Key Technologies in the Bioeconomy KTB2025

GLOBAL BIOECONOMY ALLIANCE

Global Bioeconomy Alliance

Conference 2025

Key Technologies in the Bioeconomy

Denmark, 29 September – 3 October

Contents

About the Conference

Key Technologies in the Bioeconomy is the 4th Annual Global Bioeconomy Alliance (GBA) Conference.
The conference advances sustainable solutions by fostering collaboration between researchers, industry leaders, and policymakers. It brings together key stakeholders to explore policy developments, industry advancements, and cutting-edge technological innovations shaping the future of the bioeconomy.

The program covers sustainable food production, sustainable agriculture, fermentation, biomaterials, cell-free bio-solutions, sustainable mining, as well as political perspectives and industry involvement.

Industry and Government on a Global Scale

Site visit to Kalundborg Symbiosis

In-depth Scientific Sessions

The first day focuses on industry and government on a global scale, highlighting policy and industry developments.

The second day is dedicated to a visit to Kalundborg Symbiosis, Scandinavia's largest bioindustrial cluster, where industrial symbiosis demonstrates sustainability in practice.

The last three days feature in-depth scientific sessions covering themes such as scaling bioeconomy solutions globally, sustainable food production and agriculture, cell-free biosolutions, biomaterials, sustainable mining, and fermentation as a key driver in the bioeconomy. Each session combines invited lectures from leading international experts with roundtable discussions based on submitted abstracts, fostering networking, collaboration, and knowledge exchange.

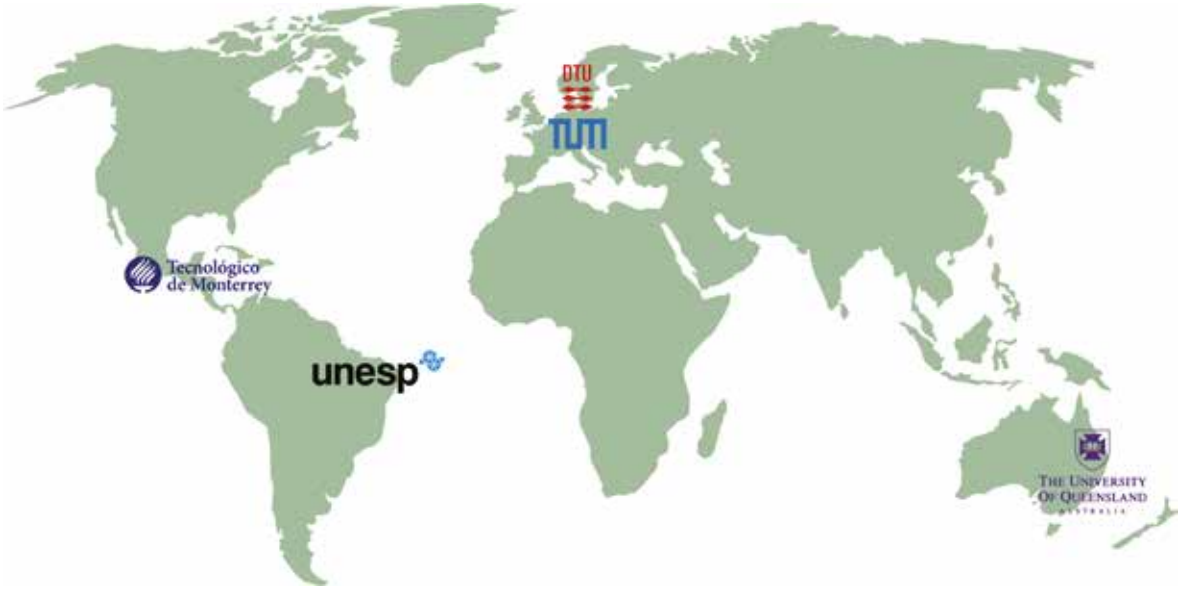
The conference also includes a poster session, giving early-career researchers the opportunity to present their work, with the winner announced at the closing session.

A highlight of the conference is the presentation by the awardee of the GBA Award for Impact and Leadership in Bioeconomy.

Let's change the world together. Welcome!

The GBA Board

About the Global Bioeconomy Alliance



The Global Bioeconomy Alliance (GBA) is a worldwide network of leading institutions dedicated to advancing the bioeconomy. Its mission is to strengthen collaboration in research, innovation, and education to accelerate the transition toward a more sustainable society and improved planetary health.

The alliance brings together top universities with strong expertise in bioeconomy-related fields:

- Technical University of Munich (Germany)
- The University of Queensland (Australia)
- Universidade Estadual Paulista (Brazil)
- Tecnológico de Monterrey (Mexico)
- Technical University of Denmark

These partners are recognized leaders in their regions, with outstanding expertise in research and teaching across bioeconomy topics.

GBA aims to foster cooperation across agriculture, technology, and social sciences to drive the bio-based economy, facilitate the transfer of knowledge and technology to avoid common pitfalls in bioeconomy initiatives, attract funding to support joint and country-specific research challenges, and build a continuously expanding network of experts committed to solving global sustainability problems.

By combining regional expertise with a shared vision, the GBA seeks to accelerate the development of a global bioeconomy and a more sustainable future.

GBA invites universities, research institutions, and organizations from around the world to join the alliance, contribute their expertise, and help shape the future of the global bioeconomy. Please reach out on: info@bioeconomy.world.

Global Bioeconomy Alliance
Annual Conference
Key Technologies in the Bioeconomy 2025

PROGRAMME

Wednesday, 1 October

09.00 - 09.25 *Light Breakfast*

09.25 - 09.30 **Welcome**
Volker Sieber, Rector, TUM Campus Straubing for Biotechnology and Sustainability
Chair of the Board, Global Bioeconomy Alliance

09.30 – 11.30 **SESSION I: BIOECONOMY – HOW TO SCALE SOLUTIONS GLOBALLY**
Chair: Paul Spee, Associate Professor in Strategy, The University of Queensland

09.30 – 10.00 **PLENARY TALK: Bioeconomy – How to Scale Solutions Globally**
Livia Cabernard, Assistant Professor, Sustainability Assessment of Food and Agricultural Systems, Technical University of Munich

10.00 – 10.30 *Coffee Break*

10.30 - 11.00 **PLENARY TALK: How the Biocapacity can Enhance the Bioeconomy**
Alcides Lopes Leão, Professor, Department of Bioprocess and Bioengineering, School of Agricultural Sciences, Campus of Botucatu, São Paulo State University, Brazil

11.00 – 11.30 **PLENARY TALK: A Sustainable Bio-platform for High Quality Microbial Protein Production**
Zhou Yan, Associate Chair (Faculty) and Professor, School of Civil and Environmental Engineering, Nanyang Technological University, Singapore

11.30 – 13.00 *Lunch*

13.00 – 14.15 **SESSION II: SUSTAINABLE FOOD PRODUCTION**
Chair: Timothy Hobley, Associate Professor, The Technical University of Denmark

13.00 – 13.30 **PLENARY TALK: Upcycling of Alkaline Maize Wastewater: From Tortilla to Lettuce**
Janet Alejandra Gutiérrez Uribe, Regional Department Head of Bioengineering and Science, School of Engineering and Sciences, Tecnológico de Monterrey

13.30 - 14.15 **Round table: Sustainable Food Production**

- **Valorisation of Soy Sidestreams via Fungal Fermentation and Bioprocess Intensification**
  Sonja Berensmeier, Professor, The Technical University of Munich
- **Integrated Dual Pathways for Fruit Waste Valorization in Food and Bioprocessing Towards a Circular Bioeconomy**
  Daniel Ojwang, Research Scientist, Kenya Industrial Research and Development Institute
- Q&A

14.15 - 14.45 *Coffee Break*

14.45 - 16.00 **SESSION III: SUSTAINABLE AGRICULTURE**
Chair: Damaris Mbui, Professor, University of Nairobi

14.45 - 15.15 **PLENARY TALK: Robotics-Assisted Discovery of New Biosolutions for the BioAg Space -Smarter AgroBiological Screening (SABS)**
Rasmus J. N. Frandsen, Professor, DTU Bioengineering, Technical University of Denmark.

15.15 - 16.00 **Round table: Sustainable Agriculture**

- **Metabolomics-Guided Discovery of Bioactive Natural Products from Soil and Marine Microbial Ecosystems for Bioeconomy Applications**
  Zeinab Khalil, Australian Research Council Future Fellow, The University of Queensland
- **Enabling Automatic Plant Disease Phenotyping through Deep Learning-Based Image Segmentation**
  Sofia Martello, PhD Student, HSWT, The Technical University of Munich
- **Enzybiotics: Innovative biocatalysts to support sustainable citriculture**
  Igor Vinicius Ramos Otero, Postdoc, São Paulo State University
- Q&A (15m)

16.00 - 17.30 **Poster Session and Refreshments**

17.30 - 18.30 *Break and Check-in*

18.30 - 20.30 *Dinner at Marienlyst*

Global Bioeconomy Alliance
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PROGRAMME

Thursday, 2 October

09.00 - 11.30 **SESSION IV: CHALLENGES AND OPPORTUNITIES IN BIOECONOMY**
Chair: Bjarke Bak Christensen, Professor, The Technical University of Denmark & Gary Schenk, Professor, The University of Queensland

09.00 - 09.30 **PLENARY TALK: Forging a Link Between Bioeconomy Resources, Biotechnology to Products and Market Specific Solutions and Services Opportunities and Challenges in Africa**
Professor Francis J. Mulaa, Associate Dean, University of Nairobi, Kenya

09.30 - 10.00 **PLENARY TALK: Industrial Microbiology as a Driver for Linking Mining and Agriculture in Chile**
Professor Pilar Parada Valdecantos, Director, Center for Systems Biotechnology (CSB), Universidad Andrés Bello, Chile

10.00 - 10.30 *Coffee break*

10.30 - 11.30 **Panel discussion: Challenges and Opportunities in Bioeconomy**

- **Livia Cabernard**, Professor, Sustainability Assessment of Food and Agricultural Systems, Technical University of Munich.
- **Alcides Lopes Leão**, Professor, Department of Bioprocess and Bioengineering, School of Agricultural Sciences, Campus of Botucatu, São Paulo State University, Brazil.
- **Professor Francis J. Mulaa**, Associate Dean, University of Nairobi, Kenya
- **Pilar Parada Valdecantos**, Professor, Director, Center for Systems Biotechnology (CSB), Universidad Andrés Bello, Chile
- **Zhou Yan**, Associate Chair (Faculty) and Professor, School of Civil and Environmental Engineering, Nanyang Technological University, Singapore

11.30 - 12.30 *Lunch*

12.30 - 13.45 **WORKSHOP: Designing Sustainable Business Ecosystems and Innovation**

Chair: TBD

Moderators:

- **Paul Spee**, Associate Professor in Strategy, The University of Queensland
- **Claudia Doblinger**, Professor for Innovation and Technology Management, The Technical University of Munich
- **Kristina Vaarst Andersen**, Associate Professor, The Technical University of Denmark
- **Brandon Weber**, Chief Research Officer, Director of Centre for Bioprocess Engineering Research, University of Cape Town
- **Puja Thiel**, Bioeconomy Impact & Partnership Lead, University of Exeter

13.45 - 14.00 *Get-ready Break*

14.00 - 16.30 **Walk to Kronborg Castle**

16.30 - 16.45 *Coffee and Cake*

16.45 - 18.00 **SESSION V: CELL-FREE BIOSOLUTIONS**

Chair: Anne S. Meyer, Professor, The Technical University of Denmark, Co-chair Lara Pfaff, Postdoc, The Technical University of Denmark

16.45 - 17.15 **PLENARY TALK: Biocatalytic Upgrading of Renewable Biomass to Chemicals and New Bio-based Materials**

Emma Masters, Director at Biozone, Principal Investigator at Bioproducts Research Lab, University of Toronto

17.15 - 18.00 **Round table: Cell-Free Biosolutions**

- **Diversity study of Alcohol Dehydrogenases through *in silico* sequence structure function analysis**
  Cecilie Nørskov Jensen, PhD Student, The Technical University of Denmark
- **Towards a universal screening platform: Harnessing cell-free protein synthesis for high-throughput protein discovery**
  Tobias Köllen, Doctoral Researcher, The Technical University of Munich
- **Engineering stable and efficient ketol-acid reductoisomerases for industrial biotransformations using ancestral sequence reconstruction**
  Oscar Paredes Trujillo, PhD Student, The University of Queensland
- Q&A (15m)

18.00 - 18.30 *Break*

18.30 - 20.30 *Dinner at Marienlyst*

Global Bioeconomy Alliance
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PROGRAMME

Friday, 3 October

09.00 - 10.15 **SESSION VI: BIOMATERIALS AND BIOMASS CONVERSION**
Chair: Michael Zavrel, Professor, The Technical University of Munich

09.00 - 09.30 **PLENARY TALK: From Supramolecular Assembly to Biobased and Bioinformed Materials for a Circular Bioeconomy**
Stephen Schrettl, Professor, Functional Materials for Food Packaging, Technical University of Munich

9.30 - 10.15 **Round table - Biomaterials and Biomass Conversion**

- **Repurposing Environmental Weeds as Biofuel Pellets for Renewable Energy Transitions**
  Bruno Rafael De Almeida Moreira, Research Fellow, The University of Queensland
- **AI-Enhanced Bioprocessing for Agrifood Residue Valorization into Protein and Bioplastics**
  Mario Torres, Bioengineer; Professor; and Researcher, Technológico de Monterrey
- Q&A (15m)

10.15 - 10.45 *Coffee Break*

10.45 - 12.00 **SESSION VII: SUSTAINABLE MINING**
Chair: Nicholas Harmer, Professor, University of Exeter

10.45 - 11.15 **PLENARY TALK**
Sue Harrison, Professor, Deputy Vice-Chancellor (Research and Innovation), The University of Queensland

