high temperature, and elevated CO₂ levels, as well as to characterize its biochemical composition. Such investigations will validate *P. acidophila* as a promising indigenous polyextremophilic microalga from Indonesia for dual applications in carbon mitigation and high-value biomass production.

Keywords: climate change, extremophilic microalgae, CO₂ sequestration, *Pumilosphaera acidophila*.

[EB-6]

DNA Barcoding and Antibacterial Activity of *Cryptocarya pulchrinervia* Indigenous Indonesia

Risma Septi Insani¹, Jesa Eranda Ramadani¹, Hendra Helmanto², Lia Dewi Juliawaty¹, Yanti Rachmayanti^{1*}

¹Division of Biochemistry and Biomolecular Engineering, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesha 10, Bandung, Indonesia

²Bogor Botanical Garden, BRIN, Jl. Ir. H. Juanda 13, Bogor, Indonesia

³Division of Organic Chemistry, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesha 10, Bandung, Indonesia

e-mail: rachmayanti@itb.ac.id

Abstract

Cryptocarya pulchrinervia (Lauraceae) is an Indonesian medicinal plant known to produce pyrone type secondary metabolites with cytotoxic potential. However, this species has not been clearly differentiated from related taxa, and no genetic data are currently available in GenBank. This study aimed to determine the morphological and genetic identity of *C. pulchrinervia* and to evaluate the antibacterial activity of its leaf and total DNA was extracted for PCR amplification of the *rbcl* and 18S rRNA genes. Amplicons were sequenced using the Sanger method and analyzed with BioEdit, BLAST, and MEGA11. Antibacterial activity was tested against *Staphylococcus aureus* using the Kirby-Bauer method. Morphological observations showed pinnate leaves, reddish scaly bark, and a tree height of approximately 20 m. The extract exhibited inhibitory zones of 0.5-5.3 mm, increasing with concentration. DNA representing the first molecular identification of this species. These results confirm the taxonomic identity of *C. pulchrinervia* and demonstrate its potential as a natural antibacterial agent for further pharmacological and conservation studies.

Keywords: *Cryptocarya pulchrinervia*, *rbcl*, 18S rRNA, DNA barcode, antibacterial.

[EB-7]
Isolation, Identification and Draft Genome Library Construction of
Acidophilic Microalgae from Indonesian Hot Springs

Berliana Gita Nurani Pertiwi, Alfredo Kono, Zeily Nurachman

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and
Natural Sciences, Institut Teknologi Bandung, Bandung, West Java, Indonesia

e-mail: zeily@itb.ac.id

Abstract

Indonesia is located within the Ring of Fire, which gives it numerous volcanic mountains, including hot springs. Hot springs are extreme ecosystems for living organisms due to their low pH and high temperatures. In these ecosystems, extremophilic microorganisms such as microalgae have been discovered. This study involved the cultivation and a series of purification steps to obtain a pure single-colony culture of extremophilic (acidophilic) microalgae from the hot springs of Kawah Kamojang, Garut, West Java. PCR using 18sM13 forward and reverse primers was conducted to amplify conserved genes, and electrophoresis results showed six bands of 500 bp in size from isolates 3p and 3sp, both originating from the same hot spring. Nucleotide analysis was subsequently performed through sequencing techniques, and a phylogenetic tree was constructed to determine the closest relatives of the identified species. Nucleotide analysis results demonstrated that isolates 3p and 3sp were single colonies, indicated by single peaks in the chromatogram. Nucleotide alignment verified that they were identical, and phylogenetic analysis identified as *Pumiliosphaera acidicola*.

Keywords: acidophilic microalgae, *Pumiliosphaera acidicola*.

[EB-8]
Analysis of Growth and Photosynthetic Capacity of Local Green
Microalgae Isolate *Chlorella* sp. ITB2 A in a Semi-Open Phototank
System

Raisya Rahmania, Rindia Maharani Putri, Alfredo Kono

Biochemistry Division, Faculty of Mathematics and Natural Sciences, Bandung Institute of
Technology, Jalan Ganesha 10, Bandung 40132, Indonesia
e-mail: rindia.m.putri@itb.ac.id

Abstract

The escalating emission of carbon dioxide (CO₂) is a major driver of the global climate crisis. Nature-based solutions, such as green microalgae, offer a promising approach to mitigating CO₂ emissions due to their high capture efficiency and rapid growth. This study aimed to isolate local green microalgal strains and evaluate their growth, biomass productivity, and photosynthetic activity in a semi-open phototank system (12 L photobioreactor) as a foundation for industrial-scale CO₂ capture technology. Green microalgae were isolated from soil collected at the Tamansari Gate of Institut Teknologi Bandung (ITB) using physical washing and streak plate methods to obtain single colonies. Species identification was performed through morphological observation and genetic characterization of the 18S rRNA gene (V4 to V5 region) using PCR, sequencing, and phylogenetic analysis. Two isolates, *Chlorella* sp. ITB2 A and *Desmodesmus* sp. ITB2 F, were successfully obtained. Large-scale cultivation was conducted using minimal Tris medium (pH 7), with daily monitoring of cell density and biomass. Photosynthetic rate during the early exponential phase was measured from oxygen evolution using an Oxygraph plus. *Chlorella* sp. ITB2 A exhibited a short adaptation phase (less 1 day) and exponential growth until day 3, followed by a decline due to contamination on day 4. Higher inoculum density improved stability, and biomass productivity reached 0.0327 g/L/day. The semi-open phototank culture showed lower photosynthetic capacity (V_{max}: 38.64 (error: 4.48) μmol O₂/hour/mg chlorophyll- K 0.5(Ci): 95.56 (error: 15.59) μM) compared to a closed flask (V_{max}: 43.08 (error: 2.59) μmol O₂/hour/mg chlorophyll- K 0.5(Ci): 25.7 (error: 1.33) μM). Future studies should focus on optimizing media and applying genetic engineering to enhance photosynthesis and reduce contamination. This study highlights the potential of local green microalgae as sustainable, fast-growing agents for CO₂ capture.

Keywords: green microalgae, CO₂ capture, photosynthesis, microalgae isolation, phototank, *Chlorella* sp.

Food Biochemistry

[FB-1]

Synergistic Enhancement of Antimicrobial Activity in *Lactococcus lactis* ATCC 11454 through CRISPR/Cas9-Mediated *ldh* Deletion and *nisRK* Overexpression

Yuli Haryani^{1,2*}, Hanan Hasan^{3,4}, Rudi Hendra^{1,2}, Benni Iskandar⁵, Yulia Andriana¹, Analdi Farniga⁶

¹Department of Chemistry, Faculty of Mathematics and Natural Sciences, Riau University, 28293 Pekanbaru, Riau, Indonesia

²Centre of Biological Innovation for Regenerative and Natural Applications, Riau University, 28293 Pekanbaru, Riau, Indonesia

³Department of Food Science, Faculty of Food Science and Technology, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia

⁴Laboratory of Halal Science Research, Halal Research Product Institute, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia

⁵Department of Pharmaceutical Technology, Sekolah Tinggi Ilmu Farmasi, Pekanbaru, Riau 28293, Indonesia

⁶School of Food Industry, King Mongkut's Institute of Technology Ladkrabang, 1 Chalong krung Rd., Ladkrabang, Bangkok 10520, Thailand

Abstract

Metabolic pathway engineering in lactic acid bacteria offers a promising approach to enhance antimicrobial metabolite biosynthesis for food preservation. In this study, a CRISPR/Cas9 system was successfully developed to delete the lactate dehydrogenase (*ldh*) gene in *L. lactis* ATCC 11454, a nisin-producing strain, to redirect carbon flux toward nisin and bacteriocin-like inhibitory substance (BLIS) production. The Cas9 nuclease (4,107 bp) was cloned into the shuttle vector pNZ8148 under the constitutive P_{nis} promoter, while a specific single-guide RNA was driven by a modified plasmid derived from pMG36e. The commonly used pMG36e vector was optimized for higher expression by replacing its native P32 promoter with the strong constitutive P8 promoter yielding P8-pMG36e. The recombinant plasmid was propagated in *E. coli* TOP10, confirmed by sequencing, and used to express sgRNA cloned into the multiple cloning site generating sgRNA_P8-pMG36e. All constructs were verified by restriction enzyme digestion and sequencing. The CRISPR/Cas9 complex successfully generated *ldh*Δ mutants, which showed reduced acidification (final pH ~6.0) and improved growth compared to the wild-type (WT). To further boost antimicrobial production, the *nisR* and *nisK* regulatory genes were expressed under the P8 promoter in pMG36e, creating *nisRK*-P8-pMG36e, which was introduced into both WT and *ldh*Δ strains resulting mutants, *nisRK*^{OE} and *ldh*Δ*nisRK*^{OE}. Comparative antimicrobial assays demonstrated significant enhancement across all mutants. The *ldh*Δ strain exhibited inhibition zones of 13.3–15.7 mm, representing ~60% improvement over WT (7.7–10.0 mm). The *nisRK*^{OE} strain showed comparable increases (13.0–15.0 mm), confirming successful transcriptional activation of the nisin biosynthetic operon. Remarkably, the double mutant *ldh*Δ*nisRK*^{OE} displayed the strongest inhibition, reaching 16.8 mm against *Staphylococcus aureus*, 19.3 mm against *Bacillus subtilis*, 14.5 mm against *Listeria monocytogenes*, and up to 16.0 mm against Gram-negative *Vibrio parahaemolyticus* and *Escherichia coli*. These findings demonstrate that *ldh* deletion effectively reroutes pyruvate metabolism away from lactic acid formation, while *nisRK* overexpression amplifies transcription of the nisin gene cluster. Their synergistic integration markedly increases antimicrobial compound biosynthesis, providing a powerful and scalable strategy for developing *L. lactis* strains with superior antimicrobial potential for biotechnological and biopreservative applications.

Keywords: antimicrobial activity, *L. lactis*, *ldh*, *nisRK*, nisin.