11.15 - 12.00 **Round table - Sustainable mining**

- **Microbially-Induced Calcite Precipitation in Co-disposed Coal Waste Systems**
  Ishaaq Hajee, Lecturer, University of Cape Town
- **From Environmental Liability to Strategic Resource: Cobalto Verde® Bioleaching Tailings for Cobalt Recovery**
  Pilar Parada Valdecantos, Centre for Systems Biotechnology Director, Universidad Andrés Bello
- **Valorisation of Bauxite Residue for Critical Metal Recovery Using Fungal Bioleaching: A Pathway Toward Circular Economy**
  Fernanda Soto-Montandon, PhD Student, The University of Queensland
- Q&A (15m)

12.00 - 13.00 *Lunch*

13.00 – 14.15 **SESSION VIII: FERMENTATION: A KEY DRIVER IN THE BIOECONOMY**
Chair: John Woodley, Professor, The Technical University of Denmark

13.00 – 13.30 **PLENARY TALK: The harder we TRY – towards low cost, fermentation-based manufacturing**
Lars Keld Nielsen, Scientific Director, Novo Nordisk Foundation Center for Biosustainability and Senior Group Leader, The University of Queensland

13.30 – 14.15 **Round table: Fermentation - A Key Driver in the Bioeconomy**

- **Engineering of *Corynebacterium glutamicum* and process development for 1,4-diaminobutane production from C1-based acetate**
  Katharina Dietz, Doctoral Candidate and Research Associate, The Technical University of Munich
- **Improving the production of Mogroside-V in *Saccharomyces cerevisiae* by developing a sucrose responsive GAL promoter system**
  Hannes Ehlert, PhD Student, The University of Queensland
- **Single-cell protein production from Mexican food industry waste via submerged fermentation**
  Aurea Karina Ramírez-Jiménez, Professor, Technológico de Monterrey
- Q&A (15m)

14.15 – 14.45 **SESSION IX: THE WORK IN THE GLOBAL BIOECONOMY ALLIANCE**
Board Members of the Global Bioeconomy Alliance

14.45 – 15.30 **SESSION X – MATCHING RESEARCHERS AND FUNDING OPPORTUNITIES**

15.30 - 15.40 **Closing Session and Poster Prize Winner Announcement**
Board Members of the Global Bioeconomy Alliance

15.40 - 18.00 *Refreshments*

17.00 – 18.30 *Break or Departure to Copenhagen, Øster Voldgade 4A/4B, 1123 Copenhagen*

18.30 – 20.30 *Dinner at Marienlyst*

Saturday, 4 October

09.00 – 10.00 *Check-out*

10.00 – 11.15 *Departure to Copenhagen, Øster Voldgade 4A/4B, 1123 Copenhagen*

Algae Farm
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Speakers

Wednesday, 1 October

Session I: Bioeconomy – How to Scale Solutions Globally

Chair: Paul Spee, Associate Professor, The University of Queensland

Livia Cabernard

Assistant Professor, Sustainability, Assessment of Food and Agricultural Systems, Technical University Munich, Germany

Talk **Bioeconomy – How to Scale Solutions Globally**

About

Livia Cabernard, born in Switzerland (1991), studied environmental sciences at ETH Zurich (2011–2017). She completed her PhD at the Institute of Environmental Engineering and the Institute of Science, Technology, and Policy at ETH Zurich (2017–2021), followed by a postdoc (2022–2023).

Since 2023, she leads the chair in Sustainability Assessment of Food and Agricultural Systems at Technical University Munich (tenure-track assistant professorship).

Her research combines life-cycle assessment, remote sensing, and economic modeling to identify impact hotspots in the global bioeconomy supply chain and assess mitigation strategies through sustainable policies.

Sustainability Assessment of Food and Agricultural Systems, Technical University of Munich.

Abstact

The bioeconomy is central to tackling the global climate and biodiversity crises, yet our research reveals a paradox: it is also a major driver of both. Since 1995, its greenhouse gas emissions have risen by 3.3 Gt CO_2-eq, while related land-use change has committed 1.4% of global species to extinction—far beyond planetary boundaries. International trade plays a decisive role: over 80% of these rising impacts are embodied in global supply chains. Tropical regions bear the heaviest burden, while imports by China, the Middle East, the United States, and Europe drives demand. Biochemicals showed the steepest rise, doubling through tropical land-use change and coal-based processing. Yet the scale of the problem also points to solutions: halting land conversion and shifting to renewable energy could cut emissions by nearly 60%, while sustainable sourcing and habitat protection can realign trade with planetary goals. This keynote explores how scaling such measures across borders can transform the bioeconomy from a source of crisis into a cornerstone of planetary resilience.

Alcides Lopes Leão

Professor, Department of Bioprocess and Bioengineering, School of Agricultural Sciences, Campus of Botucatu, São Paulo State University, Brazil

Talk **How the Biocapacity can Enhance the Bioeconomy**

About

Professor Alcides Lopes Leão, responsible for Biomass, Bioenergy, and Biobased Materials, works at UNESP, Brazil, and coordinates the RESIDUALL laboratory. He has published over 150 scientific papers, 70 newspaper articles, 40 book chapters, and 4 books. He has been a visiting professor at the University of Wisconsin (1993), Queensland University of Technology (2019-2024), and a mentor at Stirling University (2020-2023). He taught a master's course at Volkswagen AG (2005) and is UNESP's representative for GBA. He has lectured at over 150 international conferences and led more than 50 research projects.

Abstact

The biocapacity is closely linked to bioeconomy. Although in many places, most Least Developed Countries, still those values are explored below their full capacity. Key technologies can enhance the producing chain of many crops and byproducts around the world, contributing directly to reduce the social and economical stress in many economically deprived areas. The biomass cascade approach is a very positive alternative in this directions. Among the proposed alternatives we can include the biofuels, biobased materials, bio feedstocks, etc. All those products or compounds can be produced following the criteria of full plant utilization, which will bring more economical stability. Therefore we have to work in two direction: densification of the agro and aquatics producing chain and reducing the demand for non-renewable articles, most of them single-use. Finally, besides the fact that water is considered a renewable capital, we must reduce its agricultural consumption through plant breeding and biotechnologies made available throughout the world bringing sustainability to those that are the weakest points in the globe.

Speakers

Wednesday, 1 October

Session I: Bioeconomy – How to Scale Solutions Globally

Presentation by the Winner of the GBA Award

Zhou Yan

Associate Chair (Faculty) and Professor, School of Civil and Environmental Engineering, Nanyang Technological University, Singapore

Talk **A Sustainable Bio-platform for High Quality Microbial Protein Production**

About

Dr Zhou is a leading environmental engineer and biotechnologist recognized for her pioneering efforts in waste valorisation and sustainable biotechnology. Her work is defined by the strategic transformation of waste into high-value resources using microbial systems and bioprocesses, targeting key sectors in water, energy, and food systems. As a senior academic at NTU and Program Director at NEWRI, she has advanced science and technology to foster circular bioeconomy innovations that are both scalable and industrially relevant.

Abstact

The presentation will talk about an integrated bio-platform that utilizes nutrient-rich beverage wastewater streams to produce high-value single cell protein (SCP) using three microbial systems: aerobic heterotrophic bacteria (AHB), purple phototrophic bacteria (PPB), and microalgae. To support scalable downstream processing, a pilot membrane system was also designed and tested for biomass separation and concentration. Innovations included energy-efficient aeration-assisted membrane modules and fouling control strategies to maintain long-term operational stability. SCP products were evaluated as fish meal replacements through comprehensive fish trials. The trials demonstrated positive growth performance and digestibility when SCP was included in the fish diet, positioning SCP as a viable alternative protein for aquaculture applications. This project culminates in a validated, scalable platform for wastewater valorization into protein-rich biomass, with promising implications for food security, waste management, and sustainable industry practices in Singapore and beyond.

Green soybean plants
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Speakers

Wednesday, 1 October

Session II: Sustainable Food Production

Chair: Timothy Hobley, Associate Professor, The Technical University of Denmark

Janet A. Gutiérrez-Uribe

Regional Department Head of Bioengineering and Science, School of Engineering and Sciences, Tecnológico de Monterrey.

Talk **Upcycling of alkaline maize wastewater: From tortilla to lettuce**

About

Dr. Janet Gutiérrez is a full research professor at the School of Engineering and Science from Tecnológico de Monterrey. Since 2024, she is the Associate Dean of Faculty. For more than 20 years, she has been working on the phytochemistry and in nutritional biochemistry of phenolic compounds and other nutraceuticals. Particularly, her research is focused on Mexican foods such as black bean, cacti, agave and maize. She has published more than 170 papers and is the inventor of more than 10 patents. In 2020, the Mexican Academy of Science awarded her as a Distinguished Young Scientist. Co-founder of the National Network for Research on Functional Foods and Nutraceuticals (AlfaNutra).

Webpage: https://www.researchgate.net/profile/Janet_Gutierrez-Uribe
https://scholar.google.es/citations?hl=es&user=-Jyr6vNEAAAAJ

Abstact

The tortilla industry generates substantial volumes of alkaline maize cooking wastewater (nejayote). Nejayote fermentation with an alkaliphilic microorganism consortium (AMC) in a high-rate algal pond (HRAP) proved to be an alternative to reuse it in fresh food production. Fermented nejayote replaced one-third of irrigation water for lettuce (Lactuca sativa) cultivation. Lettuce length and weight, total phenolic content (TPC), and metabolomic profiles were compared against chemical fertilizer, non-fermented nejayote, and water controls. Lettuce fresh weight increased by 109.9% and TPC by 313.2% in comparison with water. In contrast, non-fermented nejayote (N) reduced lettuce fresh weight by 33.7%. Fermentation of nejayote with AMC promoted phenolic and polyphenolic accumulation as well as other molecules like fatty acids related with plant stress tolerance and membrane fluidity. This agroindustrial wastewater upcycling strategy promoted sustainable agriculture by minimizing reliance on synthetic agro-inputs, conserving freshwater, and aligning with circular economy principles.

Round Table Discussion

Valorisation of Soy Sidestreams via Fungal Fermentation and Bioprocess Intensification

Sonja Berensmeier, Sabrina Styblova, Paul Jacoby, Baghbaderani Mantri

Technical University of Munich, Bioseparation Engineering Group, Germany

Under-utilised sidestreams from soy-based food production constitute an abundant, low-cost and sustainable feedstock. We present a modular bioprocess that converts these heterogeneous residues into multiple high-value products through submerged fermentation with edible macrofungi. Thanks to their broad substrate tolerance, efficient biomass formation and innate capacity to generate flavour molecules while mitigating allergenic compounds, these fungi are ideal biocatalysts for functional-food and alternative-protein ingredients.

Continuous operation is realised with an in-line dynamic cross-flow filtration (DCF) unit that simultaneously retains and concentrates protein- and polysaccharide-rich biomass while releasing a clarified broth enriched in volatile aroma compounds. The fully digitalised DCF is now being optimised via hybrid mechanistic/machine-learning models to enhance scalability and real-time process control.

Aroma compounds are captured from the filtrate by ethanol–water solid-phase extraction, achieving up to 90 % recovery and 23-fold concentration of key flavour molecules. The retained fungal biomass can be used directly as a protein-rich ingredient; in addition, targeted cell disruption and fractionation enabled the isolation of bioactive lectins exhibiting haemagglutinating, anti-tumour and glycoprotein-binding activities.

These results demonstrate a feasible, scalable and flexible cascade process that converts industrial food waste into a portfolio of natural flavours, functional proteins and alternative-protein biomass. By integrating fungal biotechnology with intensified downstream operations, the platform exemplifies circular-bioeconomy innovation and opens new opportunities for the food, cosmetic and biopharmaceutical sectors.

Speakers

Wednesday, 1 October

Session II: Sustainable Food Production

Round Table Discussion

Integrated Dual Pathways for Fruit Waste Valorization in Food and Bioprocessing Towards a Circular Bioeconomy

Ojwang Daniel Otieno[1], Knight Moraa[1], Agatha Kemunto[1], Godfrey Mwangi[1], Mulaa F. Jakim[2]

[1]Industrial Microbiology and Biotechnology Research Center, Kenya Industrial Research and Development Institute, P.O Box 30650-00100 Nairobi, Kenya.
[2]Department of Biochemistry, University of Nairobi, P.O Box 30197-00100 Nairobi, Kenya.
Corresponding e-mail: daniel.otieno@kirdi.go.ke

Fruit-processing by-products are abundant lignocellulosic residues that are often regarded as low value and discarded, particularly in developing countries, despite being rich in high-value compounds. In this study, the feasibility of using fruit-processing wastes as substrates for mushroom cultivation was assessed. Similarly, their potential for producing lignocellulolytic enzymes through solid-state fermentation was also evaluated.

To achieve this, three oyster mushrooms (*Pleurotus sajor-caju (Fr.) Singer, P. ostreatus (Jacq.: Fr.) P. Kumm., and P. eryngii (DC.) Quel.*) were cultivated on fruit wastes including banana, mango, avocado, pineapple, orange peels, and watermelon rind, with wheat straw as the control. In parallel, crude enzyme cocktails were produced via solid-state fermentation of pineapple and passion fruit peels using a newly isolated *Aspergillus niger* KWM strain. These enzymes were subsequently applied to saccharify mushroom biomass and passion fruit peel into glucose and galacturonic acid, respectively.

This study showed that fruit peels are effective in improving mushroom growth. The yield increase of up to 28% was recorded, with *P. sajor caju* achieving the highest on avocado peel. However, not all fruit peel substrates promoted mushroom yield; performance of *P. ostreatus* reduced on orange peel and watermelon rind. Furthermore, fruit peel substrates enhanced mushroom antioxidant activity by up to 49%, with *P. eryngii* grown on avocado peel showing the highest levels. The recovered crude enzyme cocktails effectively saccharified mushroom biomass and passion fruit peel, releasing ~1.6 mg/mL glucose and 77.8 mg galacturonic acid per gram of dry substrate, respectively.

Overall, this study demonstrates a scalable circular valorization pathway, where fruit processing byproducts can be used either directly as substrates for mushroom cultivation or as feedstocks for enzyme generation, enabling their profitable utilization, particularly in developing countries where such residues are abundant yet unexploited. This dual approach offers multiple benefits of meeting food/industry demands, while facilitating waste management in line with the principles of a circular bioeconomy.

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[1] Ojwang DO, Obiero G, Midiwo J, Mulaa FJ. Strategies for improving hydrolytic efficiency of crude multienzyme extracts in mushroom processing. Heliyon 8, e11312 (2022).
[2] Ojwang DO, Obiero G, Midiwo J, Mulaa FJ. Design Strategy for effective fruit waste bioconversion with crude fungal enzyme extract. Biologia, 79, 557–568 (2024).
[3] Ojwang DO, Obiero G, Midiwo J, Mulaa FJ. Utilization of fruit waste substrates in mushroom production and manipulation of chemical composition Biocatal Agric Biotechnol 39, 102250 (2022).

Biomass
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Speakers

Wednesday, 1 October

Session III: Sustainable Agriculture

Chair: Demaris Mbui, Professor, University of Nairobi

Rasmus J.N. Frandsen

Professor, Director of IBIS, Head of DALSA, The Technical University of Denmark

Talk **Robotics-Assisted Discovery of New Biosolutions for the BioAg Space – Smarter AgroBiological Screening (SABS)**

About

Professor Rasmus J.N. Frandsen earned his PhD in fungal molecular genetics from Copenhagen University, where he studied biosynthetic pathways in the wheat pathogen *Fusarium graminearum*. He joined DTU in 2010 and is now Professor of Fungal Biotechnology and Life Science Automation. His research focuses on fungal biosynthetic pathways, the engineering of fungal cell factories, the development of new-to-nature pathways, and non-GMO solutions for the BioAg sector. In his most recent project, Smarter AgroBiological Screening (SABS) project, he led a team of microbiologists, automation experts, and data scientists to develop robotics-assisted workflows for high-throughput analysis of filamentous fungi. His current projects target microbial solutions for sustainable agriculture (biofertilizers - IBIS) and food production, including off-flavor-degrading enzymes (REFINES), and next-generation production hosts (UP-CYFUN). Rasmus is furthermore heading DTU's Arena for Life Science Automation (DALSA), a public-private co-creation space that unites mechanical/electrical/software engineering with life science to develop new robotics solutions.

Abstact

Modern agriculture's performance relies on synthetic fertilizers and pesticides; however, these also disrupt nutrient cycles, pollute the environment, and are energy-intensive. Sustainable biosolutions are necessary to ensure food production within planetary limits, but a poor correlation between laboratory assays and field performance hinders their development. The Smarter AgroBiological Screening (SABS) project at DTU tackled this challenge by implementing robotic-assisted high-throughput mycology and testing of 9k fungal isolates for their biocontrol potential. Iterative assay development enhanced predictive power, allowing for enrichment for strains with higher greenhouse performance. While data volume limited lab-to-field correlation, results showed that smarter assay design can accelerate discovery. Building on these insights, the new Initiative for Biofertilizer Innovation and Science (IBIS) will optimize the pipeline from discovery (TRL1) to validated prototype (TRL7–8), enabling faster development of microbial biofertilizers to reduce agriculture's footprint and boost food security.

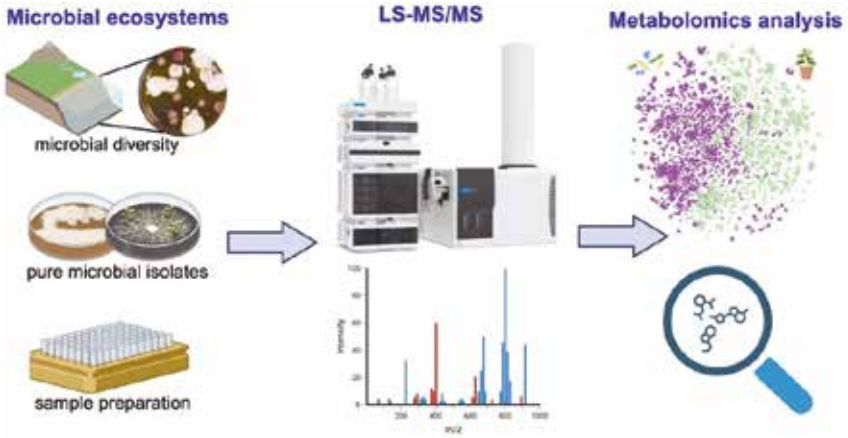
Round Table Discussion

Metabolomics-Guided Discovery of Bioactive Natural Products from Soil and Marine Microbial Ecosystems for Bioeconomy Applications

Ahmed Adel, Jolynn Kiong, **Zeinab G. Khalil**

Institute for Molecular Bioscience, Australian Institute for Bioengineering and Nanotechnology, UQ Biosustainability Hub, The University of Queensland, St Lucia, QLD 4072, Australia

The untapped metabolic potential of soil and marine microbes offers a powerful frontier for sustainable bioeconomy solutions [1]. We present M³i (**M**icrobial **M**etabolomics and **M**ultiomics for **I**nnovation), an integrated platform that combines microbial cultivation, advanced metabolomics, and multiomics-guided bioinformatics to accelerate the discovery of novel bioactive compounds for agricultural and environmental applications. We have built one of Australia's largest living libraries of soil-derived microbes, collected in partnership with citizen scientists [2]. In parallel, we explore marine microbial diversity from coastal sediments and sponge-associated ecosystems [3]. Using an OSMAC (One Strain Many Compounds) strategy alongside high-resolution MS/MS profiling, the M³i platform screens thousands of microbial extracts for antimicrobial, antifungal, and plant-beneficial activities. Advanced bioinformatics tools, including chemical space exploration, spectral similarity clustering, substructure guided molecular discovery, bioactivity guided metabolomics were used to dereplicate known compounds, predict novel structures, and map biosynthetic diversity across environments. This integrative platform highlights the essential role of microbial metabolites in driving innovative, sustainable solutions for next-generation bioeconomy applications.



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[1] **Zeinab G. Khalil**, Thulasi Sritharan, Angela A. Salim and Robert J. Capon. MATRIX: A Platform for Cultivation Profiling and Bioactive Discovery in Natural Products Research. *Frontiers in Natural Products*, 1-13, (2025).

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[3] **Zeinab G. Khalil**, Pablo Cruz-Morales, Cuauhtemoc Licona-Cassani, Esteban Marcellin and Robert J. Capon. Inter-Kingdom beach warfare: Microbial chemical communication activates natural chemical defences. *The ISME journal*, 13(1), 147-158, (2019).

Speakers

Wednesday, 1 October

Session III: Sustainable Agriculture

Round Table Discussion

Enabling Automatic Plant Disease Phenotyping through Deep Learning-Based Image Segmentation

Sofia Martello, Nikita Genze, Dominik Grimm

TUM Campus Straubing for Biotechnology and Sustainability & Weihenstephan-Triesdorf
University of Applied Sciences, Straubing, Germany

Developing disease-resistant crops is essential for sustainable agriculture. However, traditional phenotyping methods used to assess plant traits, such as disease severity, remain a major bottleneck in modern breeding programs due to their subjectivity and labor intensity [1]. To overcome these limitations, we present a deep learning-based approach for high-resolution, image-based phenotyping of naturally infected barley leaves. This method enables a more accurate, scalable, and reproducible assessment of foliar disease traits.

Our approach leverages multiclass semantic segmentation models trained on expert-annotated scans of field-grown barley leaves infected with brown rust (*Puccinia hordei*) and ramularia (*Ramularia collo-cygni*). We evaluate convolutional deep learning architectures such as U-Net, as well as hybrid variants incorporating modern token-mixing mechanisms, based on their ability to precisely delineate and classify disease lesions. Preliminary results indicate reliable and consistent segmentation performance across diverse barley genotypes, with high lesion detection accuracy.

Ongoing work focuses on quantifying lesion coverage, count, and spatial distribution from the predicted segmentation maps to enable trait-based comparisons across different genotypes. To support breeders in their workflows, we are developing a browser-based interface for real-time visualisation, inspection, and export of various disease metrics, ensuring accessibility for researchers and breeders.

By enabling automated, trait-specific phenotyping under real field conditions, this approach addresses a critical technological need for a sustainable agriculture. It facilitates data-driven genotype selection and supports the development of robust, low-input crop varieties essential for a resilient agricultural future.

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Enzybiotics: Innovative biocatalysts to support sustainable citriculture

Igor Vinicius Ramos Otero[1*]; Mario Nicolas Caccalano[1]; Caio Felipe Cavichia Zamunér[1]; Henrique Ferreira[1]

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Endolysins are bacteriophage-derived enzymes expressed during the late stage of lytic infection. Predominantly classified as hydrolases, they degrade the bacterial cell wall, enabling the release of viral progeny [1]. These enzymes have been extensively investigated as promising alternatives for controlling pathogenic bacteria; however, their potential applications in agriculture remain largely unexplored [2]. Citrus canker, an incurable disease caused by the Gram-negative bacterium *Xanthomonas citri* subsp. *citri* (*X. citri*), is currently managed through integrated practices, including the application of copper-based compounds. Besides their toxicity and phytotoxicity, the accumulation of copper in orchards may drive the emergence of resistant *X. citri* strains. In this context, our research group has identified endolysins from different *X. citri*-infecting phages and is evaluating their potential for disease control. Among them, CP2-07 is a globular endolysin that appears to lack the canonical β-hairpin motif typically found in lysozymes, while conserving critical residues in its catalytic cleft. CP2-07 exhibited muramidase activity against purified *X. citri* peptidoglycan, demonstrating good thermostability (T_m = 52 °C) and the ability to refold after thermal denaturation at 90 °C, while retaining its initial activity. CP2-07 displayed bactericidal effects against *X. citri* at 100 µg/mL and effectively promoted cell lysis during the mid-log phase, although activity required EDTA as a membrane permeabilizer. To overcome this limitation, we are currently engineering CP2-07 and other endolysins fused with polycationic peptides. This modification is expected to facilitate their translocation across the outer membrane of Gram-negative bacteria, such as *X. citri*, enabling direct access to the peptidoglycan layer, eliminating the need for additives. Although still in progress, our findings highlight the potential of endolysins as a foundation for innovative, biocatalysis-based strategies aimed at controlling economically relevant bacterial phytopathogens.

Keywords: Endolysins; *Xanthomonas citri*; Biocontrol.

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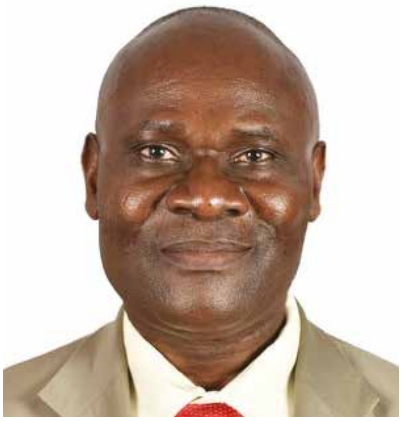
Speakers

Thursday, 2 October

Session IV: Challenges and Opportunities in Bioeconomy

Chairs: Bjarke Bak Christensen, Professor, The Technical University of Denmark & Gary Schenk, Professor, The University of Queensland



Francis J. Mulaa

Professor, Associate Dean, University of Nairobi, Kenya

Talk **Forging a Link Between Bioeconomy Resources, Biotechnology to Products and Market Specific Solutions and Services Opportunities and Challenges in Africa.**

About

Professor Francis Mulaa is an academic broad scientist currently serving as the Deputy Vice Chancellor, Research, Innovation and Enterprise (RIE) at the University of Nairobi, Kenya. He is the coordinator of AFTREC, a Pan-African network of engineering and technology-focused universities to accelerate workforce development, knowledge creation, and entrepreneurship that drives inclusive digital transformation in Africa. He has founded a startup company based on one of the industrial biotechnology patents arising from earlier work using industrial enzymes, biotechnology.

Abstact

Africa is well endowed with bio-resources that can be harnessed to stimulate economic growth and integrate the region to the wider global bioeconomy. Harnessing these bio-resources is key in addressing development challenges such as health, food and nutrition security, and sustainable utilization of natural resources for industrial development.

African countries should explore biotechnology to gain advantages from early entry into circular pathways of organizing production activities, such as exchanging bioresources and residual streams and building business synergies. Barriers for the transformation of bioresources to a circular economy including enabling policies exist, but, we argue, African countries are less locked-in to linear practices and infrastructures. There are great opportunities if circular industrialization strategies could be addressed ambitiously, wisely and in a timely manner. Industries should therefore seek, to exploit the window of opportunity in bioeconomy to steer the rising industrialization in a circular direction.

Pilar Parada Valdecantos

Professor, Director, Center for Systems Biotechnology (CSB), Universidad Andrés Bello, Chile

Talk **Industrial microbiology as a driver for linking mining and agriculture in Chile.**

About

Pilar Parada, Director of the Centre for Systems Biotechnology at Andrés Bello University (Chile), is a biochemist with more than two decades of experience in strategy and innovation in science and biotechnology. She is an expert in linking academic research with the needs of industry to drive productive transformations, particularly in the mining and agri-food sectors, with a particular focus on circular economy and sustainability. She has a strong track record of patents filed and granted, as well as awards for her achievements as an inventor and innovator. Her leadership roles at Universidad Andrés Bello, Fraunhofer Chile Research and Biosigma S.A. demonstrate her extensive experience in project management and executive leadership in biotechnology and bioleaching.

Abstact

Industrial microbiology is unlocking innovative pathways that connect Chile's two strategic sectors: mining and agriculture. Our Cobalto Verde® project harnesses native microbial consortia to bioleach cobalt from mine tailings, delivering a low-carbon, circular, and locally sourced supply of this critical metal for the global energy transition. In parallel, the Agrosimbiosis® program transforms agricultural and agro-industrial waste into high-value ingrdientes, biofertilizers and soil amendments through targeted microbiome enhancement. Together, these initiatives illustrate how microbiology can drive circular innovation, restore soil health, and significantly reduce greenhouse gas emissions, as verified through Life Cycle Assessments (LCA). The next step is to pilot these technologies in a mining city such as Copiapó, where desertified and degraded soils offer a unique opportunity to create true industrial symbiosis between agriculture and mining. Chile thus provides a scalable living lab for resource-based economies seeking to decouple growth from environmental impact and accelerate a resilient, low-carbon bioeconomy.