[FB-2]
Variation of IPTG Inducer Substitution on the Expression of the
xynBTN63D Gene Encoding the Endo- β -1,4-D-Xylanase in
Escherichia coli BL21 (DE3)

Anak Agung Istri Ratnadewi¹, Waode Mia, Wuryanti Handayani, Tinok Dwi Ananda,
Ni Nyoman Tri Puspaningsih²

¹Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas
Jember, Jl. Kalimantan No. 37, Jember 68121, East Java, Indonesia

²Department of Chemistry, Faculty of Sciences and Technology, Universitas Airlangga,
Kampus C Mulyorejo, Surabaya, 60115, Indonesia

e-mail: istri_dewi.fmipa@unej.ac.id

Abstract

The endo- β -1,4-D-xylanase enzyme is a member of the glycoside hydrolase (GH) family that hydrolyzes xylan into xylooligosaccharides (XOS). The xynBTN63D gene is a mutation of the xynBT gene from *Bacillus* sp. This gene was transformed in the pET30a(+) plasmid and expressed in *Escherichia coli* BL21(DE3) to produce the endo- β -1,4-D-xylanase enzyme (xynBTN63D). This expression system is generally induced using IPTG, but its relatively expensive price makes it less efficient for industrial-scale production. This study aimed to evaluate the potential of galactose and lactose as IPTG replacement candidates in expressing the xynBTN63D gene. Production was carried out in trace element defined media (MTE-IDP000045023(2016)) with the addition of 0.5 mM IPTG, 50 mM lactose, and 50 mM galactose. Cells were expressed for 16 hours after induction at 37°C. The expression of the xynBTN63D gene was analyzed using the Miller method (DNS), hydrolysis of pNP-X, pNP-Ara substrates, the Bradford method, SDS-PAGE, and TLC. The results showed that all inducer variations and without inducer had a molecular mass of ~30 kDa, indicating successful expression. The IPTG inducer produced the highest protein content and activity, followed by galactose and lactose. TLC results showed that the hydrolysis product was XOS in the form of xylotriose (X3) in all inducer variations. Overall, galactose and lactose showed the ability to induce target gene expression, although their effectiveness was lower than IPTG. Thus, galactose and lactose have the potential to be substituted inducer candidates for IPTG in the production of endo- β -1,4-D-xylanase (xynBTN63D) enzymes based on the lac operon expression system.

Keywords: endo- β -1,4-D-xylanase, expression gene, IPTG inducer, xynBTN63D.

[FB-3]
Response Surface Optimization of Black and Green Tea Kombucha
Fermentation and Its Impact on Bioactivity, Chemistry, and Sensory
Quality

Shabarni Gaffar^{1,2}, Prangesti Andi¹, Opik Taufiqurrohman², Safri Ishmayana¹*

¹Chemistry Department, Faculty of Mathematics and Natural Sciences, Universitas
Padjadjaran, Jl. Ir. Soekarno Km. 21, Jatinangor, Sumedang, West Java, Indonesia

²Post Graduate School, Universitas Padjadjaran, Jl. Dipatiukur no. 35, Bandung, West Java,
Indonesia

Abstract

Tea (*Camellia sinensis*) is a widely consumed beverage plant known for its diverse bioactive compounds and health benefits. Kombucha, a fermented tea drink produced by a symbiotic culture of bacteria and yeast (SCOBY), undergoes biochemical transformations that enhance its functional properties. This study used Response Surface Methodology (RSM) with a Central Composite Design (CCD) to optimize the fermentation time and temperature of black and green tea kombucha, using DPPH radical scavenging activity as the response variable. Under the optimized conditions, antioxidant and antibacterial activities, ethanol content, total acidity, total flavonoid and polyphenol contents, and sensory acceptance were evaluated. The optimal fermentation duration was 15.4 days, with temperatures of 25.6 °C for green tea and 22.5 °C for black tea kombucha. The IC₅₀ values for antioxidant activity were 179.49 ppm and 345.35 ppm, respectively. Both types of kombucha showed antibacterial activity against *Staphylococcus aureus* (2 mm and 1.5 mm inhibition zones) and *Escherichia coli* (2.5 mm and 2.25 mm). Green tea kombucha contained higher total polyphenol (10.33 mg GAE/g) and flavonoid (0.34 mg QE/g) contents than black tea kombucha (3.87 mg GAE/g and 0.20 mg QE/g). It also exhibited higher acidity (0.80%) and ethanol content (0.50% v/v) compared to black tea kombucha (0.58% and 0.41% v/v). Sensory evaluation indicated that panelists preferred black tea kombucha. Overall, RSM successfully optimized fermentation parameters, showing that green tea kombucha exhibits stronger bioactivity and higher metabolite content, while black tea kombucha provides greater sensory acceptance.

Keywords: kombucha, fermentation, bioactivity, chemical properties, sensory quality.

Health

[H-1]

Molecular Insights into Novel IDS Mutations: Protein Structural and Biomarker Correlations in Indonesian Patients with Hunter Syndrome

Steven Arianto^{1,2}, Poernomo Soeharso³, Damayanti Rusli Sjarif^{4}*

¹Department of Chemistry, Faculty of Mathematics and Natural Sciences, Bandung Institute of Technology, Jalan Ganesha 10, Bandung 40132, Indonesia

²Institusi Department of Medical Laboratory Technology, Hermina Institute of Health, Jalan Jatinegara Barat 126, Jakarta 13320, Indonesia

³Department of Medical Biology, Faculty of Medicine, Universitas Indonesia, Jalan Salemba Raya 6, Jakarta 10430, Indonesia

⁴Department of Paediatrics, National Hospital of Cipto Mangunkusumo, Jalan Pangeran Diponegoro 71, Jakarta 10430, Indonesia

e-mail: ukk.npm.idai@gmail.com

Abstract

Mucopolysaccharidosis type II (MPS II, Hunter syndrome) is a rare X-linked lysosomal storage disorder caused by mutations in the iduronate-2-sulfatase (IDS) gene. Pathogenic variants impair IDS enzyme activity, leading to the accumulation of glycosaminoglycans (GAGs), particularly heparan sulfate (HS) and dermatan sulfate (DS). This study aimed to investigate IDS gene mutations in Indonesian MPS II patients, construct 3D structural protein models, and correlate mutation types and structural alterations with urinary HS and DS levels. Genomic sequencing of the IDS gene was performed in seven clinically diagnosed patients. Detected variants were classified, and three-dimensional protein models were generated *in silico*. Urinary HS and DS levels were quantified using enzyme-linked immunosorbent assay (ELISA) and correlated with mutation types, structural findings, and enzyme replacement therapy (ERT) history. Seven IDS mutations were identified, comprising nonsense (1/7), deletion (2/7), insertion (1/7), and missense variants (3/7), including two novel mutations not previously reported. Structural modeling revealed conformational alterations that may disrupt enzymatic function. Urinary HS was consistently elevated across patients, whereas DS levels showed variable patterns, with some remaining within the normal range. Biomarker variability was influenced by mutation type, mutation location, timing of diagnosis, ERT duration, and patient-specific treatment response. This study identifies novel IDS mutations in Indonesian patients with MPS II and highlights the importance of integrating genetic, structural, and biochemical analyses. These findings provide molecular insights that may improve diagnostic precision, prognostic evaluation, and personalized therapeutic strategies.

Keywords: dermatan sulfate, heparan sulfate, IDS, mutation, protein.

[H-2]

Efficacy Test of Master Diagnostic Kit for *Salmonella typhi* Targeting the *sifA* Gene in Chicken Samples

Valia Rahma^{1,2}, Fauzan Alipsyah^{1,2}, Fuzi Rahmawati^{1,2}, Hana Fajriah^{1,2}, Okky Rizky Pratama^{1,2}, Vinka Juniaty Lestari^{1,2}, Wanda Hanifa^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{1,2}, Royna Rahma Musie^{1,2}, Irwan Saputra^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Aulanni'am⁴, Hesham Ali El-Enshasy^{5,6}, Muktiningsih Nurjayadi^{1,2*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asjari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Lembaga Penelitian dan Pengabdian Kepada Masyarakat, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁵Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁶School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Baru, Malaysia

⁷City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandria, Egypt

Abstract

Salmonella typhi is foodborne pathogen that causes typhoid fever in cases of food poisoning. The *sifA* gene plays a crucial role in maintaining the integrity and stability of SCVs, preventing fusion with lysosomes and IL-1beta, thus enabling *Salmonella typhi* to survive and replicate within host cells. Previous research has developed a prototype detection and validation kit using the real-time PCR method, which is a fast, sensitive, and accurate detection method. This study aims to test the efficacy of the prototype kit for the detection of foodborne pathogen in chicken samples by comparing culture, PCR, and real-time PCR method. Primers of *sifA* *S. typhi* amplified bacterial culture DNA isolates and artificially contaminated chicken samples used as positive controls at 216 bp, respectively obtained Ct value at 10.55 ± 0.20 and Ct value at 14.01 ± 0.16 with Tm value at 82.09 ± 0.16°C and Tm 82.32 ± 0.09°C. In the culture method, a sampling technique was carried out by swabbing the surface of 30 chicken samples. Of these, 30 samples tested positive on each selective media. The PCR method and real-time PCR showed amplification results in 30 samples with *sifA* *S. typhi*. The Ct value obtained in front of the cut-off value and the Tm value was in accordance with the positive control, which was 82.32 ± 0.09°C. Based on the results, it can be concluded that the bacteria detection kit with rt-PCR is proven to provide effective, efficient, specific, and sensitive.

Keywords: foodborne disease, *Salmonella typhi*, *sifA*, detection kit, efficacy test.

[H-3]
Rational Design and In Silico Validation of a Potent Multi-Epitope
Vaccine Candidate Against Dengue Virus

Poppy Mai Versiska^{1,2}, Marselina Irasonia Tan³, Reza Aditama¹, Dessy Natalia^{1}*

¹Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Bandung, West Java, Indonesia

²Faculty of Health Sciences, Muhammadiyah University of Metro, Metro, Lampung, Indonesia

³School of Life Science and Technology, Institut Teknologi Bandung, Bandung, West Java, Indonesia

*dessynatalia@itb.ac.id

Abstract

Dengue remains a significant global health concern, particularly affecting populations in tropical and subtropical regions, with over 100 countries considered endemic. Despite various control efforts, the lack of effective antiviral treatments and the challenges in vaccine development due to the virus's high genetic diversity have limited progress. This study utilized reverse vaccinology and immunoinformatics approaches to design a multi-epitope vaccine targeting all four serotypes of the dengue virus. Highly conserved and immunogenic CTL, HTL, and B-cell epitopes were identified and assembled into a single vaccine construct with appropriate adjuvants and linkers to enhance immunogenicity. The construct demonstrated favorable physicochemical properties, including stability, solubility, and non-allergenicity. Tertiary structure modeling and refinement revealed a reliable 3D conformation, supported by a valid Z-score, ERRAT quality factor, and Ramachandran plot analysis. Molecular docking analysis revealed high binding affinities between the designed vaccine and key immune receptors, namely BCR, TCR, and TLR4, with binding energies of -15.2, -15.6, and -18.0 kcal/mol, respectively. These interactions suggest the potential to activate both adaptive and innate immune responses. In silico immune simulations indicated a robust immune response, including the formation of memory cells and cytokine production. Notably, population coverage analysis revealed a global coverage of 96.65%, with high efficacy in endemic regions such as Brazil, India, and Indonesia. These findings demonstrate the promising potential of the designed vaccine, although further in vitro and in vivo validations are required to confirm its safety and immunogenicity.