SESSION IV: Challenges and Opportunities in Bioeconomy Panel Discussion

Livia Cabernard, Assistant Professor, Sustainability Assessment of Food and Agricultural Systems, Technical University of Munich

Alcides Lopes Leão, Professor, Department of Bioprocess and Bioengineering, School of Agricultural Sciences, Campus of Botucatu, São Paulo State University, Brazil.

Francis J. Mulaa, Professor, Associate Dean, University of Nairobi, Kenya

Pilar Parada Valdecantos, Professor, Director, Center for Systems Biotechnology (CSB), Universidad Andrés Bello, Chile

Zhou Yan, Associate Chair (Faculty) and Professor, School of Civil and Environmental Engineering, Nanyang Technological University, Singapore

Workshop:
Designing Sustainable Business Ecosystems and Innovation

This workshop explores how sustainable business ecosystems can address pressing societal challenges—such as the energy transition—by overcoming barriers and leveraging synergies. Through panel discussion and active audience participation, it fosters dialogue across diverse perspectives. The aim is to develop a shared understanding of ecosystem dynamics and to identify opportunities for collaborative research and innovation.

Moderators:

Kristina Vaarst Andersen, Associate Professor, The Technical University of Denmark

Claudia Doblinger, Professor for Innovation and Technology Management, The Technical University of Munich

Paul Spee, Associate Professor in Strategy, The University of Queensland

Puja Thiel, Bioeconomy Impact & Partnership Lead, University of Exeter

Brandon Weber, Chief Research Officer, Director of Centre for Bioprocess Engineering Research, University of Cape Town

Speakers

Thursday, 2 October

Session V: Cell-Free Biosolutions

Chair: Anne S. Meyer, Professor, The Technical University of Denmark,
Co-Chair Lara Pfaff, Postdoc, The Technical University of Denmark

Emma Master

Professor, Director at Biozone, Principal Investigator at Bioproducts Research Lab, University of Toronto

Talk Biocatalytic upgrading of renewable biomass to chemicals and new bio-based materials

About

Emma Master is a Professor at the University of Toronto and Adjunct Professor at Aalto University (Finland). In July 2023, she became Director of the BioZone Centre for Applied Bioscience and Bioengineering, and in 2025 she became the inaugural Robert Korthals Chair in Sustainability. The aim of her research is to develop enzymes that customize nature's most abundant structural polymers for use in renewable and value-added materials. She was awarded a Finland Distinguished Professor Fellowship and a European Research Council Consolidator grant to expand her research network in Europe. In 2020, she was awarded an EU Horizon grant to integrate bioscience, computational sciences and materials sciences in circular bio-based economy frameworks. She also led the Genome Canada "Synbiomics" project, which involved four Canadian universities and seven industry partners from across the bioproduct value chain, and now leads the NSERC CREATE for BioZone: an open science centre for industrial biotechnology in the circular economy. To scale-up and de-risk most promising biotechnologies, she co-founded YZymes Inc in 2021 to accelerate technology translation and benefits to diversified biorefineries.

Abstact

Genomics initiatives have uncovered the critical importance of microbial enzymes to expanding the range of products that can be made from plant biomass (i.e., lignocellulose). So far, most applications of such enzymes focus on the deconstruction of lignocellulose to monosaccharides and monolignols for subsequent fermentation to fuels and target chemicals. While necessary for capturing the full potential of renewable plant biomass, this approach inevitably foregoes the benefit of upgrading the energy and carbon already fixed in structures. In this presentation, I will describe our efforts to discover and develop enzymes and enzyme systems that introduce new chemical and physical functionality to underused lignocellulose fractions, leading to lignocellulosic building blocks primed for use in value-added applications, including use as crosslinkers and plant-based polyamines. In particular, this presentation will describe our characterization and application of carbohydrate oxidoreductases oxidases, carbohydrate-active transaminases, and microbial expansin-related proteins.

Round Table Discussion

Diversity study of Alcohol Dehydrogenases through *in silico* sequence structure function analysis

Jensen, C. N.[1]*, Pfaff, L.[1], Schenk, G.[2], Agger, J. W.[1], & Meyer, A. S.[1]

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[2] Australian Institute for Bioengineering and Nanotechnology, School of Chemistry and Molecular Biosciences, University of Queensland, QLD 4072, Australia

Carbon dioxide (CO_2) is a major driver of global warming and reducing the continued emissions is crucial to mitigating irreversible climate change. Atmospheric CO_2 represents a valuable carbon resource that can be converted into high-demand chemicals via sustainable pathways. A promising green approach involves a cell-free enzyme cascade that converts thermodynamically stable CO_2 into methanol. This cascade involves three microbial oxidoreductases: formate dehydrogenase (EC 1.2.1.2), formaldehyde dehydrogenase (EC 1.2.1.46) and alcohol dehydrogenase (ADH, EC 1.1.1.1).

This project focuses on the final step of the enzymatic cascade, catalyzed by ADH: an often-overlooked enzyme with significant potential as a C1-converting biocatalyst. ADHs are ubiquitous and can be found in all domains of life from bacteria, fungi, and plants to mammals. Consequently, this enzyme class comprises a wide range of oxidoreductases that have evolved to catalyze reversible oxidation of alcohols to the corresponding carbonyl products with broad specificity. ADHs utilize various metals, cofactors, or prosthetic groups, each characteristic of distinct ADH types. The overarching aim of this research is to elucidate sequence structure function relationships across the diverse ADH classes.

Identification of ADH sequences employed *in silico* studies that included genome mining of microbial genomes via sequence retrieval from the US National Center for Biotechnology Information database (NCBI), protein BLAST analyses, and AlphaFold 3 predictions of structures. From these initial studies, selected candidates were further studied through bioinformatic techniques to investigate the sequence structure function relationship across the different types of ADHs. This understanding lays the foundation for future wet lab experiments, in which these candidate enzymes will be recombinantly expressed, purified, and characterized with a particular focus on structural stability, solvent robustness, and catalytic efficiency.

Novel insights into microbial ADHs, their metallo-catalytic mechanisms, and structural features will advance the understanding of how ADHs can be optimized for enzymatic reaction cascades and yield unique foundational knowledge of the parameters governing reversible redox processes.

Speakers

Thursday, 2 October

Session V: Cell-Free Biosolutions

Round Table Discussion

Towards a universal screening platform: Harnessing cell-free protein synthesis for high-throughput protein discovery

Tobias Köllen, Volker Sieber,

Chair of Chemistry of Biogenic Resources, Technical University of Munich, Campus for Biotechnology and Sustainability, 94315 Straubing, Germany; Catalysis Research Center, Technical University of Munich, 85748 Garching, Germany

Enzymes are indispensable tools for the bioeconomy, enabling sustainable routes for biomass valorization, green chemistry, and the production of high-value chemicals. The discovery of novel enzymes is therefore a key challenge in biotechnology. Traditionally, enzyme candidates are expressed and screened in *Escherichia coli*, taking advantage of its robustness and well-established molecular toolbox. However, this approach is limited by host-specific expression biases. *E. coli*'s codon usage strongly influences which proteins can be expressed efficiently, restricting discovery pipelines to enzymes that align with its translational preferences. As a result, a large fraction of potentially valuable enzymes remains inaccessible using cell-based workflows.

Cell-free protein synthesis (CFPS) offers a powerful alternative. By decoupling protein expression from the constraints of living hosts, CFPS systems allow open access to and control over every step of protein synthesis. In this work, we employ the bottom-up, fully reconstituted PURE system to develop a highly flexible protein screening platform. PURE's defined composition, built from purified translation components, provides a unique opportunity to fine-tune expression environments with precision using co-factors or chaperones to enhance folding and activity. Because the translational machinery is highly conserved across organisms, PURE can also be adapted to mimic the codon usage preferences of diverse species. By supplementing or fully replacing the native tRNA pool with defined sets of rare tRNAs, we demonstrate that PURE can overcome codon usage bias and unlock the expression of proteins that are challenging in *E. coli*. This strategy significantly broadens the accessible sequence space for enzyme discovery.

We propose that integrating PURE into enzyme discovery pipelines will accelerate the identification of novel biocatalysts, reduce host-related bottlenecks, and expand the diversity of enzymes available for industrial application. In doing so, PURE-based screening provides a powerful tool for advancing the bioeconomy toward more efficient and sustainable bioprocesses.

Engineering stable and efficient ketol-acid reductoisomerases for industrial biotransformations using ancestral sequence reconstruction

Oscar Paredes Trujillo, Damian Hine, Gabriel Foley, Luke Guddat, Volker Sieber, Mikael Boden, Gerhard Schenk

The global economy has remained predominantly linear, and a shift towards circular processes that reuse waste streams and mitigate the unsustainable consumption of natural resources is urgently required. Here, enzyme engineering is employed to optimise a sustainable manufacturing process at lab scale, whereby a renewable feedstock (sugar) is converted to a platform chemical, isobutanol, which in turn can be used to produce biofuels and biomaterials [1]. The slowest step of this process, the conversion of (*S*)-2-acetolactate to 2,3-dihydroxyisovalerate, is catalysed by ketol-acid reductoisomerase (KARI) (Figure 1), an NAD(P)H-dependent enzyme [2]. To generate a portfolio of candidate KARIs for optimised isobutanol production, we applied ancestral sequence reconstruction (ASR) which recovered ancestor variants representing the KARI diversity across the tree of life and exposed evolutionary events underpinning the mixed functional profiles we observe in extant KARIs [3]. Ancestral variants were expressed, purified and their catalytic properties evaluated, revealing that the majority have improved catalytic efficiency (k_{cat}/K_m) and thermal stability when compared to the benchmark KARIs. Moreover, some variants exhibited increased isobutanol tolerance and total turnover numbers (TTNs) >10^6, greatly enhancing their potential for use in commercially viable industrial processes. Importantly, our results showcase ASR as a robust approach for leveraging structural and functional properties evolved in different species and environments to design optimised biocatalysts.

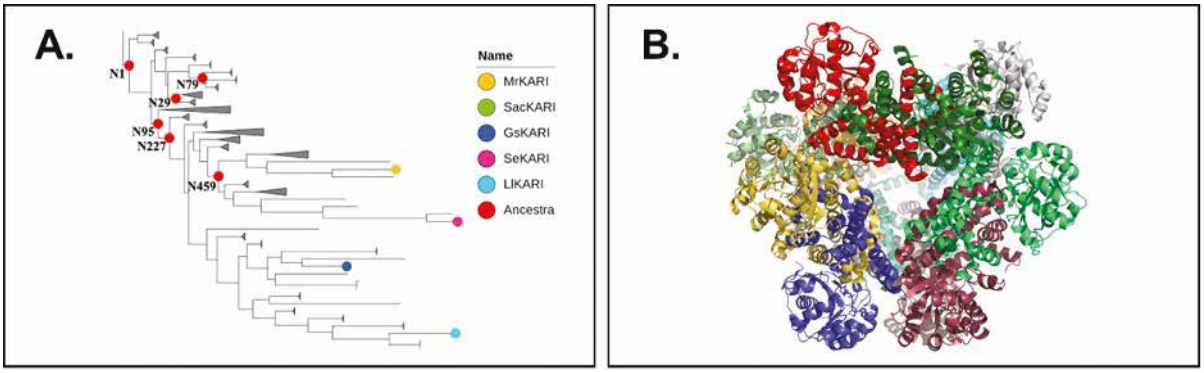

Figure 1: A) Phylogenetic tree of Class I KARIs, highlighting selected extant representatives and ancestors chosen for enzymatic characterisation. B) Graphical representation of the structure of KARI from *Saccharolobus solfataricus*.

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Aerial top view of Drinking Water Treatment plants. Microbiology of drinking water production
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Speakers

Friday, 3 October

Session VI: Biomaterials and Biomass Conversion

Chair: Michael Zavrel, Professor, Dr., The Technical University of Munich

Stephen Schrettl

Professor, Functional Materials for Food Packaging, Technical University of Munich

Talk **From Supramolecular Assembly to Biobased and Bioinformed Materials for a Circular Bioeconomy**

About

Stephen Schrettl is Professor at the Technical University of Munich (TUM) School of Life Sciences, where he researches new materials that combine performance with sustainability. His work explores supramolecular polymers, bio-inspired and responsive systems, and their use in areas such as food packaging. He coordinates the BayWater project, an academic initiative focused on sustainable water management and material systems. He also serves as Head of International Relations for the TUM School of Life Sciences, fostering global collaboration. Beyond academia, he advises the start-up Beworm, which develops innovative solutions for plastic degradation.

Abstact

Supramolecular polymers are created by assembling monomeric building blocks through directional, non-covalent interactions. Their reversible linkages endow the resulting materials with dynamic features such as healing, reprocessability, and responsiveness, opening routes toward advanced and sustainable material systems. In this presentation, we highlight recent advances in harnessing supramolecular assembly to enhance mechanical performance, implement new functions, and create robust materials that approach the properties of commodity plastics. Building on these fundamentals, we explore how the integration of biobased building blocks and, importantly, bioinformed design principles inspired by natural materials can accelerate the transition toward sustainable alternatives. The combination of molecular-level design with both renewable resources and bioinspired strategies provides opportunities to develop materials that are recyclable and adaptable for real-world applications. Our results illustrate how supramolecular strategies can contribute to the broader goals of the circular bioeconomy by linking fundamental innovation with practical sustainability

Round Table Discussion

Repurposing Environmental Weeds as Biofuel Pellets for Renewable Energy Transitions

Bruno Rafael de Almeida Moreira[a], Sameer Punde[b], Damian Hine[a], Sudhir Yadav[a]

[a] The University of Queensland St Lucia QLD 4072, Australia
[b] WorkEco Pvt Ltd, Taringa QLD 4068, Australia

Abstract: Progress toward net-zero emissions is increasingly constrained by sustainable feedstock supply. This study explores a globally overlooked solution: valorising invasive environmental weeds as standard-compliant biofuel pellets. In Australia, and across much of the Global South, these weeds are abundant, fast-growing, and ecologically damaging. Yet they remain underutilised. If converted into high-quality pellets, they could support both residential heating and industrial power generation, especially in regions where biomass is accessible but underexploited [1]. We assessed 15 species, including Weeds of National Significance, for composition and particle size to evaluate densification via mechanical interlocking and lignin-mediated cohesion (Fig. 1). A 3 × 3 matrix of temperature (25/50/100 °C) and pressure (50/100/150 bar) yielded 135 pellet types. Fuel quality (density, durability, calorific value, ash/mineral content) was benchmarked against ENplus® and ISO 17225 standards. Brazilian Nightshade (24.1% lignin) achieved ≈19 MJ kg^{-1} and 97.3% durability, meeting critical thresholds. However, species such as Mexican Ruellia and Singapore Daisy had high ash (≈36.5% and 11.1%) and elevated N, S, K, Na, raising fouling risks. Higher temperature and pressure improved durability and energy density, though unit density remained a constraint, as identified by machine-learning algorithms for key predictors and optimal conditions. This work shifts the focus from proof of combustion to proof of standard. It offers a replicable model for the Global South to lead in biomass innovation, while inviting Global North collaboration on technology transfer, standard harmonisation, and carbon accounting. By transforming a shared ecological burden into a renewable asset, this research supports more inclusive, circular, and energy transitions worldwide.

Figure: Schematic of the pathway for converting weed biomass into solid biofuel.

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Speakers

Friday, 3 October

Session VI: Biomaterials and Biomass Conversion

Round Table Discussion

AI-Enhanced Bioprocessing for Agrifood Residue Valorization into Protein and Bioplastics

Cecilia L. Martínez-Camarillo[+1], Paola C. Gutiérrez-Rangel[+1], Lynette M. Pacheco-Hernández[+1], Ulises A. Salas-Villalobos[1,2], Alberto Santos-Delgado[2], **Mario A. Torres-Acosta**[*1,3]

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[2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Building 220 Søltofts Plads, 2800 Kongens, Lyngby, Denmark.

[3] The Advanced Centre for Biochemical Engineering, Department of Biochemical Engineering, University College London, London WC1E 6BT, United Kingdom.

Agrifood residues pose a growing environmental and economic challenge worldwide. Their valorization into value-added products offers a sustainable solution. This work explores two bioconversion strategies: (i) whey valorization into single-cell protein (SCP) using mixed cultures of a lactose-consuming microorganism with Saccharomyces cerevisiae, and (ii) polyhydroxybutyrate (PHB) production by the halophile Halomonas campaniensis from orange peel residues. Factorial designs and response surface methodology were applied to optimize biomass generation by varying substrate concentrations, fermentation time, and mixed-culture conditions. Optimal SCP production required co-inoculation of both microorganisms, supplementation with glucose to enhance S. cerevisiae growth, and harvesting at 12 hours. PHB yields were maximized using 40–60% orange peel extract, balancing limonene inhibition with biomass accumulation over 48 hours. To extend experimental insights, artificial neural networks were trained with augmented datasets, enabling prediction of untested fermentation scenarios. Careful selection of variables was critical to avoid dimensionality issues while improving model robustness. These predictive tools are being integrated into techno-economic analyses to identify cost-efficient operating strategies. Overall, combining experimental design with AI/ML approaches accelerates process optimization, reduces laboratory workload, and enhances knowledge extraction. This integrated framework demonstrates the potential of digital bioprocessing for the sustainable revalorization of agrifood residues into protein and bioplastics.

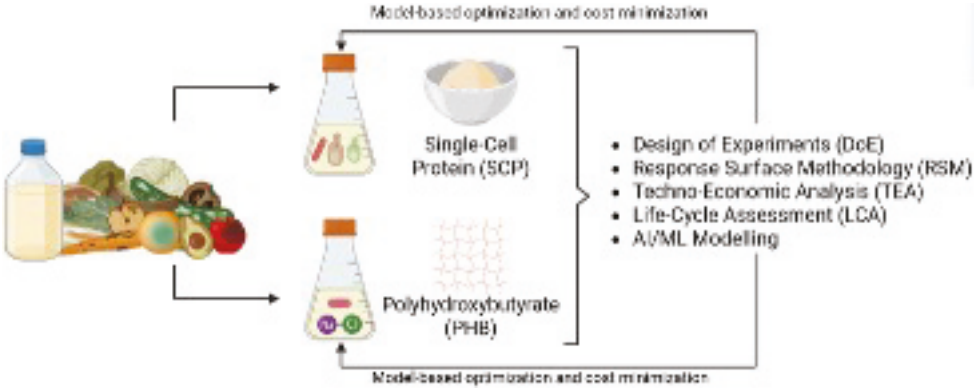

Figure 1. Graphical abstract representing the use of agrifood residues to perform fermentation using mixed microbial cultures for SCP production and halophilic bacteria for PHB generation. Additionally, the different techniques for analysis are shown.

Biogas plant for power generation and energy generation
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Speakers

Friday, 3 October

Session VII: Sustainable Mining

Chair: Nicholas Harmer, Professor, University of Exeter

Sue Harrison

Professor, Deputy Vice-Chancellor (Research and Innovation), University of Queensland, Australia

About

Professor Sue Harrison is Deputy Vice-Chancellor: Research and Innovation at the University of Queensland, since May 2025. Prior to this, she held positions of the University of Queensland's Executive Dean of the Faculty of Engineering, Architecture, and Information Technology (EAIT) in which she focused on the delivery of leading edge educational programs and research addressing global challenges and delivering transformational excellence, the University of Cape Town's Deputy Vice-Chancellor: Research and Internationalization championing research, innovation, postgraduate studies, and internationalization with a strong focus on embedding social responsiveness into research, and the South African Research Chair in bioprocess engineering, hosted by UCT. Sue has a long track record in management and leadership in the academic arena.

Sue is an active researcher in bioprocess engineering and its application to the circular economy, green technologies for the resource sectors and improved health care and well-being. Her research integrates fundamentals of process engineering and molecular & microbiology across applications including biominerals engineering, bioenvironmental systems, valorizing & repurposing waste, bioproducts and algal biotechnology. Integrating microbial dynamics and structure-function relationships informs building robust & resilience bioprocesses and novel bioproducts. Using IDTD research, she seeks sustainable approaches to mineral & water-sensitive systems.

Round Table Discussion

Microbially-Induced Calcite Precipitation in Co-disposed Coal Waste Systems

Ishaaq A. Hajee

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Acid rock drainage (ARD) is recognized as the single biggest environmental concern affecting the mining and mineral industry that deleteriously affects underground water resources and surrounding terrestrial ecosystems. Limiting the access of natural oxidants to the sulfide-containing mineral is, therefore, paramount to prevent the oxidation reactions that promote ARD. Co-disposal techniques, which aim to reduce the permeation of oxidants to acid-generating fractions by increasing the physical and chemical stability of wastes, involve the co-mingling of complementary mine wastes. The co-disposal technique was combined with microbially-induced calcite precipitation (MICP), where 12 bioreactors were setup with different packing configurations, inoculated with ureolytic bacteria *S. pasteurii*, and irrigated with a $CaCl_2$-rich cementation solution. Building on a previous investigation where MICP formation in co-disposed coal waste was demonstrated, the robustness of the hybrid MICP-co-disposal method was evaluated. The microbially-stabilised beds were subjected to acidified water at a pH comparable to acid rain for 240 days, where their structural stability and neutralisation capacity were constantly monitored. The cemented bioreactors maintained their neutralizing capacity for the entire irrigation period and contrasted the behaviour of the non-cemented controls, which ultimately yielded acidic leachate due to the repeated exposure of the sulphide-containing mineral waste to gaseous and aqueous oxidants. The results suggested that the hybrid MICP-co-disposal system is promising for long-term ARD prevention, even under highly acidic conditions.

Keywords: Acid Rock Drainage, Microbially-Induced Calcite Precipitation, Co-disposal

Speakers

Friday, 3 October

Session VII: Sustainable Mining

Round Table Discussion

Valorisation of Bauxite Residue for Critical Metal Recovery Using Fungal Bioleaching: A Pathway Toward Circular Economy

Fernanda Soto-Montandon[1,2]; Luke Webster[1,2]; Rosemary Gillane[1,2]; Esteban Marcellin[1]; Susan T.L. Harrison[3] and Denys Villa-Gomez[1,2]

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[3] University of Queensland, 4072, QLD, Australia

Bauxite residue (BR), a by-product of alumina refining, is one of the most abundant industrial wastes on Earth [1]. To date, approximately 4 billion tonnes have been stockpiled in disposal sites worldwide, with an additional 140-150 million tonnes generated annually [2]. BR is characterized by high alkalinity and salinity, posing significant environmental risks [3]. BR also represents an untapped source of critical metals (CM)-including rare earth elements and vanadium-necessary for sustainable technologies such as solar panels, electric vehicles, and clean energy systems [4].

This study introduces an innovative biotechnological approach for extracting critical metals from BR using bioleaching agents produced by filamentous fungi-*Aspergillus niger and Penicillium oxalicum*-isolated from global bauxite mine sites [5, 6]. These fungi produce organic acids that lower the alkalinity of BR while simultaneously solubilizing the target metals, thereby facilitating their mobilization into the soluble phase. The results obtained thus far demonstrate that *A. niger* and *P. oxalicum* tolerated concentrations of up to 10% w/v and 5% w/v, respectively, with only slight inhibition. Both strains exhibited a high neutralisation capacity, reducing significantly the pH. Leaching studies revealed that low concentrations of organic acids achieved higher extraction efficiencies for critical metals than mineral acids of equivalent normality and molarity. This underscores the potential of organic acids for the targeted recovery of metals associated with these phases and highlights the importance of metal-organic complex solubility in facilitating metal separation from the solid matrix.

This investigation proposes a novel, scalable biotechnological platform for the transformation of hazardous waste into a valuable resource while reducing environmental impact. This aligns with SDG 12 by promoting responsible consumption, resource efficiency, and reduced toxic waste generation.

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Round Table Discussion

From Environmental Liability to Strategic Resource: Cobalto Verde® Bioleaching Tailings for Cobalt Recovery

Pilar Parada Valdecantos, Director

Center for Systems Biotechnology (CSB), Universidad Andrés Bello, Chile

Speakers

Wednesday, 3 October

Session VIII: Fermentation: A Key Driver in the Bioeconomy

Lars Keld Nielsen

Professor, Scientific Director, Novo Nordisk Foundation Center for Biosustainability and Senior Group Leader, University of Queensland

Talk The harder we TRY – towards low cost, fermentation-based manufacturing

About

Professor Lars Nielsen is a Senior Group Leader at the Australian Institute for Bioengineering and Nanotechnology at The University of Queensland. He leads the development of experimental and computational tools to analyse and design complex biological systems. His expertise in metabolic modelling and flux analysis is available nowhere else in Australia – and in few labs across the world. Professor Nielsen's studies of biological systems as diverse as bacteria, baker's yeast, sugarcane, insects, and mammals have attracted industrial partnerships with companies including Dow, Metabolix, Amyris, LanzaTech, Boeing, Virgin Australia, and GE. Professor Lars Nielsen is also a Scientific Director at the Novo Nordisk Foundation Center for Biosustainability at the Technical University of Denmark within the team of Quantitative Modelling of Cell Metabolism, which analyses quantitative multi-omics datasets, using them to produce fine-grained numerical descriptions of biological processes that can guide environmentally crucial metabolic engineering projects.

Abstact

The 21st Century – the Century of Biology – started with great optimism over the potential for biotechnology to replace conventional chemical products and processes with better, cleaner, and cheaper alternatives. This hope was further stoked by rapidly increasing oil prices through the 00s, leading to large investments in industrial biotechnology. A quarter way through the century, biotechnology has delivered tremendous value in the fine chemicals area, while the promised contribution towards net zero has largely been absent. This talk will explore where fermentation based production may fit in the future sustainable chemical industry and what technological advances can be leveraged to make fermentation-based production viable for more products.

Round Table Discussion

Engineering of *Corynebacterium glutamicum* and process development for 1,4-diaminobutane production from C1-based acetate

Katharina Dietz[1], Bastian Blombach[1,2]

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[2] SynBiofoundary@TUM, Technical University of Munich, Straubing, Germany

The presented project aims for the fermentative production of 1,4-diaminobutane (DAB, trivial name putrescine) from C1-based acetate using *Corynebacterium glutamicum*. DAB is a valuable monomer for the synthesis of polyamide plastics which are currently produced from fossil raw materials. [1] This project pursues an alternative microbial process based on acetate, an underexploited carbon source that can be sustainably produced e.g. via acetogenic gas fermentation relying solely on CO_2/CO and H_2. [2] In doing so, the socio-economic and environmental risks associated with agriculturally derived substrates can be avoided. In addition, nitrogen valorization is addressed by using ammonia salts from wastewater treatment to produce the nitrogen-containing compound DAB.

The established platform organism *C. glutamicum* holds GRAS status and is primarily known as amino acid producer. The Gram-positive and glyoxylate-positive bacterium can readily metabolize acetate as sole carbon and energy source and tolerates elevated concentrations of acetate (40 g L^{-1}) and DAB (66 g L^{-1}), making it a promising host for the presented approach. [3,4] In a previous study, DAB production was enabled by heterologous expression of the ornithine decarboxylase SpeC of *E. coli*, leveraging the native arginine biosynthesis. Subsequent engineering of the biosynthetic route and the central metabolism led to strain NA6 which achieved a product yield of 0.26 g DAB per g glucose. [5,6]

In this study, strain NA6 was genetically adapted to improve DAB production from acetate. Initial small-scale screening experiments identified promising candidate strains with product yields ranging from 0.13 – 0.20 g DAB per g acetate. Consequently, selected *C. glutamicum* DAB producers were cultivated in a batch fermentation at 500 mL scale, reaching a final product titer of 1.26 g L^{-1} and a yield of 0.10 g DAB per g acetate (60 mg L^{-1} h^{-1}). The current focus lies on bioprocess development. Particularly carbon-limited fed-batch strategies using highly concentrated acetic acid feed streams are applied with the objective to further enhance productivity to 1 g L^{-1} h^{-1}.