Keywords: multi-epitope, dengue virus, reverse vaccinology.

[H-4]

Metabolomic Analysis to Evaluate the Effect of Fermentation Agitation and Type of Extraction Solvent on Co-Culture of *Penicillium* sp. *LBKURCC34* and *Staphylococcus aureus*

Yuana Nurulita^{1*}, Rahmi Ramadani¹, Mohammad Rafi², Titania Tjandrawati Nugroho¹

¹Department of Chemistry, Faculty of Mathematics and Natural Sciences, University of Riau, Pekanbaru, Indonesia- 28293

²Department of Chemistry, Faculty of Mathematics and Natural Sciences, IPB University, Bogor, Indonesia- 16680

Abstract

The potential for discovering new antibiotic alternatives through the exploration of local microbes from Riau as a source of bioactive compounds is significant. However, isolating active compounds using a guided assay approach presents challenges due to the limited amount of extract and the low yield obtained from microbial fermentation. To address these challenges, it is crucial to optimize fermentation production factors, such as the impact of agitation and extraction solvents, to enhance the production of bioactive compounds. This study seeks to assess the effects of agitation fermentation and type of extraction solvents in the liquid fermentation of a co-culture of *Penicillium* sp. *LBKURCC34* and *Staphylococcus aureus* in the production of antimicrobial compounds and to conduct an analysis of the metabolite profile using an untargeted metabolomics approach based on LC-HRMS Q Orbitrap. The fermentation data underwent analysis using Xcalibur, MS-DIAL, and GNPS software multivariate analysis was employed to identify the bioactive compounds generated. The results indicated that intensive agitation treatments yielded a different compound composition compared to non-agitation treatments. Furthermore, technical-grade and pro-analysis solvents did not result in differences in the extracted compound composition in non-agitated treatments but showed variations in agitated treatments. Several identified bioactive compounds exhibit potential for further development. The compounds that were identified included cyclo(phe-pro), cyclo(val-pro), and maculosin, astaxanthin, harmaline, phenalinolactone a, gossypetin, sanguinarine, and dinactin.

Keywords: antimicrobial activity, metabolomics analyses, co-culture fermentation, *Penicillium* sp. *LBKURCC34*.

[H-5]
Polyvinyl Alcohol Hydrogel Incorporated Keratin and Sericin for
Elastic Implants Technology

Moch Saifur Rijal¹, Arie Wibowo², Lia Amelia Tresna Wulan Asri²

¹Doctoral Program of Material Science and Engineering, Faculty of Mechanical and
Aerospace Engineering, Institut Teknologi Bandung.

²Material Science and Engineering Research Group, Faculty of Mechanical and Aerospace
Engineering, Institut Teknologi Bandung.

Abstract

Osteoarthritis (OA) is the most common form of arthritis and a major contributor to disability in the elderly population. Biomaterials such as hydrogels offer promising alternatives to synthetic osteochondral implants due to their biocompatibility and ability to mimic native tissue properties. This study reports the successful fabrication of polyvinyl alcohol (PVA)-based hydrogel implants incorporated with keratin and sericin via a freeze-thawing technique. Keratin was isolated from sheep wool using the 2-mercaptoethanol reduction method, while sericin was extracted from silkworm cocoons through degumming. The incorporation of these natural proteins significantly enhanced the mechanical properties and biocompatibility of the hydrogels, as demonstrated through in vitro evaluations. The resulting hydrogels exhibited a gel fraction exceeding 92% and a swelling ratio increase of over 100%, indicating improved structural integrity and water absorption capacity. These findings highlight the high potential of keratin- and sericin-enhanced PVA hydrogels as implantable materials for osteochondral tissue repair.

Keywords: keratin, sericin, PVA, hydrogel, implant.

[H-6]
Comparative Genomics and Genome Mining of Novel Antimicrobials
from Gili Meno Lake, Indonesia (Dry Season)

Muhammad Daffa Aubin^{1}, Nashita Saaliha¹, Ernawati Arifin Giri-Rachman¹,
I Dewa Made Kresna¹,*

¹School of Life Science and Technology, Bandung Institute of Technology
Jalan Ganesha 10, Bandung 40132, Indonesia

Abstract

Antimicrobial resistance is a global health threat based on the report by WHO in 2023. High number of pathogens shown to be resistant highlights the urgent need to discover new antimicrobials to combat these pathogens. Gili Meno lake, Lombok, Indonesia has been found to have elevated salt content compared to seawater surrounding the island, indicating the evolution of diverse microbial communities of the lake with the potential to be explored for their ability to produce antimicrobials. This research involves isolating bacteria from Gili Meno Lake water and sediment samples during the dry season, while also examining their potential to produce novel antimicrobial compounds. To support this data, a comparative genomic study also has been done to close relatives of the identified isolates to assess their potential for producing new antimicrobial compounds based on their biosynthetic gene cluster profiles. This study began with bacterial isolation performed on three types of enrichment media, followed by a challenge test to evaluate the isolates inhibitory activity against the growth of Gram-negative and/or Gram-positive bacterial models. Isolates showing activity has been identified based on their 16S rRNA gene sequences and these identification results will serve as the basis for searching the NCBI database for the whole genome sequences (WGS), allowing for a comparative study of the BGC profiles in each WGS. Results showed that out of a total of 29 purified isolates, 12 exhibited antimicrobial production activity against the Gram-positive bacteria model *B. subtilis* and/or the Gram-negative bacteria model *E. coli*. Two selected isolates were identified as *Bacillus amyloliquefaciens* KPCG13 and *Paenibacillus polymyxa* KPSI22. Comparative analysis of the closest genome sequences of these two isolates available in the database revealed the identification of a total of 11 biosynthetic gene clusters (BGCs) capable of producing 9 compounds already known to possess antimicrobial activity. Meanwhile, 2 other gene clusters are predicted to be capable of producing derivatives of known compounds or novel compounds, namely Tridecaptin derivatives and a hybrid polyketide peptide compound. Further research is needed to verify the existence of these two gene clusters and their products in the Gili Meno Lake isolates, and it is hoped that this information can aid in the discovery of new bioactive compounds to address the AMR problem in Indonesia and the world.

Keywords: antimicrobials, Gili Meno Lake, genome mining, *Bacillus amyloliquefaciens*, *Paenibacillus polymyxa*.

[H-7]

Development and Experimental Validation of an Optimized mRNA-Based Multi-Epitope Therapeutic Vaccine Candidate for Chronic Hepatitis B

*Patricia Gita Naully¹, Marselina Irasonia Tan², Reza Aditama³, Husna Nugrahapraja²,
Aluicia Anita Artarini⁴, and Ernawati Arifin Giri-Rachman^{2*}*

¹Doctoral Program of Biology, School of Life Science and Technology, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia

²School of Life Science and Technology, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia *erna_girirachman@itb.ac.id

³Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia

⁴School of Pharmacy, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia

Abstract

Chronic hepatitis B (CHB) remains a major global health concern due to the persistence of covalently closed circular DNA (cccDNA), which maintains viral replication and immune tolerance. Current antiviral therapies can suppress viral replication but fail to eradicate cccDNA, underscoring the need for therapeutic vaccines capable of restoring hepatitis B virus (HBV)-specific immunity. This study reports the development and experimental validation of an optimized mRNA-based multi-epitope therapeutic vaccine candidate targeting the hepatitis B core (HBc) and X (HBx) proteins. Computational analyses integrating reverse vaccinology and immunoinformatics were employed to identify immunodominant T- and B-cell epitopes and to predict the structural stability and receptor interactions of the designed antigen. The corresponding mRNA construct was further optimized through codon adaptation, untranslated region (UTR) engineering, anti-reverse cap analog (ARCA) capping, and poly(A) tailing to enhance molecular stability and translational efficiency. Secondary structure modeling demonstrated favorable folding with efficient translation initiation and elongation potential. The synthesized mRNA exhibited high purity and successfully expressed the encoded antigen in HEK293T cells, as verified by quantitative fluorescence analysis and confocal microscopy. These findings provide experimental evidence supporting the feasibility of an optimized multi-epitope mRNA therapeutic vaccine for chronic hepatitis B and highlight the effective integration of computational design with molecular validation in vaccine development.

Keywords: chronic hepatitis B, mRNA vaccine, multi-epitope, therapeutic vaccine.

[H-8]

Efficacy Test of Master Diagnostic *Vibrio parahaemolyticus* with toxS Gene Target in Food Sample

Hana Fajriah^{1,2}, Fauzan Alipsyah^{1,2}, Fuzi Rahmawati^{1,2}, Okky Rizky Pratama^{1,2}, Valia Rahma^{1,2}, Vinka Juniaty Lestari^{1,2}, Wanda Hanifa^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{2,3}, Royna Rahma Musie^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Novi Wulandari⁴, Aulanni'am⁵, Hesham Ali El-Enshasy^{6,7,8}, Muktiningsih Nurjayadi^{1,2*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asj'ari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Lembaga Penelitian dan Pengabdian Kepada Masyarakat, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Biomedic Laboratory Rolabdokkes, Police Medical and Health Center, Jl. Trunojoyo, Jakarta, 12110, Indonesia

⁵Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁶Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁷School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Baru, Malaysia

⁸City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandria, Egypt

Abstract

Foodborne diseases pose a significant threat to human health, with seafood often being a common source of contamination. *Vibrio parahaemolyticus* is one of foodborne pathogen that frequently found in seafood, capable of causing Vibriosis. To address the spread of such foodborne diseases, rapid and sensitive detection methods are needed, such as Real Time Polymerase Chain Reaction (RT PCR). This study aims to evaluate the efficacy of a prototype detection kit targeted toxS gene *Vibrio parahaemolyticus* in seafood samples using the rt PCR method. Cut off testing was performed to determine the maximum value at which a sample is deemed positive- results indicated a cut off value of 28.36 with a standard deviation of 0.38 for *Vibrio parahaemolyticus* using the toxS primer. The positive control consisted of pure culture DNA isolate and shrimp samples artificially contaminated with the target bacteria. When tested by PCR, these produced an amplicon product of 173 bp, while rt PCR yielded a Ct of 12.13 for the pure isolate and 12.91 for the contaminated sample. The melting curve values were 85.09 for the pure isolate and 85.01 for the contaminated sample. Based on PCR amplification with the toxS primer, the positive control produced a 173 bp amplicon product, whereas none of the six samples did. The rt PCR test results for the six shrimp samples showed no contamination by *V. parahaemolyticus*. According to the rt PCR amplification results with the toxS primer, each sample had a Ct value exceeding the cut off, with Ct values ranging from 32.27 to 35.24, and exhibited melting curve peaks distinct from the positive control. The results are consistent with conventional PCR testing, where no *V. parahaemolyticus* contamination was found in the samples. These findings suggest that the development of the prototype detection kit for foodborne pathogen bacteria has been successfully achieved.

Keywords: foodborne disease, *Vibrio parahaemolyticus*, real-time PCR, efficacy, detection kit.

[H-9]

Potential of ebpS Gene as a Target Detection for *Staphylococcus aureus* using real-time Polymerase Chain Reaction

Fauzan Alipsyah^{1,2}, Valia Rahma^{1,2}, Fuzi Rahmawati^{1,2}, Hana Fajriah^{1,2}, Okky Rizky Pratama^{1,2}, Vinka Juniaty Lestari^{1,2}, Wanda Hanifa^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{2,3}, Royna Rahma Musie^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Vira Saamia⁴, Aulanni'am⁵, Hesham Ali El-Enshasy^{6,7,8}, Muktiningsih Nurjayadi^{1,2*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asjari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Institute for Research and Community Service, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Center Forensic Laboratory of the Criminal Investigation, Police of the Republic of Indonesia, Cipambuan Babakan Madang, Bogor, 16810, Indonesia

⁵Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁶Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁷School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Bahru, Malaysia

⁸City of Scientific Research and Technological Applications, New Borg El Arab, Alexandria, Egypt

Abstract

Foodborne diseases are illnesses resulting from the consumption of food contaminated with pathogenic microorganisms, among which bacteria represent a predominant group. *Staphylococcus aureus* is a well-known foodborne pathogen responsible for food poisoning and gastrointestinal infections. Owing to its superior rapidity, sensitivity, and specificity compared to conventional detection methods, real-time PCR has become a preferred approach for the molecular identification of pathogenic bacteria. This study aimed to establish a rapid, sensitive, and specific real-time PCR assay for the detection of *S. aureus* targeting the ebpS gene. The optimized annealing temperature for the ebpS primer was determined to be 60C, yielding an amplicon of 174 bp. The primer set efficiently amplified the target sequence with a mean Ct value of 12.7 +/- 0.11 and a melting temperature (Tm) of 80.83C +/- 0.01. Furthermore, the ebpS primer pair successfully discriminated *S. aureus* from non-target bacterial species based on distinct Ct and Tm profiles. The limit of detection (LoD) achieved in this assay was 3.2 pg/uL, corresponding to a Ct value of 24.02, which equates to approximately 9.186 x 10¹ CFU. The cut-off threshold was established at a Ct value of 32.08. Collectively, these results demonstrate that the ebpS based real-time PCR assay provides a reliable, sensitive, and specific method for the detection of *Staphylococcus aureus* in foodborne pathogen surveillance.

Keywords: foodborne disease, foodborne pathogen, *Staphylococcus aureus*, ebpS, real-time polymerase chain reaction.

[H-10]

Efficacy Test of the Master Diagnostik *Cronobacter sakazakii* with grxB Gene Target in Infant Formula Milk Samples

Fuzi Rahmawati^{1,2}, Hana Fajriah^{1,2}, Wanda Hanifa^{1,2}, Valia Rahma^{1,2}, Fauzan Alipsyah^{1,2}, Okky Rizky Pratama^{1,2}, Vinka Juniaty Lestari^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{2,3}, Royna Rahma Musie^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Novi Wulandari⁴, Aulanni'am⁵, Hesham Ali El-Enshasy^{6,7,8}, Muktiningsih Nurjayadi^{1,2*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asjari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Lembaga Penelitian dan Pengabdian Kepada Masyarakat, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Biomedic Laboratory Rolabdokkes, Police Medical and Health Center, Jl. Trunojoyo, Jakarta, 12110, Indonesia

⁵Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁶Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁷School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Baru, Malaysia

⁸City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandria, Egypt

Abstract

Infant formula serves as a source of nutrition during growth, but its quality and safety cannot guarantee protection from pathogenic bacterial contamination such as *Cronobacter sakazakii*, which can cause foodborne disease such as necrotizing enterocolitis (NEC) and even death. To mitigate this risk, a rapid and sensitive detection method, such as real-time Polymerase Chain Reaction (Real-time PCR), is essential. This study evaluated the efficacy of a prototype foodborne pathogen detection kit designed to target grxB gene *Cronobacter sakazakii* in various infant formula samples by comparing three methods: conventional culture, PCR, and real-time PCR. The positive controls for the PCR and real-time PCR methods in this study included pure culture DNA isolates and artificially contaminated infant formula samples, amplified using grxB gene primers, resulting in amplicon sizes of 151 bp with Ct values of 13.97 at a Tm of 86.08C and 14.35 at a Tm of 85.83C. Results from the three methods for 20 infant formula samples indicated that no colonies grew on MacConkey Agar (MCA) media using the culture method. Additionally, the PCR amplicon results showed that 16 samples produced amplicon products matching the positive control size of 151 bp. In contrast, the real-time PCR method revealed that 19 samples had Ct values below the cut-off, with Ct 30.84 +/- 1.10 and Tm 85C +/- 1, producing a specific single peak identical to the positive control, indicating these samples tested positive for the bacteria. Based on these three detection methods, the prototype kit for detecting foodborne pathogens effectively identifies the presence of *Cronobacter sakazakii* in infant formula milk.

Keywords: foodborne disease, *Cronobacter sakazakii*, real-time PCR, efficacy test, detection kit.

Efficacy Test of the Master Diagnostic *Escherichia coli* Targeting the *acrF* Gene in Food Samples

Okky Rizky Pratama^{1,2}, Fuzi Rahmawati^{1,2}, Wanda Hanifa^{1,2}, Valia Rahma^{1,2}, Fauzan Alipsyah^{1,2}, Hana Fajriah^{1,2}, Vinka Juniaty Lestari^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{2,3}, Royna Rahma Musie^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Vira Saamia⁴, Aulanni'am⁵, Hesham Ali El-Enshasy^{6,7,8}, Muktiningsih Nurjayadi^{1,2*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asj[^]ari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Lembaga Penelitian dan Pengabdian Kepada Masyarakat, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Center Forensic Laboratory of the Criminal Investigation, Police of the Republic of Indonesia, Cipambuan Babakan Madang, Bogor, 1681, Indonesia.

⁵Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁶Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁷School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Baru, Malaysia

⁸City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandra, Egypt

Abstract

Foodborne diseases are a global health concern caused by the consumption of food contaminated with pathogenic microorganisms. Notably, around 70% of diarrhea cases are attributed to food containing disease-causing agents, with *Escherichia coli* being a primary culprit. Consequently, the need for rapid, accurate, and sensitive detection methods to identify microbial contamination in food products is paramount. This study aim to assess the efficacy of a prototype diagnostic kit designed to detect *Escherichia coli* targeted *acrF* gene, in various chicken meat samples using three detection methods: conventional culture, PCR, and real-time PCR. Pure culture DNA isolates and chicken meat samples artificially inoculated with *E. coli* were used as positive controls, showing Ct values of 10.23 and 11.26, respectively. The results of testing 18 chicken meat samples using these three methods demonstrated that the culture method produced pink colonies on MacConkey Agar (MCA), indicating lactose fermentation by *E. coli*. PCR amplification with the *acrF* gene primer generated an amplicon of 169 bp, while the real-time PCR method yielded Ct values below the cut-off threshold and displayed a single specific melting peak consistent with the positive control. All chicken meat samples tested positive for *Escherichia coli* contamination. Comparative analysis indicated that the real-time PCR method was the most accurate, sensitive, efficient, and rapid. Thus, the Master Diagnostic *Escherichia coli* prototype kit targeting the *acrF* gene proved effective for detecting *E. coli* contamination in food samples.

Keywords: foodborne pathogen, *Escherichia coli*, *acrF*, real-time polymerase chain reaction, efficacy, detection kit.

[H-12]

Efficacy Test of Master Diagnostic *Shigella flexneri* with sfmD Gene Target on Chicken Samples

Wanda Hanifa^{1,2}, Fuzi Rahmawati^{1,2}, Hana Fajriah^{1,2}, Valia Rahma^{1,2}, Fauzan Alipsyah^{1,2}, Okky Rizky Pratama^{1,2}, Vinka Juniaty Lestari^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{2,3}, Royna Rahma Musie^{1,2}, Irwan Saputra^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Aulanni'am⁴, Hesham Ali El-Enshasy, Muktiningsih Nurjayadi

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asjari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Lembaga Penelitian dan Pengabdian Kepada Masyarakat, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁵Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁶School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Baru, Malaysia

⁷City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandria, Egypt

Abstract

Shigella flexneri causes Shigellosis, a disease transmitted through contaminated food. Of all deaths caused by diarrhea, 15% are due to dysentery, with *Shigella flexneri* being the most prevalent *Shigella* bacterial species in Indonesia. Based on this factor, testing for microbial contamination content such as pathogenic bacteria in food is very necessary, using methods like Polymerase Chain Reaction (PCR) and Real-time PCR. In this study, an efficacy test was conducted to observe the effectiveness of a prototype foodborne pathogen detection kit that had been designed to detect *Shigella flexneri* in various chicken meat samples by comparing three methods: conventional culture, PCR, and real-time PCR. DNA isolates from pure cultures and chicken meat samples contaminated with *S. flexneri* bacteria were used as positive controls, with respective ct values of 12.99 and 13.07. The results from testing 24 chicken meat samples using the three testing methods showed that, in the culture method, specific colonies grew on Salmonella Shigella Agar (SSA) media. Based on PCR amplification results using the sfmD gene primer, the amplicon product had a bp value of 155 bp. Meanwhile, in the RT-PCR method, the Ct value obtained was lower than the cut-off value and produced a specific single peak identical to the positive control. The efficacy test results for the chicken meat samples showed that all 24 samples tested positive for *S. flexneri* contamination. Based on the results of the three detection methods, it is concluded that the real-time PCR method is accurate, efficient, sensitive, and rapid for detection. This proves that the Master Diagnostic *Shigella Flexneri* prototype kit targeting the sfmD gene in food samples is effective.

Keywords: foodborne pathogen, *Shigella flexneri*, real-time PCR, efficacy test, detection kit.