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Speakers

Wednesday, 3 October

Session VIII: Fermentation: A Key Driver in the Bioeconomy

Round Table Discussion

Improving the production of Mogroside-V in *Saccharomyces cerevisiae* by developing a sucrose responsive GAL promoter system

Hannes Ehlert, James J. DeVoss, Birgitta E. Ebert

The University of Queensland, Brisbane/Australia

Mogroside-V is a glucosylated triterpenoid with an intense sweetening property 250 times that of household sugar, with only a fraction of the caloric value. The agricultural production of the compound is limited due to the specific environmental conditions required by the native plant *Siraitia grosvenorii*. The extract is also often tainted by off-tasting precursors and byproducts, making the biotechnological production of Mogroside-V attractive to increase yield and purity [1,2]. Recently, the de novo synthesis of Mogroside-V in the chassis organism *Saccharomyces cerevisiae* has been reported [3]. The heterologous pathway was expressed using GAL promoters, which are autoinducible in the absence of glucose after deleting the GAL80 gene. To still achieve the glucosylation of the triterpenoid backbone, ethanol and glucose need to be fed in a finely tuned ratio, which complicates the production.

We are developing a regulatory circuit for the autoinduction of the strong GAL promoters in the presence of the cheap carbon source sucrose. Sucrose can be split into fructose, which can be shuttled into the carbon metabolism of the cell, and glucose, which can be used to decorate the carbon backbone of the target compound. Using an auxin degradation system and tightly regulated, sucrose-responsive promoters, we can selectively degrade GAL repressors in the presence of sucrose and the absence of extracellular glucose [4,5]. This activates the GAL promoters, allowing for strong, autoinducible protein expression after a diauxic growth in which first glucose is consumed for cell growth until the culture switches into production mode utilising sucrose. We believe this system will benefit the production of all glucosylated natural products and make sucrose more accessible as a carbon source for precision fermentation.

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Round Table Discussion

Single-cell protein production from Mexican food industry waste via submerged fermentation

Leal-Urbina, E.[1], Dufoo-Hurtado, E.[1], Tec-Caamal, E.[1], Gaytán-Martínez, M.[2], Fernández-Cervantes, M.[1], **Ramírez-Jiménez, A[1]*.**

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Meeting rising global protein demands, expected to increase by 50% by 2050 [1], while managing agro-industrial waste, presents a critical challenge for the bioeconomy. This study introduces a low-impact bioprocess for single-cell protein (SCP) production using agave bagasse, a lignocellulosic byproduct from the Mexican mezcal industry, which generates an estimated 141 tons of bagasse monthly [2]. Bagasse was dried, milled (<1.7 mm), and enzymatically hydrolyzed using Cellic CTec2 and HTec2 in distilled water for 24 h, producing fermentable sugars at 16-17 g/L. These hydrolysates were the sole carbon source in submerged fermentations with *Saccharomyces cerevisiae* (T=30°C, 200 RPM, 72 h, pH 5.3) and *Aspergillus oryzae* (T=30°C, 200 RPM, 72 h, pH 5.7), cultivated in nitrogen-supplemented media (Figure 1). SCP production was measured through dry weight, OD600, sugar consumption (DNS, HPLC), and total protein content (Kjeldahl). *A. oryzae* yielded the highest biomass (up to 80 g/L), due to its enzymatic adaptability to complex substrates, while *S. cerevisiae* reached a biomass concentration of 32.6 g/L. Protein quantification revealed significantly higher yields in fungal fermentations, with up to 17.5 g protein per 100 g dry biomass and 11.48 g/L of protein in the culture medium, outperforming yeast-based SCP by over 40-fold. These results support the use of agave bagasse as a regionally abundant source for sustainable protein production and highlight its potential role in circular bioeconomy models, promoting waste reduction and resource efficiency.

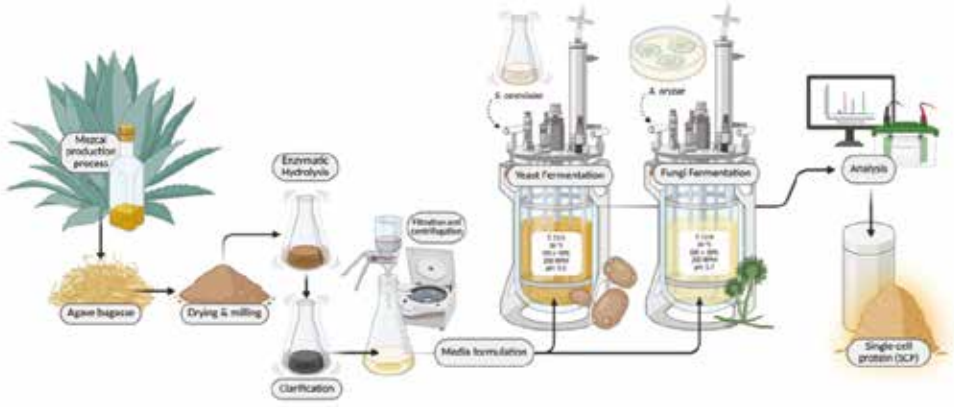

Figure 1. Bioprocess summary and fermentation conditions for *S. cerevisiae* and *A. oryzae*. Created in Biorender.

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Photobioreactor in algae fuel biofuel industry
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Poster 1

Unlocking the Nutritional Potential of *Nannochloropsis oceania*: A Novel Microalgae Ingredient for Sustainable Future Foods

Oladipupo Q. Adiamo, Saleha Akter, Eshetu M. Bobasa and Yasmina Sultanbawa

Centre for Nutrition and Food Sciences, Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Indooroopilly, QLD 4068, Australia.

Climate change significantly affects agricultural production, reducing arable land while global demand for agricultural products continues to rise. To sustainably feed nearly 8 billion people, more eco-friendly food sources must be established, and traditional food systems must transform to incorporate more sustainable and scalable practices [1] that are environmentally friendly, cost effective, culturally acceptable and ensure food security and health and nutrition equity for current and future generations [2].

Microalgae, a sustainable production system, has attracted interest as a food or ingredient because of its environmental benefits, like the ability to utilise carbon dioxide (CO_2), and abundance in nutrients and bioactive compounds, such as proteins, lipids, minerals and phytochemicals [3]. Furthermore, microalgae do not depend on freshwater and can thrive in non-potable water like seawater, reducing freshwater dependency. Microalgae can also be produced on non-arable lands that are unsuitable for traditional agriculture [4]; therefore, microalgae offer potential economic and environmental benefits for countries with expansive arid regions like Australia.

Despite the potential of microalgae as a food ingredient, their inclusion in commercial food products, particularly of new microalgae strains like *Nannochloropsis oceania,* is hindered by several challenges including regulatory and safety concerns, low shelf-life stability and poor nutrient bioavailability. This study specifically addresses the challenge of nutrient bioavailability by investigating the impact of post-production drying techniques (freeze-drying and spray drying) on the structural integrity of *Nannochloropsis oceania* cells. The study evaluates how structural changes influence nutrient release during digestion and absorption using a combination of microscopic analysis, *in vitro* gastrointestinal simulations and intestinal cell culture models.

Our previous findings on related microalgae strains, such as *Nannochloropsis oculata* demonstrated an increase in protein digestibility from 56% to 67% following ultrasonication. The current study will provide valuable insights into the nutritional and potential health benefits of *Nannochloropsis oceania*, thereby facilitating new product development and enhancing industry uptake of the microalgae as a novel ingredient.

Moreover, this project directly aligns with the Sustainable Development Goals (SDGs #2, #12 and #13) by promoting the development of sustainable food solutions that effectively address limitations associated with soil and freshwater resources through innovative cultivation of microalgae on arid lands.

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Poster 2

Data-driven prediction of sustainability performance for industrial biotechnology solutions at an early R&D stage

Tova Alenfalk, Sumesh Sukumara, Marjan Mansourvar, Line H. Clemmensen

Engineering and design decisions made early in the development of new industrial biotechnology solutions presumable influence the final bioprocess design, including its environmental impact. Early-stage sustainability assessments can therefore help guide the bioprocess development towards more sustainable solutions. However, these are typically challenging to conduct due to limited knowledge about the final process design. Machine learning (ML) techniques could potentially offer a valuable tool assisting early-stage sustainability assessments of emerging biotechnology solutions to ensure that these innovations truly support long-term sustainability goals.

Through a structured literature review, we identify opportunities, challenges, and research gaps for applying ML in early-stage sustainability assessment of biotechnology solutions. Although ML is increasingly applied in both biotechnology and sustainability assessments, its use for early-stage sustainability assessments in biotechnology remains limited. ML models capable of forecasting the final sustainability impacts from early-stage R&D data could contribute significantly to more informed decision-making during the bioprocess development. However, their development is hindered by challenges such as data scarcity and lack of integration of sustainability assessment models with experimental workflows. We have outlined strategic recommendations and future research priorities aimed at overcoming these limitations. Addressing these challenges could enable predictive, data-driven guidance for more sustainable bioprocess designs already at an early R&D stage.

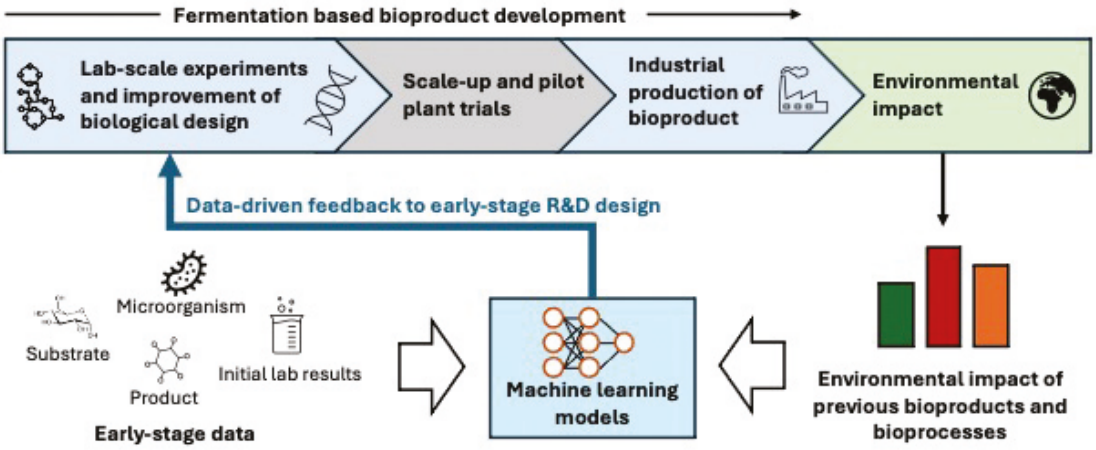

Figure 1: Potential integration of machine learning tools to assess the sustainability of industrial biotechnology solutions early in the bioprocess development pipeline. By learning from sustainability data of already developed bioprocesses, machine learning techniques could potentially find relationships between data available at an early R&D stage and corresponding sustainability impacts, enabling data-driven feedback towards more sustainable designs.

Poster 3

Upcycling Agro-Industrial Food Waste into Sustainable Composite Boards for General-Purpose and Interior Applications

Nelson W. Barasa[1,2], Thomas O. Mbuya[1], Meisam Jalalvand[2], Anand S. Ramesh[3]

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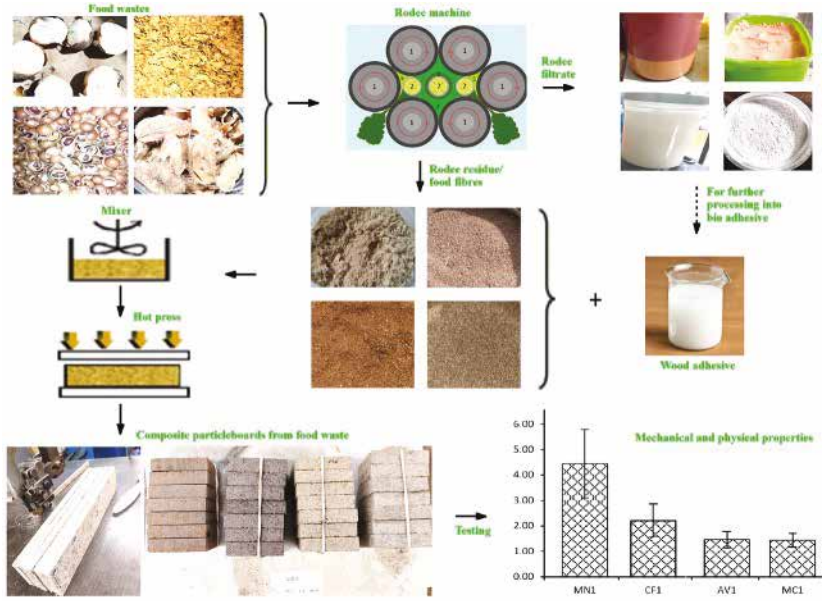
[2] University of Southampton, Faculty of Engineering and Physical Sciences, Southampton, UK
[3] University of Copenhagen, Forest & Landscape, Faculty of Life Sciences, Copenhagen, Denmark.



The rapid increase in agro-industrial food waste in urban Africa presents both an environmental burden and a valuable bioresource. This study advances the circular bioeconomy by upcycling food processing residues into composite boards, with the aim of reducing pressure on virgin wood resources and petrochemical resins. Composite boards were fabricated from food waste with wood resins. Experimental evaluation of properties revealed that food waste-derived composites with 50% resin meet performance requirements for P1 and P2 boards, and are hence potentially suitable for general-purpose and interior applications [1]. Ongoing research seeks to demonstrate that hybridization of these wastes can significantly enhance strength and moisture resistance [2]. Parallel efforts are directed toward developing biobased adhesives derived from food waste streams to provide a sustainable alternative to formaldehyde-based resins. This work underscores the potential of food waste valorization into high-value green composites for furniture and construction, which, if scalable, can help tackle global challenges of waste, deforestation, and fossil-based chemicals.

Keywords: Food waste, composite boards, circular bioeconomy, sustainable adhesives

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Poster 4

The Role of Law in Standardisation of Synthetic Biology

Goncagul Cengiz Baris

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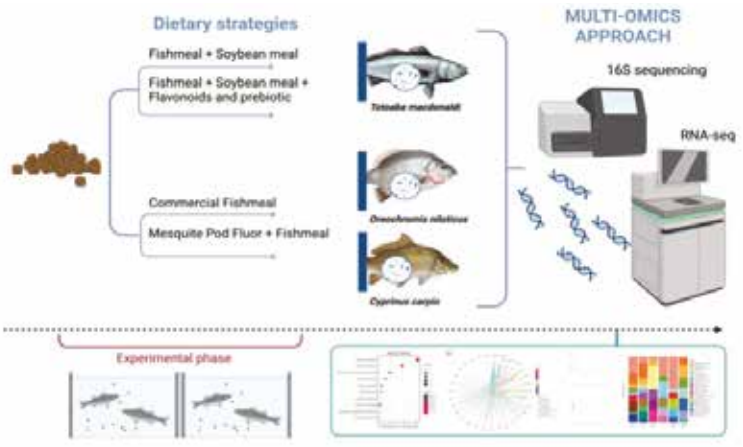
Standards play a critical role in scientific and technical communication. They also facilitate the circulation, translation and industrial application of scientific knowledge and the interoperability of products. For standards to operate effectively, they need to be readily available, easily accessible, and mobile. Intellectual property protection over standards has the potential to limit the effectiveness of standards by making them difficult to access and use. This research looks at the potential ways in which intellectual property impacts on the operation of technical standards in synthetic biology. More specifically, it looks at potential ways in which these limitations may be minimised.

Poster 5

Multi-omics evaluation of sustainable dietary alternatives in aquaculture: an integrative approach to enhance fish nutrition and production

Presenting author: **Maria Fernanda Barragan Longoria, PhD student.**



Aquaculture plays a crucial role in global food security, yet it faces growing challenges related to feed sustainability, fish health, and environmental impact [1]. This study proposes an integrative omics-based approach for evaluating alternative dietary ingredients in aquaculture, focusing on species of commercial importance in Mexico: *Totoaba macdonaldi, Cyprinus carpio* and *Oreochromis niloticus.*

This research incorporates a species-specific approach, recognizing that each aquaculture species presents individual nutritional requirements and physiological responses. To address this, different dietary strategies were developed and evaluated for each fish: (I) Supplementation of soybean-based diets with flavonoids and prebiotics (quercetin, epicatechin, and inulin) in *Totoaba macdonaldi*; (II) Mesquite (*Prosopis laevigata*) pod flour as a partial fishmeal replacement in *Cyprinus carpio*; (III) Mesquite (*Prosopis laevigata*) pod flour as a partial fishmeal replacement in *Oreochromis niloticus.* In addition to evaluating conventional physiological indicators, such as growth performance and biochemical profiles, each study integrates molecular and metabolic responses, and gut microbiota modulation, to provide a more comprehensive understanding of dietary effects. Through RNA-seq transcriptomics and 16S metagenomics, the study aimed to identify complex biological responses induced by dietary supplementations, elucidating gene regulatory networks, metabolic pathways, and microbiota-driven interactions. Results showed that these functional supplementation strategies led to improvements in growth performance, modulation of lipid metabolism, and favorable modulation in gut microbiota. Additionally, transcriptomic analyses identified metabolic pathways related to lipid utilization and cellular energy homeostasis, suggesting a diet-induced response in molecular processes linked to nutrient metabolism [2],[3]. This research contributes to the development and understanding of nutritionally effective feeding strategies that respond to the expanding aquaculture sector, while advocating a strategic shift toward sustainable supplementation practices that align with the goals of the global bioeconomy. By reducing dependence on fishmeal and promoting the use of cost-effective, functional ingredients, this approach has the potential to strengthen the economic viability, sustainability, and food security of aquaculture systems, particularly in developing regions where feed costs and environmental constraints are major limiting factors.

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Poster 6

Liquid/liquid extraction for *in-situ* removal of isobutanol from fermentation broth containing wheat straw hydrolysate

Jennifer Borger, Michael Zavrel

Technical University of Munich Campus Straubing

The Synergy Fuels project aims to develop an integrated biorefinery concept utilizing biomass and Power-to-X technology for renewable fuel production. As a part of this initiative, the Professorship of Bioprocess Engineering at TUM Campus Straubing is focusing on isobutanol production via fermentation using genetically engineered strains of *Corynebacterium glutamicum* and wheat straw hydrolysate as substrate. Due to the toxicity of isobutanol at concentrations as low as 20 g L^{-1}, *in-situ* product removal (ISPR) is an essential step to enable efficient fermentation. Liquid/liquid extraction (LLE) was selected as the most suitable ISPR approach to be applied to this process.

Several promising organic solvents were identified and tested to determine their partition coefficients for isobutanol and their biocompatibility with *C. glutamicum*. Solvents which did not inhibit glucose consumption for up to 24h under aerobic conditions were categorized as biocompatible: oleyl alcohol, tris(2-ethylhexyl) phosphate (TEHP), tributyrin, and corn oil. Oleyl alcohol and TEHP were further investigated due to their relatively high partition coefficients and dissimilar densities with water. The presence of wheat straw hydrolysate (WSH) in the aqueous phase was observed to enhance isobutanol partitioning compared to glucose-containing media or water.

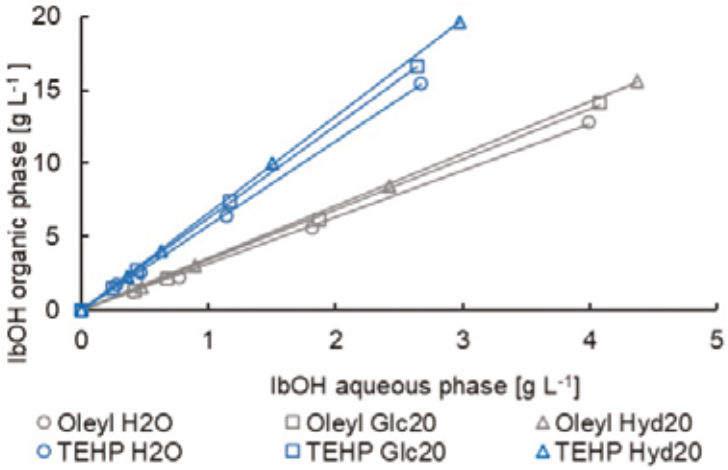

Figure 1: Partitioning of different initial isobutanol concentrations between aqueous and organic phases after saturation. Initial isobutanol concentrations in the aqueous phase were 1, 2, 5, and 10 g L^{-1}. Aqueous phases used were distilled water (circles), CGXII media containing 20 g L^{-1} glucose (squares), and CGXII media containing 20 g L^{-1} of WSH (triangles). Organic phases used were oleyl alcohol (grey) and TEHP (blue). Slopes of the lines represent the partition coefficients.

Under anaerobic fermentation with *C. glutamicum*, both oleyl alcohol and TEHP were observed to negatively affect substrate uptake and isobutanol production rates. To address this, a membrane-based separation approach is under development to reduce direct cell-solvent contact while maintaining extraction efficiency. These findings contribute to the advancement of ISPR strategies for bio-based isobutanol production and support the wider development of the bioeconomy.

Poster 7

Antifungal Potential of Bacterial Isolates from Mexican Ecosystems for Controlling Anthracnose in Avocado

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Anthracnose, caused by *Colletotrichum* spp., is one of the most severe diseases affecting avocado production. This study explores the search of biocontrol agents by the bioprospection of actinobacteria from two unique Mexican ecosystems: Cuatro Ciénegas, an oligotrophic desert valley with extreme nutrient imbalances, and the Calakmul Biosphere Reserve, the second-largest tropical humid forest in the Americas.[1,2]

A total of 142 actinobacterial isolates were tested for antagonistic activity against *Colletotrichum*. Strains displaying mycelial inhibition were selected, and their crude extracts were assessed through *in vitro* and *in vivo* assays. *In vitro* tests demonstrated up to 49% reduction in mycelial growth and up to 100% inhibition of sporulation. The *in vivo* assays showed up to 100% reduction in anthracnose symptoms on avocado fruits.

To elucidate the antifungal metabolites, the genomes of the most effective strains were analyzed for biosynthetic gene clusters (BGCs) potentially linked to antifungal activity. Genomic analysis revealed BGCs associated with antifungal compounds, elicitors, and fungicide-enhancing metabolites, suggesting multiple modes of action. Additionally, fractionation of the crude extracts was performed to identify the active compounds. The integration of genomic and metabolomic data determine whether the responsible molecule is known or represents a novel fungicidal compound. These findings highlight the potential of actinobacteria from extreme environments as promising sources for biocontrol agents, paving the way for sustainable alternatives to synthetic fungicides in avocado production.

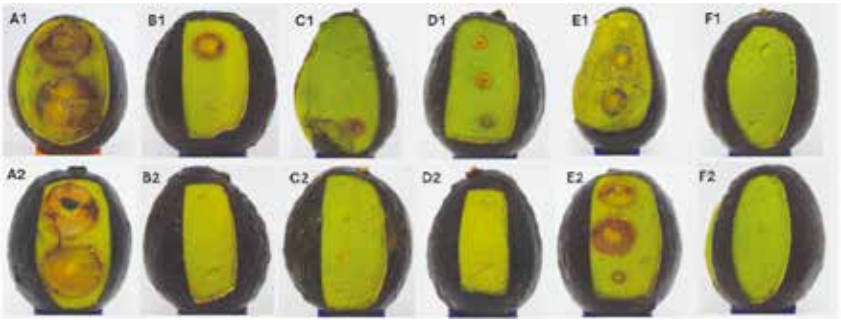

Figure 1.Effect of actinobacteria extracts on lesion size reduction caused by *Colletotrichum* spp. A) Control fruits. B-F) Fruits treated with extracts from isolates. The number "1" indicates assays with *C. acutatum* and "2" with *C. gloeosporioides*

References:

[1] Souza, V., & Eguiarte, L. E. (2018). In the Beginning, There Was Fire: Cuatro Ciénegas Basin (CCB) and the Long History of Life on Earth. Cuatro Ciénegas Ecology, Natural History and Microbiology, 21–33. doi:10.1007/978-3-319-93423-5_2

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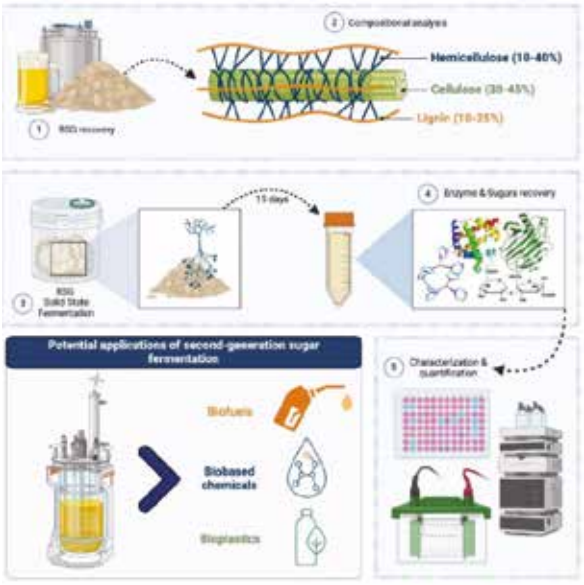
Poster 8

Fungal lignocellulolytic enzyme profiling: evaluating the potential for enhancing brewer's spent grains saccharification

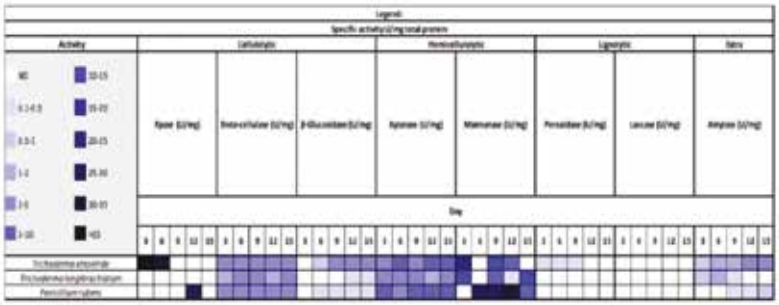
Sara Saldarriaga-Hernandez, Anahid Esparza-Vasquez, Diego Villalvazo-García, José María García-Rodríguez, Mauricio Zavala-Campos, Rosa Leonor Gonzalez-Díaz, Lorena Amaya-Delgado, Elisabeth Tamayo, J. Philipp Benz, **Danay Carrillo-Nieves***

Brewer's spent grains (BSG), a major brewing byproduct, represent a sustainable source of structural carbohydrates for second-generation (2G) sugar production. This study evaluates the potential of native Mexican lignocellulolytic fungi for enhancing BSG saccharification via solid-state fermentation (SSF). BSG compositional analysis revealed 37.5% cellulose, 8.7% hemicellulose, and 17.5% lignin, supporting its suitability as a bioconversion feedstock[1].



Fungal strains including *Trichoderma atroviride* (NBRC 101776), *Penicillium rubens* (CBS 129667) and *Trichoderma longibrachiatum* isolate PC1, were isolated, identified through ITS sequencing, and confirmed with TEF1 sequencing for *Trichoderma* spp.

Enzymatic profiling under SSF showed that *T. atroviride* exhibited the highest cellulase and xylanase activities (FPase: 0.488 U/mL, ß-glucosidase: 0.055 U/mL, xylanase: 0.125 U/mL), whereas P. rubens displayed the highest mannanase activity (0.419 U/mL). SDS-PAGE of crude and partially purified extracts revealed distinct protein bands corresponding to cellulases, ß-glucosidases, amylases, and xylanases, indicating enzyme diversity among native isolates[1]. These findings highlight the potential of BSG as a substrate for cost-effective enzyme production and provide insights into strain selection for lignocellulosic biomass valorization. The study underscores the integration of agro-industrial residues into circular bioeconomy strategies, demonstrating that native fungal strains can significantly enhance enzymatic hydrolysis while reducing reliance on commercial enzyme cocktails. This approach contributes to sustainable bioprocessing and supports the development of bio-based products from brewing byproducts.



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Poster 9

From Research to Commercialization: A Pipeline for Early Assessment of Bio-processes

Presenting Author: **Shahaf Cohen**

How much uncertainty can be reduced when considering further investment into early-stage bio-process development? Developing a generalized computational pipeline that connects strain design to techno-economics and environmental sustainability metrics - bridging the gap between lab-scale proof-of-concept and industrial scale-up will help answer this question.