Stability Assessment of a Prototype Master Diagnostic Kit for Detecting *Salmonella typhi*, *Shigella flexneri*, and *Escherichia coli*

Vinka Juniaty Lestari^{1,2}, Valia Rahma^{1,2}, Okky Rizky Pratama^{1,2}, Fauzan Alipsyah^{1,2}, Wanda Hanifa^{1,2}, Hana Fajriah^{1,2}, Fuzi Rahmawati^{1,2}, Jefferson Lynford Declan^{1,2}, Siti Fatimah^{1,2}, Anisa Fitriyanti^{2,3}, Royna Rahma Musie^{1,2}, Irma Ratna Kartika^{1,2}, Ika Keumala Fitri^{1,2}, Futi Kusumawati^{1,2}, Aulanni'a⁴, Hesham Ali El-Enshasy^{5,6,7}, Muktiningsih Nurjayadi^{1,2*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Negeri Jakarta, Gedung KH. Hasjim Asj'ari, 5th Floor, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

²Research Center for Detection of Pathogenic Bacteria, Lembaga Penelitian dan Pengabdian Kepada Masyarakat, Universitas Negeri Jakarta, Jl. Rawamangun Muka, Jakarta Timur, 13220, Indonesia

³Department of Chemistry, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, 16424, Indonesia

⁴Biochemistry Laboratory, Faculty of Sciences, Brawijaya University, Indonesia

⁵Innovation Center in Agritechology for Advanced Bioprocessing (ICA), Universiti Teknologi Malaysia (UTM), Pagoh, Johor, Malaysia

⁶School of Chemical and Energy Engineering, Faculty of Engineering, Universiti Teknologi Malaysia (UTM), Skudai, Johor Baru, Malaysia

⁷City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandria, Egypt

Abstract

Foodborne pathogens remain a major threat to global public health, emphasizing the urgent need for rapid, accurate, and versatile diagnostic systems applicable in both laboratory and field settings. This study focused on the laboratory-scale development and stability evaluation of a prototype Master Diagnostic Foodborne Pathogen Detection Kit targeting *Salmonella typhi* (sifA gene), *Shigella flexneri* (sfmD gene), and *Escherichia coli* (acrF gene). The kit's stability was assessed under two storage conditions (-20 °C and 4 °C) for 90 days. Results demonstrated that both temperatures effectively preserved reagent performance, with -20 °C recommended for long-term storage and 4 °C suitable for short-term or routine use, based on Ct (threshold) and Tm (melting temperature) values. However, repeated freeze-thaw cycles reduced reagent stability. Performance testing using two Real-Time PCR instruments showed no significant variation in detection results, confirming strong cross-platform compatibility. Overall, the developed prototype exhibited consistent stability, accuracy, and robustness, supporting its potential as a reliable and rapid diagnostic tool for detecting foodborne pathogens

Keywords: foodborne pathogens, diagnostic kit, real-time PCR, stability test, molecular detection.

[H-14]

Expression, Purification, and Characterization of Hepatitis B VLP using LEGO Vaccine Concept

Fatiha Khairunnisa^{1,2,3*}, Amir Zaki Abdullah Zubir^{1,2}, Kang Lan Tee^{1,2}, Tuck Seng Wong^{1,2}

¹UK-South East Asia Vaccine Manufacturing Research Hub (UK-SEA Vax Hub), University of Sheffield, Sheffield, United Kingdom

²Department of Chemical and Biological Engineering, Faculty of Engineering, University of Sheffield, Sheffield, United Kingdom

³Department of Chemistry, Faculty of Science and Technology, Airlangga University, Surabaya, Indonesia

e-mail: fatiha.khairunnisa@fst.unair.ac.id

Abstract

The COVID-19 pandemic and the emergence of new viral infectious disease outbreaks stress a global demand for innovative vaccine platforms to address our preparedness for the next pandemic. Virus like particles (VLPs) are considered to represent a cutting-edge vaccine platform against prevalent and emergent diseases due to their naturally non infectious, structural resemblance to viruses, and excellent immunogenicity. The UK SEA Vax Hub is currently developing a LEGO vaccine platform to accommodate rapid vaccine design and manufacturing, focusing on connectivity, flexibility, and stability. In this research, Hepatitis B (HB) VLP with N and C terminal polyhistidine tags using the LEGO vaccine concept are explored. The correct assembly of the LEGO vaccine was identified in silico. N His HB VLP and C His HB VLP LEGO vaccine plasmid was constructed using Golden Gate Assembly and transformed into *E. coli DH5 alpha*. Colonies were selected for plasmid extraction, and successful assembly was confirmed by DNA gel electrophoresis and sequencing. The protein was expressed in *E. coli BL21 (DE3)* using 150 micro-M IPTG at 30 degree C overnight. The soluble proteins were purified using immobilized metal affinity chromatography (IMAC) nickel resin. Physicochemical characterizations of the HBcAg VLPs were performed using SDS PAGE, dynamic light scattering (DLS), and transmission electron microscopy (TEM). The N His HB VLP and C His HB VLP were correctly assembled and validated by DNA gel and sequencing. Both HB VLPs were successfully expressed. The molecular weight of HB VLP was observed at 22 kDa using SDS-PAGE, and the particle size radius was measured at range of 16 to 22 nm using both DLS and TEM. HBcAg VLP produced using the LEGO vaccine concept has been successfully expressed, purified, and physicochemically characterized. Our finding shows that the LEGO vaccine platform is a suitable alternative method to rapidly create and test vaccines.

Keywords: expression, purification, characterization, hepatitis B, VLP, LEGO vaccine concept.

[H-15]
Tuning the Structure and Bioperformance of Doped Biphasic
Calcium Phosphate Biomaterial Toward Next Generation Bone
Tissue Engineering

Sabrina Ocha Felinda, Fainan Failamani, Irma Mulyani

Department of Chemistry, Faculty of Mathematics and Natural Sciences, Institut Teknologi
Bandung, Jl. Ganesha No. 10, Bandung 40132, Indonesia

e-mail: sabrina.ocha.f@gmail.com

Abstract

Biphasic calcium phosphate (BCP), composed of hydroxyapatite (HAp) and beta tricalcium phosphate (BTCP), combines chemical stability, biocompatibility, bioactivity, and a suitable degradation rate for bone regeneration. However, pure BCP exhibits low mechanical strength and limited thermal stability. To address these limitations, cationic substitution within the HAp lattice using essential metal ions was employed. Magnesium (Mg) and zinc (Zn) were selected as dopants for their key roles in bone metabolism and tissue formation. Mg improves crystal lattice regularity and enhances bioactivity by promoting osteoblast proliferation, while Zn strengthens intercrystalline bonding, promotes mineralization, provides antibacterial properties, and inhibits osteoclastic resorption. Their combined incorporation is expected to synergistically enhance structural stability and osteoconductivity. Mg and Zn doped HAp powders were synthesized via coprecipitation using $\text{Ca}(\text{NO}_3)_2 \cdot 4\text{H}_2\text{O}$ and $(\text{NH}_4)_2\text{HPO}_4$ precursors ($\text{Ca}/\text{P} = 1.67$). Dopants from $\text{Mg}(\text{NO}_3)_2 \cdot 6\text{H}_2\text{O}$ and $\text{Zn}(\text{NO}_3)_2 \cdot 6\text{H}_2\text{O}$ solutions (1 to 5 mol) were added during precipitation to ensure direct lattice incorporation. The precipitates were dried (100°C) and calcined (700 to 800°C). BTCP was synthesized separately ($\text{Ca}/\text{P} = 1.5$), then combined with MgZn doped HAp (60 per 40) through mechanochemical mixing and sintered at 800°C for 4 hours. Powder X-ray diffraction (PXRD) confirmed HAp and BTCP phases without secondary formation. Diffraction peaks shifted toward higher 2θ angles with increasing dopant concentration, indicating lattice contraction due to Ca substitution by smaller Mg and Zn ions. Rietveld refinement showed preferential substitution at Ca(2) sites with greater than 90 percent occupancy. Dual Mg and Zn doping improved thermal stability, phase balance, and bioactivity, confirming BCP potential as a next generation bone regenerative biomaterial.

Keywords: biphasic calcium phosphate, doping, Mg Zn, PXRD, rietveld refinement.

[H-16]

Chemical Modification of Inulin via Acetylation: Optimization, Physicochemical Characterization and Antibacterial Evaluation

Abdur Rahman Arif¹, Muhamad Nasir³, Atthar Luqman Ivansyah², Rukman Hertadi¹

¹Division of Biochemistry and Biomolecular Engineering, Faculty of Mathematics and Natural Sciences, Bandung Institute of Technology, Jalan Ganesha No. 10, Bandung 40132, Indonesia.

²Division of Inorganic and Physical Chemistry, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Bandung 40132, Indonesia

³Environmental Nanotechnology Research Group, Research Center for Environmental and Clean Technology, National Research and Innovation Agency (BRIN), Bandung, 40135, Indonesia

e-mail: rhertadi@itb.ac.id

Abstract

This study investigates the chemical modification of inulin via acetylation to improve its structural and functional properties, emphasizing process optimization, physicochemical characterization, and antibacterial evaluation. The acetylation process was optimized using variations in temperature, reaction time, and sodium acetate concentration, achieving optimal conditions at 70 °C, 36 h, and 0.18 percent catalyst concentration. Fourier Transform Infrared (FTIR) analysis revealed a new absorption band at 1747 cm⁻¹ corresponding to carbonyl (C=O) stretching, while ¹H NMR spectra showed new signals at delta 2.0-2.2 ppm confirming the presence of acetyl (COCH₃) groups with a degree of substitution of 75.51 percent. X-ray diffraction (XRD) indicated reduced crystallinity (from 19.12 to 15.10%) and increased amorphous regions. SEM micrographs showed a morphological transition from aggregated granules to fragmented porous structures, corroborated by BET analysis that confirmed mesoporous formation with increased surface area and pore volume. The acetylated inulin exhibited antibacterial activity against *Escherichia coli* and *Staphylococcus aureus* in vitro. These findings demonstrate that controlled acetylation effectively tailors the structural and functional properties of inulin, providing a promising route for developing antibacterial biopolymers with potential applications in biomedical and food packaging materials.

Keywords: inulin, acetylation, optimization, physicochemical characterization, antibacterial activity.

[H-17]
Carotenoids Profile of Seaweed *Halimeda* sp. Harvested In Two
Different Seasons

Dwindi Agryanti Johar, Zeily Nurachman, AB Susanto, Yanti Rachmayanti

Division of Biochemistry and Biomolecular Engineering, Faculty of Mathematics and
Natural Sciences, Bandung Institute of Technology, Jalan Ganesha No. 10, Bandung 40132,
Indonesia

Abstract

Research on the utilization of seaweed as a source of xanthophyll, particularly from tropical species *Halimeda* sp., remains limited, despite seaweed being an essential commodity for Indonesia's economy. This study examines the xanthophyll profile of these two species harvested from Pantai Kartini, Jepara, during the rainy and dry seasons. The majority of Indonesia's seaweed production is still exported in raw or dried form due to the limited information on the variation and characteristics of its bioactive compounds, particularly xanthophyll. Therefore, this research aims to identify the variation and types of xanthophyll. Additionally, it evaluates its potential as an antibacterial and anticancer compound. Seaweed samples are harvested in two different seasons to assess the environmental conditions influence on xanthophyll content. Xanthophyll is extracted using the Supercritical Fluid Extraction (SFE) method, which is recognized as an environmentally friendly and efficient technique. The obtained extract is then analyzed using High-Performance Liquid Chromatography (HPLC), UV-Vis spectroscopy, FTIR, and LC-MS to determine its chemical structure. The antibacterial activity is tested using the well diffusion method, while the anticancer activity is assessed against MCF-7 breast cancer cells using the Presto Blue assay. The results of this study are expected to show significant variations in the types and concentrations of xanthophyll in *Sargassum* sp. and *Halimeda* sp. across the two different seasons. Xanthophyll extracted from these species is anticipated to exhibit strong antibacterial activity against specific pathogens and significant anticancer activity against MCF-7 cells. The hypothesis of this study suggests that polluted environmental conditions at Pantai Kartini may enhance xanthophyll production with higher biological activity. This research contributes to revealing the characteristics of xanthophyll from tropical seaweed and its applications in the health sector while also offering a solution to increase the added value of Indonesia's seaweed commodities by transforming raw products into high-value processed products.

Keywords: xanthophyll, seaweed, supercritical fluid extraction (SFE), bioactive, anticancer.

[H-18]

The Study of Campesterol as a Therapeutic Agent Candidate

Rina Budi Satiyarti, Sri Novianti

Chemistry department, Science and Technology Faculty, UIN Sunan Gunung Djati Bandung,
Indonesia

e-mail: rinabudisatiyarti@uinsgd.ac.id

Abstract

Secondary metabolite based medicine is important to develop. It is because secondary metabolites reduced side effect as a medicine, have diverse structure and multi targeted actions. The aim of this research is to explore potential of fitosterol derivate, namely campesterol in the pharmaceutical field. The research was conducted computationally, for docking analysis there was used glucose transporter 4 (GLUT4) protein as a target. The stages of the research were biological activity of campesterol using PASS test, pharmacokinetic profile evaluation using Lipinski rule and ADME, and molecular docking using autodock. The result showed that campesterol has several biological activity as antihypercholesterolemia, wound healing agent, and antitoxic. Lipinski and ADME analysis showed campesterol is qualified to be a therapeutic agent. Docking analysis between campesterol and GLUT4 protein showed affinity binding value at -10,2 kkal/mol, which was mean it has significant hydrophobic interaction. Binding campesterol changed GLUT4 conformation therefore promote more efficient interaction, and surprisingly showed positif effect to its activity. The conclusion of this research is that campesterol has a potential as therapeutic agents. It need further research to study campesterol as a ligand for GLUT4 protein in order to prove that campesterol has an antiglicemic activity.

Keywords: secondary metabolite, campesterol, biological activity, GLUT4 protein.

[H-19]

Development of Multimeric Bann-Rbd Fusion Protein as A Covid-19 Vaccine Candidate

Ozi Jumadila, Ihsanawati, Dessy Natalia

Institut Teknologi Bandung

Abstract

The COVID-19 pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has had profound global health and economic impacts. Despite widespread vaccination efforts, continued viral mutations underscore the need for next-generation vaccines with enhanced immunogenicity and safety. Among the various vaccine platforms—such as inactivated, mRNA, DNA, viral vector, and protein subunit vaccines—the protein subunit approach has shown strong potential due to its safety profile, non-infectious nature, and ability to induce robust immune responses when combined with suitable adjuvants. The receptor-binding domain (RBD) of the SARS-CoV-2 spike protein is a key antigenic target, as it mediates viral entry by binding to the human angiotensin-converting enzyme 2 (ACE2) receptor. Multimeric RBD constructs have been demonstrated to elicit stronger neutralizing antibody responses compared to monomeric forms. The aim of this study was to develop a vaccine candidate based on a multimeric RBD subunit protein. The RBD multimer was engineered through genetic fusion of the gene encoding the RBD protein with the gene encoding the β -annulus (Bann) peptide derived from Tomato bushy stunt virus (TBSV). The Bann peptide is known to self-assemble into virus-like nanocapsules, and thus, the fusion protein was expected to form a multimeric Bann-RBD structure. Molecular modeling of the Bann-RBD multimer was performed in silico. The gene encoding Bann-RBD was cloned into the pPICZ α A expression vector for expression in the *Pichia pastoris* X33 system. This expression system was chosen due to its ability to produce high levels of recombinant protein and to perform post-translational modifications necessary for generating functional proteins. The expressed Bann-RBD protein was purified using metal ion affinity chromatography, followed by biochemical and biophysical characterization, as well as immunological assays. The development of the Bann-RBD multimeric protein vaccine candidate comprises several key research stages. In the initial phase in silico modeling of the Bann-RBD multimer structure was performed to design a fusion between the Bann peptide and the RBD protein, ensuring the RBD domains are oriented toward the surface of the multimer. Epitope prediction analysis for B cells and T cells was also conducted in silico to evaluate the immunogenic potential of the Bann-RBD protein. Subsequently, the gene encoding Bann-RBD was cloned into the pPICZ α A expression vector for expression in the *P. pastoris* X-33 system. This was followed by optimization of expression conditions, protein production, and purification of the recombinant Bann-RBD protein using affinity chromatography with Ni-NTA resin. Biochemical and biophysical characterizations of the Bann-RBD protein included SDS-PAGE analysis, deglycosylation using the Endo-Hf enzyme, amino acid sequence verification, and glycopeptide analysis via LC-MS/MS. The molecular size of the Bann-RBD multimer were assessed using dynamic light scattering (DLS) and transmission electron microscopy (TEM). An antigenicity study was conducted to evaluate the interaction between the Bann-RBD protein and specific antibodies. Immunogenicity studies were performed by administering the Bann-RBD protein, both with and without the Alum-CpG adjuvant, to BALB/c mice in three doses spaced 21 days apart. Preliminary toxicity assessments were carried out in silico, followed by monitoring of body weight, temperature, and the injection site. Immune responses were evaluated from mouse serum using indirect ELISA, while neutralizing activity was assessed through competitive ELISA.

Keywords: COVID-19, multimeric protein, RBD, subunit vaccine, β -annulus.

[H-20]

PHB-Ectoine Microparticles (MPs) with Rhamnolipid Formulation: A Triple-Action System for Skin Protection

Alma Tyara Simbara, Rukman Hertadi

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Science, Institut Teknologi Bandung

Abstract

The skin functions as a biological barrier that protects the body from ultraviolet radiation, microorganisms, and chemical agents. Maintaining its integrity is essential to prevent irritation, inflammation, and infection. Conventional skincare formulations often rely on synthetic surfactants and UV filters that may cause cytotoxicity and are poorly biodegradable. Therefore, this study investigates the use of natural and biocompatible compounds, namely poly(3-hydroxybutyrate) (PHB), ectoine, and rhamnolipid, to develop a multifunctional and eco-friendly protective system for skin applications. PHB and ectoine were covalently linked through EDC-mediated crosslinking to form PHB-Ectoine microparticles, which were subsequently dispersed in rhamnolipid. Fourier transform infrared spectroscopy confirmed the formation of amide bonds, while scanning and transmission electron microscopy revealed spherical particles with a dual-layer structure. The average particle size was 1.28 micrometers in water and 0.53 micrometers in rhamnolipid, with a zeta potential of -61.47 millivolts, indicating good colloidal stability. Functional assays demonstrated that the microparticles protected 96.77 percent of zein protein from denaturation, showed a sun protection factor of 5.64 with 82.3 percent UVB protection, and enhanced antibacterial activity when combined with rhamnolipid, producing an inhibition zone of 472 square millimeters against *Staphylococcus aureus*. In conclusion, this study successfully developed a biodegradable triple-action microparticle system combining PHB, ectoine, and rhamnolipid that provides anti-irritant, anti-UVB, and antibacterial protection, showing strong potential for use in sustainable skincare formulations.

Keywords: PHB-Ectoine, rhamnolipid, skin protection.

[H-21]
The Effect of N331Q Mutation on the Multimer Formation of COVID-19 Vaccine Candidate Bann-RBD

*Epafroditus Kristiadi Susetyo, Ozi Jumadila, Fernita Puspasari, Ihsanawati, Dessy Natalia**

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia

*email: dessynatalia@itb.ac.id

Abstract

Coronavirus disease 2019 (COVID19) is a disease caused by severe acute respiratory syndrome coronavirus 2 infection. Vaccination with receptor binding domain (RBD) of the viral spike (S) glycoprotein induces the production of neutralization antibody. RBD multimerization increases immunogenicity. Fusion of RBD with beta annulus (Bann) polypeptide could induce multimer formation. Glycan at N331 is predicted to pose steric hindrance to BannRBD multimerization. The purposes of this research were to express the gene encoding BannRBDN331Q and to characterize BannRBDN331Q protein. Expression of the gene encoding BannRBDN331Q in *Pichia pastoris* was induced by the addition of 2 percent methanol for 72 hours at 30 degrees Celsius and 225 rpm. The protein was concentrated by tangential flow filtration. BannRBDN331Q was purified with agarose NiNTA resin and eluted predominantly with 100 mM imidazole. Analysis of the pure protein showed that BannRBDN331Q is a protein with a molecular mass of about 34 kDa. Enzyme linked immunosorbent assay showed that the produced BannRBDN331Q interacts with S1 IgG human monoclonal antibody with an absorbance at 450 nm of 0.8078 pm 0.0257. Dynamic light scattering analysis showed that BannRBDN331Q could form multimers at protein concentrations of 3.5 mM, 1.75 mM, and 0.875 mM with sizes of (29.73 pm 9.81) nm, (26.20 pm 8.65) nm, and (20.58 pm 6.56) nm, respectively. Transmission electron microscopy image showed that BannRBDN331Q could form multimers as nanoparticles ranging from about 20 nm to about 40 nm. The results of this research showed that BannRBDN331Q multimers had a size smaller than BannRBD multimers, but less interaction with antibody compared to BannRBD multimers. Therefore, the N331 glycan is suspected to play an important role in the interaction between BannRBD with antibody, presumably by keeping the BannRBD multimer size large so that it could more easily interact with more antibodies.

Keywords: SARS-CoV-2, Bann-RBD, glycosylation, multimerization, nanoparticle.

[H-22]

Genome Mining-Based Exploration of Novel Antimicrobial Compounds from Gili Meno Lake Bacterial Isolates During the Rainy Season

Nashita Saaliha

Institut Teknologi Bandung

Abstract

Exploring natural products from microbes is a crucial approach in the discovery of new antibiotics to combat the global threat of antimicrobial resistance (AMR). AMR occurs when microorganisms evolve and become resistant to common drugs, like antibiotics, leading to widespread disease and increased mortality. The continuous rise of AMR and the scarcity of new antibiotic classes discovered since 1987 have created an urgent need for novel antimicrobial agents. One promising source is microorganisms living in extreme environments, such as Gili Meno salt lake (Lombok), with its high salinity of 54.00 ± 0.82 ppt, as they produce unique secondary metabolites as an adaptive response. This study aimed to isolate and identify microbes from Gili Meno salt lake, a habitat for halophilic microorganisms, and explore their potential for antimicrobial production through the analysis of biosynthetic gene clusters (BGCs). Lake water and sediment samples were collected, and the microbes were isolated. Their antimicrobial activity was tested against the model pathogens *Escherichia coli* (Gram-negative) and *Bacillus subtilis* (Gram-positive) using a *double-layer agar* challenge test. The species of the active isolates were identified through 16S rRNA gene sequencing. Subsequently, genome mining was performed using the AntiSMASH software on available *whole genome* data from the identified species in public databases to pinpoint BGCs with the potential to produce new antibiotics. A 2D structural visualization of the predicted final products was also conducted. Based on the research findings, 40 microbial isolates were successfully obtained, with 11 showing antimicrobial activity. Of these 11 isolates, two species were identified based on the 16S rRNA gene sequencing results: *Bacillus paralicheniformis* and *Priestia megaterium*. The genome mining analysis of these isolates revealed two potential BGCs, one similar to Paeninodin and the other to Amyloliquecidin GF610. The predicted 2D structures of the final products from these BGCs identified the compounds Paeninodin B, PamA1, and PamA2, providing a starting point for further research in the development of new antimicrobial compounds.

Keywords: antibiotic, secondary metabolites, biosynthetic gene clusters, genome mining.

[H-23]

Cloning and Expression of the Gene Encoding Protease from the Marine Bacterium *Bacillus amyloliquefaciens* ABBD

Muhammad Adlan^{1,2}, Retno Arianingrum², Fernita Puspasaria¹, Dessy Natalia^{1,3}, Ihsanawati^{1*}

¹Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132

²Departement of Chemistry Education, Faculty of Mathematics and Natural Sciences, Universitas Negeri Yogyakarta, Jl. Colombo No.1 Karangmalang Yogyakarta 55281

³Biosciences and Biotechnology Research Centre, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132

*email: ihsanawati@itb.ac.id

Abstract

Proteases are enzymes that catalyze the hydrolysis of peptide bonds in proteins, producing oligopeptides or amino acids. The gene encoding protease (*sub*) from the marine bacterium *Bacillus amyloliquefaciens* ABBD (1665 bp) had been previously sequenced, but its expression had not yet been reported. This study aimed to clone and express the *sub* gene in *Escherichia coli* and characterize the recombinant protease. The *sub* gene was amplified by PCR, inserted into pGEM-T Easy for cloning, and subsequently subcloned into the expression vector pET16b. The recombinant plasmid pET-16b-*sub* was used to transform *E. coli* BL21(DE3), and the gene expression was induced with IPTG. The electrophoresis (SDS-PAGE) analysis showed a distinct protein band of approximately 65 kDa, corresponding to the expressed Sub protease. The enzyme was soluble and exhibited proteolytic activity, as indicated by clear zones in the halo assay. The amino acid sequence analysis and structural modeling revealed that the Sub protease possesses the conserved catalytic triad Asp–His–Ser, typical of serine proteases. These findings demonstrate that the successful cloning and expression of the *sub* gene, providing a basis for further biochemical and structural characterization of the recombinant protease.

Keywords: *Bacillus amyloliquefaciens* ABBD, gene expression, *Escherichia coli*, recombinant plasmid, protease.

[H-24]

CRISPR-Cas9-Based Electrochemical Biosensor for the Detection of Katg Gene Mutation in Isoniazid-Resistant Tuberculosis

Yeni Wahyuni Hartati^{1,4*}, Dika Apriliana Wulandari¹, Muhammad Ihda Hamlu Liwaissunati Zein², Salma Nur Zakiyyah², Safri Ishmayana¹, Mehmet Ozsoz^{1,3}, Irkham^{1,4*}

¹Department of Chemistry, Faculty of Mathematics and Natural Science, Universitas Padjadjaran, Sumedang 45363, Indonesia

²Department of Chemistry “Giacomo Ciamician”, Alma Mater Studiorum - University of Bologna, Bologna 40126, Italy

³Department of Biomedical Engineering, Near East University, Mersin 99138, Turkey

⁴Study Center of Sensor and Green Chemistry, Faculty of Mathematics and Natural Science, Universitas Padjadjaran, Bandung 40132, Indonesia

email: yeni.w.hartati@unpad.ac.id; irkham@unpad.ac.id

Abstract

Multidrug-resistant tuberculosis (MDR-TB) remains a significant challenge in tuberculosis (TB) treatment due to simultaneous mutations in the *rpoB* and *katG* genes, conferring resistance to rifampicin and isoniazid. Current diagnostic methods, including culture-based and molecular techniques, often suffer from prolonged turnaround times and limited sensitivity, with many molecular assays predominantly targeting *rpoB* mutations while overlooking *katG*, which is crucial for confirming MDR-TB. This study develops a CRISPR/Cas9-based electrochemical biosensor for selective and rapid detection of *katG* mutations. A target-specific guide RNA (gRNA) was designed using the Benchling CRISPR tool, considering off-target effects, specificity, and cleavage sites within the *Mycobacterium tuberculosis* genome. The selected gRNA achieved the highest on-target score of 61.2 and off-target score of 49.0 at cut position 2928, with a PAM sequence of AGG. The gRNA's effectiveness was demonstrated through an electrochemical biosensor employing a gold-modified screen-printed carbon electrode (SPCE/Au), confirmed by an increased current response using [Fe(CN)₆]^{3-/4-} as a redox probe. The detection mechanism relies on DNA probe hybridization with the mutated target DNA, forming double-stranded DNA (dsDNA) that is recognized and cleaved by the Cas9-gRNA complex. This cleavage significantly reduces the ferrocene oxidation signal, indicating the presence of the mutation. In contrast, non-mutated target DNA produces a nondetectable ferrocene signal. The analytical performance of the CRISPR/Cas9 electrochemical biosensor shows a low detection limit of 5.0837 aM, with a detection range of 101 to 106 aM, offering a sensitive and specific platform for rapid *katG* mutation detection in MDR-TB diagnostics.

Keywords: biosensor, CRISPR-Cas9, drug resistance, gene mutation, *Mycobacterium tuberculosis*.

Others

[0-1]

Expression of Serine Hydroxymethyltransferase (SHMT) through Metagenomic Approach

Puspa Sari Dewi, Akhmaloka

Biochemistry & Biomolecular Engineering Research Group, Faculty of Mathematics and Natural Sciences, Institut Teknologi
Bandung, Jl. Ganesha No. 10, Bandung 40132, Indonesia

Abstract

Indonesia is known for its rich biodiversity, including the presence of diverse thermophilic microorganisms. The genes were obtained through a metagenomic approach from microbial communities in the Domas Crater, West Java, to explore potential thermostable enzymes for industrial application. The serine hydroxymethyltransferase (SHMT) gene was successfully amplified from metagenomic DNA by conserved SHMTs region-specific primers. Sequence homology analysis confirmed the similarity of the gene to the SHMTs from *Metallosphaera* sp. The amplified fragment of approximately 1,307 bp was ligated into pET-30a(+) and expression in *E. coli* BL21(DE3). Expression was carried out by inducing 1 mM IPTG at 37 °C. SDS-PAGE analysis revealed a distinct protein band of approximately 47.5 kDa, consistent with the predicted molecular weight of SHMT. Compared with a previous study that used lysozyme-based lysis, the SDS-based method produced clearer soluble protein, suggesting an improvement in protein recovery. The crude extract showed retro-aldol cleavage activity toward DL-phenylserine, producing benzaldehyde with a maximum specific activity of 3.44 U·mg⁻¹ under experimental conditions 70 °C and pH 7.5, with the highest activity observed at 0.75% SDS. These findings demonstrate the successful metagenomic identification and recombinant expression of a thermostable SHMT, highlighting its potential for further biochemical characterization.

Keywords: metagenomics, SHMT, thermostable enzyme, Domas Crater.

[O-2]

Expression and Characterization of Recombinant Major Ampullate Spidroin Subtype-2 (MaSp2) in *Pichia pastoris*

Tamamal Afiah Purnomo¹, Nur Alia Oktaviani^{2,3}, Fernita Puspasari¹, Ihsanawati¹,
Keiji Numata^{2,3}, Dessy Natalia^{1,4}

¹Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia

²Biomacromolecules Research Team, Center for Sustainable Resource Science, RIKEN, 2-1 Hirosawa, Wako, Saitama 351-0198, Japan

³Department of Material Chemistry, Kyoto University, Nishikyo-ku, Kyoto 615-8510, Japan

⁴Biosciences and Biotechnology Research Centre, Institut Teknologi Bandung, Jl. Ganesa No. 10, Bandung, 40132, Indonesia

Abstract

Dragline silk, secreted by the major ampullate glands of spiders, plays essential roles in mobility and defense. It exhibits exceptional toughness and elasticity, often surpassing synthetic fibers in performance. This silk is primarily composed of major ampullate spidroins (MaSp1 and MaSp2, predominantly) which consist of a central repetitive region flanked by conserved N- and C-terminal domains. The repetitive region of MaSp2 has glycine-rich and poly-alanine composition, interspersed with glutamine, proline, serine, and tyrosine. The GPGXX motif is the fingerprint sequence of MaSp2 which contributing to β -turn structures and elasticity. While the amino acid composition is central to MaSp2 assembly, emerging evidence suggests that post-translational modifications (PTMs)—particularly phosphorylation and hydroxylation—may modulate conformational dynamics and promote liquid-liquid phase separation (LLPS), potentially influencing fibrillization. In this study, we constructed a synthetic MaSp2 (N-R12-C) gene and inserted it into the pPICZA shuttle vector under the control of the AOX1 promoter for expression in *Pichia pastoris*. The plasmid was integrated into the *P. pastoris* genome via homologous recombination at the AOX1 promoter locus. Our result indicates that *P. pastoris* was able to express recombinant MaSp2 following methanol induction. SDS-PAGE and Western blot analysis revealed an apparent molecular weight higher than predicted, suggesting the occurrence of post-translational modifications.

Keywords: dragline silk, major ampullate spidroin-2 (MaSp2), *Pichia pastoris*, post-translational modification (PTM).

[0-3]
Identification of Pitcher Plant (*Nepenthes sp.*) Types using Deep
Learning-Based Models

Budi Asmanto^{1,2}, Mahfut^{3}, La Zakaria⁴, Tristiyanto⁵*

¹Doctoral Student, Faculty of Mathematics and Natural Sciences, Lampung University

²Information System Department, Faculty of Vocation, Muhammadiyah Metro University

³Department of Biology Study, Faculty of Mathematics and Natural Sciences, Lampung
University mahfut.mipa@fmipa.unila.ac.id

⁴Department of Mathematics, Faculty of Mathematics and Natural Sciences, Lampung
University

⁴Department of Computer Science, Faculty of Mathematics and Natural Sciences, Lampung
University

Abstract

Pitcher plants (*Nepenthes sp.*) are carnivorous plants with high ecological and aesthetic value, as well as economic potential in horticulture and conservation. These plants are susceptible to various diseases that can disrupt their growth and productivity. Rapid and accurate disease identification and diagnosis are crucial for implementing appropriate control measures to prevent further damage. In the digital era and advances in artificial intelligence technology, the use of deep learning for plant image processing offers an innovative solution for automatically detecting and classifying plant diseases. This research aims to develop and implement a convolutional neural network (CNN)-based deep learning model to identify disease types and diagnose pitcher plants using digital images of diseased leaves and pitchers. Image datasets were collected from various field sources and literature, followed by data augmentation, labeling, and preprocessing to improve the quality and quantity of training data. Various CNN architectures, such as ResNet, VGG, and EfficientNet, were evaluated to determine the optimal model based on accuracy, precision, recall, and F1-score metrics. Deep learning is an effective technology in supporting the health management of carnivorous plants, especially pitcher plants, and opens up opportunities for the development of smartphone-based applications or automatic monitoring systems for real-time disease detection.

Keywords: *Nepenthes sp.*, pitcher plant, deep learning, convolutional neural network, identification of pitcher.

[O-4]

In Silico Multiligand Analysis of *Spirulina platensis* Bioactive Compounds Targeting IL-6, EGFR, FGFR1, and MMP9 for Wound Healing

Agnia Muftiasih¹, Heli Siti Halimatul Munawaroh^{1,2}, Siti Aisyah¹

¹Study Program of Chemistry, Faculty of Mathematics and Natural Sciences of Education, Universitas Pendidikan Indonesia

²Pusat Halal Universitas Pendidikan Indonesia

Abstract

Chronic diabetic wounds involve dysregulated inflammation, impaired proliferation, and aberrant remodeling. This study investigates the wound-healing potential of *Spirulina platensis* bioactive compounds using an in silico multi-ligand docking strategy against four key targets: Interleukin-6 (IL-6), Epidermal Growth Factor Receptor (EGFR), Fibroblast Growth Factor Receptor-1 (FGFR1), and Matrix Metalloproteinase-9 (MMP9). Target proteins and candidate ligands were curated and prepared, the docking protocol was validated, and simulations were performed with AutoDock Vina supported by Autodock Tools. Results were visualized in BIOVIA Discovery Studio and PyMOL. Among all combinations tested, the acacetin-pinocembrin-gallic acid-quercetin set yielded the most favorable binding energies (-15.27 to -27.25 kcal/mol), outperforming single-ligand docking. The predicted interactions suggest simultaneous modulation of inflammatory signaling (IL-6), stimulation of cell-proliferation pathways (EGFR and FGFR-1), and regulation of extracellular-matrix turnover (MMP9), indicating a synergistic multi-target mechanism relevant to diabetic wound repair. Overall, *Spirulina*-derived compound combinations display coherent polypharmacology that could support and accelerate wound healing. These findings provide a mechanistic rationale for developing *Spirulina*-based topical therapeutics, while acknowledging the need for subsequent in vitro and in vivo validation to confirm efficacy and safety.

Keywords: *Spirulina platensis*, molecular docking, multi-ligand, wound healing, interleukin-6 (IL-6), Epidermal Growth Factor Receptor (EGFR), Fibroblast Growth Factor Receptors-1 (FGFR1), and Matrix Metalloproteinase-9 (MMP9).

[0-5]
Evaluation of α -amylase Inhibitory Potential of *Carica papaya* Seed
Extracts

Tina Dewi Rosahdi, Tomi Silahudin, Nunung Kurniasih, Assyifa Junitasari, Yusuf Rohmatulloh

Department of Chemistry, Faculty of Science and Technology, UIN Sunan Gunung Djati
Bandung

Abstract

Diabetes mellitus (DM) is a metabolic disorder characterized by elevated blood glucose levels resulting from impaired insulin secretion or action. One preventive strategy to manage hyperglycemia involves inhibiting α -amylase activity, thereby slowing the breakdown of complex carbohydrates into glucose. In this study, the inhibitory effectiveness of *Carica papaya* seed extracts, specifically the n-hexane, ethyl acetate, and ethanol fractions, against alfa amylase activity was evaluated. The assays were conducted in vitro using a UV-Vis spectrophotometer, and enzymatic activity was determined by the 3,5-dinitrosalicylic acid (DNS) method. Phytochemical analysis indicated that all extracts contained flavonoids, whereas only the n-hexane extract exhibited the presence of steroids. The α -amylase activity was measured at 160 U/mL. The IC₅₀ values were 173.65 mg/mL for the n-hexane extract, 183.69 mg/mL for the ethyl acetate extract, and 172.52 mg/mL for the ethanol extract. Based on these IC₅₀ values, all extracts demonstrated weak alfa amylase inhibition, as values exceeding 150 mg/mL indicate low inhibitory potency. Overall, *Carica papaya* seed extracts showed mild α -amylase inhibitory potential, suggesting limited efficacy in modulating postprandial blood glucose levels.

Keywords: α -amylase, enzyme inhibition, *Carica papaya* seed extract.

[O-6]

Water-Based Extraction and Characterization of κ -carrageenan from *Eucheuma spinosum* for Future Biomedical Applications

Mamay, Rukman Hertadi

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and Natural Sciences, Bandung Institute of Technology

Abstract

κ -carrageenan, a sulfated polysaccharide from red seaweeds, is widely recognized for its gel-forming ability and biocompatibility, making it a promising material for biomedical applications. This study reports a green and simple extraction method to isolate κ -carrageenan from *Eucheuma spinosum* using a simple, water-based method without chemical reagents to ensure safety for biomedical use. The extraction yielded 40.6% κ -carrageenan. Fourier Transform Infrared (FTIR) spectroscopy showed characteristic bands at 1259 cm^{-1} (S=O stretching of sulfate ester), 930 cm^{-1} (3,6-anhydro-D-galactose), and 845 cm^{-1} (galactose-4-sulfate), confirming the κ -type structure. The $^1\text{H-NMR}$ spectrum revealed typical G4S and DA resonances, further verifying its identity. The sulfate content was 27.6%, within the typical range for κ -carrageenan. Gelation tests indicated strong gel formation in the presence of K^+ ions, demonstrating its characteristic ionic gelation behavior. This study presents an eco-friendly and non-toxic process for producing functional κ -carrageenan from *E. spinosum*, which may serve as a safe and sustainable candidate for future biomedical applications.

Keywords: κ -carrageenan, *Eucheuma spinosum*, water-based extraction, gelation, biomedical application.

[O-7]
Isolation and Characterization of Growth and Photosynthetic
Activity of the Green Microalgae *Chlorella* sp. ITB1

Laura Adilla, Rindia Maharani Putri, Alfredo Kono

Biochemistry and Biomolecular Engineering Research Division, Faculty of Mathematics and
Natural Sciences, Bandung Institute of Technology

e-mail: rindia.m.putri@itb.ac.id

Abstract

One effort to mitigate CO₂ emissions, a primary cause of global warming, is through the development of microalgae-based CO₂ capture technology. As photosynthetic organisms, microalgae can sequester CO₂ from the atmosphere and convert it into biomass, thus holding potential as a medium for both capturing and converting CO₂ into functional compounds. This study aimed to isolate green microalgae from the ITB campus environment, analyze the growth profile of the local isolate, and determine its photosynthetic rate under different media conditions: a minimal medium and a nutrient-rich medium. In this study, soil samples were collected from five locations within ITB (locations 1, 2, 3, 4, and 5). An isolate from location 2 (in front of the Chemical Engineering Laboratory) was successfully purified into a single green microalgal colony through physical washing, serial dilution, and streaking on a solid medium. Identification based on cell morphology and the 18S rRNA gene sequence (V4–V5 region) revealed that the isolate belongs to the genus *Chlorella*, which was subsequently named *Chlorella* sp. ITB1. The growth profile was assessed in TAP (nutrient-rich) and Tris minimal (minimal nutrient) media through daily measurements of cell density, optical density, chlorophyll concentration, pH, and dry biomass. Furthermore, the photosynthetic rate of the microalgae grown in both media (TAP vs Tris minimal) was measured using an Oxygraph+. The growth profile and biomass yield of *Chlorella* sp. ITB1 were higher in the TAP medium (1.95 g/L/day) compared to the minimal Tris medium (1.15 g/L/day). The photosynthetic activity of *Chlorella* sp. ITB1 was also more efficient in the TAP medium, as indicated by a lower $K_{0.5}$ (C_i) value for inorganic carbon (C_i) ($19.42 \pm 3.90 \mu\text{M}$) compared to the minimal Tris medium ($35.96 \pm 1.20 \mu\text{M}$). However, the maximum photosynthetic rate (V_{max}) was recorded to be higher in the minimal Tris medium ($44.34 \pm 0.29 \mu\text{mol O}_2 \text{ h}^{-1} \cdot \text{mg}^{-1}$ chlorophyll) compared to the TAP medium ($35.10 \pm 1.44 \mu\text{mol O}_2 \text{ h}^{-1} \cdot \text{mg}^{-1}$ chlorophyll). This suggests that the Tris minimal medium could not efficiently induce the CO₂-concentrating mechanism (CCM), as is commonly found in the model green microalga, *Chlamydomonas reinhardtii*. This difference indicates that the regulation and effectiveness of the CCM in *Chlorella* sp. ITB1 differ from that of *C. reinhardtii*, warranting further studies to elucidate its photosynthetic adaptation mechanisms and CCM activation under various environmental conditions.

Keywords: green microalgae, *Chlorella* sp., CO₂ capture, photosynthesis, CCM.