Building on the work of Zhuang et.al [1], the current framework integrates pathway modeling via GEMs into a dynamic flux balance analysis (dFBA) with a population-aware fed-batch bioreactor model. This setup allows simulation of key process variables—such as productivity, substrate usage, and metabolic shifts—under aerobic fermentation conditions.

The system is designed to support future expansion toward comprehensive and automated techno-economic and sustainability assessments.. In later stages, a neural network module will be trained to predict optimal and realistic process outcomes by balancing trade-offs between yield, time, cost, and environmental impact.

This modular pipeline aims to support early decision-making by enabling researchers and companies to explore the process performance of engineered strains **before** entering costly scale-up or industrial validation stages.

Reference:

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Poster 10

Genome engineering barley root systems for future climates.

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Clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR associated proteins, collectively CRISPR-Cas, have emerged as a critical tool in crop improvement. CRISPR-Cas provides the capacity to develop crop lines ready for future harsher climates, and to contribute to a more sustainable agricultural system. One consequence of the traditional focus of crop breeding programs being on above-ground traits is the inadvertent fixation of genetic variation controlling root system architecture. In some countries, specific CRISPR technologies have been deregulated and therefore show strong potential for incorporation into breeding programs. This work is centred around the use of CRISPR-Cas technology to optimise the root system architecture of barley for yield stability through generating edited lines with enhanced water and nutrient use efficiencies. Target genes were translated from work in the model species *Medicago* and *Arabidopsis*, where *C-TERMINALLY ENCODED PEPTIDE RECEPTOR 1 (CEPR1)* has been shown to exert dramatic control over root system architecture. In barley, the loss-of-function *cepr1* allele led to the production a novel root system architecture with a dramatically steep and compact root system. Our future research aims to test our barley *cepr1* lines both in the field and under conditions of imposed nutrient and water-stress, as well as targeting genes downstream of *cepr1* for editing. This traits integration into breeding programs may be used to produce more sustainable elite ideotypes for regions experiencing reduced rainfall.

Poster 11

LiveSen-MAP

Josef Eiglsperger and LiveSen-MAP consortium

Empowering Sustainable Agriculture through Real-Time Nutrient Monitoring and Precision Fertilization
Nitrogen is a fundamental nutrient for plant growth and a key driver of agricultural productivity. However, its widespread use in the form of synthetic fertilizers has led to significant inefficiencies and environmental concerns. Globally, only about 50% of applied nitrogen is taken up by crops, with the remainder lost to the environment - contributing to water pollution, soil degradation, and 5-7% of global greenhouse gas emissions. Improving nitrogen use efficiency is therefore essential for achieving climate-smart, economically viable agriculture.

The **EIC-funded LiveSen-MAP project** is addressing this challenge by developing a novel biosensor platform that enables real-time, in-field measurement of nutrient concentrations - starting with nitrate - in plant sap. This user-friendly technology empowers farmers to make data-driven fertilization decisions, applying the right amount of nutrients at the right time and place. By integrating biosensor data with remote sensing and agronomic models, we aim to optimize nutrient management across diverse cropping systems and environmental conditions.

Our first field campaign involved 35 farmers managing 60 fields across more than 600 hectares in the Straubing region of Bavaria, Germany. The second campaign, currently underway, expands the scope to over 100 farmers with in total 180 fields or ~3000 hectare across Germany and European countries. Preliminary results show that nitrate fertilizer use can be reduced by up to 20% without compromising yield, demonstrating the potential of this approach to enhance both sustainability and profitability.

To ensure broad adoption and systemic impact, we are working closely with stakeholders across the agricultural value chain - including chambers of agriculture, farmer associations, advisory services, and machinery cooperatives. Our interdisciplinary team combines expertise in plant physiology, sensor engineering, data science, and agronomy to deliver a holistic solution that supports the digital transformation of agriculture.

By 2026, we aim to bring a market-ready, scalable technology to farmers across Europe and beyond. LiveSen-MAP represents a significant step toward climate-neutral agriculture by reducing fertilizer dependency, improving resource efficiency, and supporting resilient food systems. Our vision is to empower every farmer with the tools to understand and manage plant nutrition in real time - paving the way for a more sustainable and productive agricultural future.

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Poster 12

Food Composition Databases in the Food System: A Global Survey and Analysis

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Food composition databases are valuable sources of food nutrient and composition information across the global food system. Studying them by using a food systems approach gives understanding for driving food system change, transition and transformation as it considers the complexity of food systems, defines key interrelationships and shows the value across the whole food system that food composition data has.

This is the first stage of a study of the global status of food composition databases. It took a rigorous, analytical approach by doing a systematic search to find all the food composition databases online in the world and analysed the content of each of them. It then used a food systems approach to analyse food composition data through the food system including the activities, drivers and outcomes surrounding it [1,2].

The systematic search found over 140 data sets available online which varied in the foods and processing methods they included and the number of nutrients for which values were provided. This helped to map the framework around food composition across the global food system. It shows how composition changes through the activities of the food system, from agriculture and post-harvest through processing and value-adding to diets and consumption. The effects and outcomes that food composition have include the utilisation of food, effects on individual and population health, and the on-going social benefits from the continued use of traditional and indigenous foods. Environmental drivers include soil and climate, and socio-economic and socio-technical drivers include policies and the impact of science, research and technology on the activities that affect composition. Future changes that have potential to create on-going change and transitions include increased sensitivity of analytical methods for testing composition and foodomics analysis, advances in food science including new or more advanced processing technologies and the effects of climate change. Characterising food composition at a global level enables the effective analysis of its role in the food system, generates new insights, can support change and transition to take place and can build the foundation for transformation.

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Poster 13

Efficient Production of Hydrolysate from Various Lignocellulosic Feedstocks at High Dry Matter Load

Nico Geisler, Sri Ravichandran Mahalakshmi, Michael Zavrel

Technical University of Munich, Campus Straubing for Biotechnology and Sustainability, Professorship for Bioprocess Engineering, Straubing, Germany

The transition to a sustainable and circular bioeconomy must involve the efficient valorization of lignocellulosic biomass, a widely available and renewable resource that is not in competition with the food and feed industry. Its conversion into sugar-rich hydrolysates for the subsequent biotechnological production of bio-based fuels and chemicals makes it a promising alternative to fossil-based feedstocks. However, the natural recalcitrance of lignocellulosic biomass to enzymatic degradation remains a significant challenge. Therefore, the establishment of a robust and broadly applicable process to convert lignocellulosic feedstocks into capable hydrolysates is the first essential step in the emerging value creation chain.

In this study, twelve different lignocellulosic feedstocks were systematically investigated, encompassing a wide range of structural and compositional characteristics. The selection included various agricultural residues, hardwood, and softwood to ensure broad process applicability and to highlight the influence of biomass type on process performance. All feedstocks were subjected to dilute acid pretreatment at a dry matter load of 20 wt.-%, followed by enzymatic hydrolysis. Uniquely, the developed process omitted the commonly used washing step to reach neutral pH after dilute acid pretreatment. Instead, pH adjustment was carried out directly in the same reaction vessel, which conserved water, time, energy, and eliminated sugar losses that can occur during solid-liquid separation and washing.

Enzymatic hydrolysis was performed under standardized conditions across all feedstocks using an optimized experimental setup. The generated hydrolysates showed combined sugar concentrations of up to 149.8 ± 0.4 g L^{-1} and the integrated process reached total glucan conversion rates of up to 98.0 ± 0.7 %, depending on the biomass type. In general, feedstocks with lower lignin content exhibited higher total glucan conversion rates, but not necessarily higher combined sugar yields due to the feedstocks' compositional differences in cellulose and hemicellulose fractions. The process demonstrated robust performance for most of the investigated substrates and provides an efficient way to directly compare the conversion capability of various lignocellulosic feedstocks into hydrolysates under identical conditions.

By achieving high combined sugar yields and high total glucan conversion rates at high dry matter loadings via direct pH adjustment, the streamlined and feedstock-agnostic process improves the availability of capable second-generation hydrolysates in lab-scale. These findings contribute to the development of tolerant fermentation processes and to the conceptualization of commercially viable biorefineries that support the transition to a bio-based economy.

Poster 14

Towards Precision Weed Control: Site-Specific Management Using UAVs and Deep Learning

Nikita Genze, Jan Jänicke, Maria Vilsmeier, Johanna Pfeiffer, Vladyslav Pitsyk, Stefan Kopfinger, Michael Grieb, Markus Gandorfer, Dominik G. Grimm

Weeds remain one of the most persistent threats to global crop productivity, competing with crops for water, nutrients, and sunlight while acting as hosts for various pests and diseases. Conventional weed management strategies rely heavily on chemical herbicides. However, this dependence has led to the emergence of herbicide-resistant weed species, raised serious environmental and human health concerns, and contributed to soil and water contamination. While physical practices, such as mechanical weeding, can help reduce or replace chemical inputs, they often require more labor and can result in unintended negative consequences, such as soil erosion. As a result, these alternatives face limitations in scalability and adoption, particularly in large-scale farming operations.

Recent advances of Unmanned Aerial Vehicles (UAVs) offer new opportunities for scalable, environmentally responsible weed control. UAVs can rapidly collect high-resolution imagery over large agricultural fields, providing a non-invasive method for monitoring weed distribution. However, developing a robust weed detection system is challenging due to several factors, such as inconsistent illumination from changing weather conditions or diverse weed species and their growth stages. Additionally, the variability in soil types, farming practices, and cultivation techniques encountered in real-world field conditions affect the consistency and accuracy of detection systems.

Our work leverages Deep Learning (DL) techniques to overcome those challenges and enable precise, automated weed detection in UAV imagery, focusing on sorghum and maize fields. By integrating optimized UAV operations with DL-based image analysis, we generate accurate maps that differentiate between crops and weeds. These spatially resolved maps can guide autonomous robotic systems for precision mechanical weeding or enable localized, reduced-volume herbicide applications.

The primary objectives of this research are to reduce herbicide dependence, minimize soil disturbance, and enhance the scalability of sustainable agriculture systems. In doing so, our approach supports improved crop yields through timely and targeted interventions, while also lowering the environmental footprint of weed control practices.

Ultimately, this work advances the practical implementation of smart, data-driven crop protection systems. By integrating UAV-based monitoring with robust DL models, we offer a scalable solution for site-specific weed management that aligns with the goals of climate-resilient and ecologically sustainable farming. Our approach not only addresses immediate agronomic challenges but also contributes to the long-term transformation of agricultural practices toward a more resource-efficient and environmentally responsible bioeconomy.

Poster 15

Unexpected mechanisms of stabilisation of the prokaryotic ribosome

William S. Stuart[1,2], Michail N. Isupov[2], Mathew McLaren[1,2], Christopher H. Jenkins[3], Adam Monier[1], Bertram Daum[1,2], Isobel H. Norville[2,3], Vicki A.M. Gold[1,2], **Nicholas J. Harmer[1,2]**

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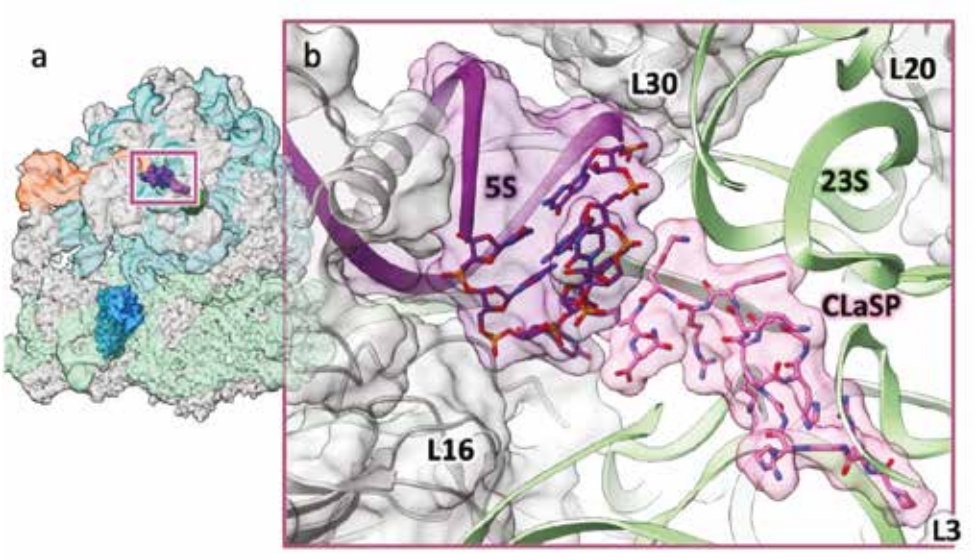
Q fever is a global zoonotic disease associated with sheep and cattle, causing both economic losses to agriculture and long-term chronic infections (e.g. Q-fever fatigue syndrome) in approximately 10% of infected humans. *Coxiella burnetii*, the causative agent, is a small obligate intracellular pathogen capable of surviving long periods in a metabolically constrained spore-like state. Current chronic Q-fever treatment is a (minimum 18 month) high dose regimen of hydroxychloroquine and doxycycline. To better understand how the *Coxiella* ribosome maintains function through months in a metabolically constrained state, we determined the structure of this ribosome from cells grown to a point where most cells have differentiated to the spore-like state. The *Coxiella* ribosome has a fragmented RNA previously seen in other ribosomes. Here, this is stabilised by a novel 22 amino acid peptide that interacts with the 23S and 5S RNA to help stabilise the 50S ribosome. Approximately half of these ribosomes formed a complex with a hibernation factor. Surprisingly, this hibernation factor included a cold-shock protein domain that has not previously been observed in ribosome. The cold-shock domain occupies the mRNA entrance tunnel and binds the 3' end of the 16S RNA. This likely confers protection from RNAses, helping to maintain ribosome integrity in the spore state. Phylogenetic analysis showed that this hibernation factor arrangement is found in many proteobacteria and nitrifying bacteria but rarely outside this group. The *Coxiella* ribosome reveals two new mechanisms for bacterial ribosomes to maintain stability during normal operation and during extended periods of inactivity.



Poster 16

Engineering Biocatalytic Pathways for Formaldehyde Fixation and Sugar Synthesis

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The selective conversion of single-carbon (C1) feedstock such as formaldehyde into complex functionalized biomolecules represents a major challenge in the development of sustainable and circular carbon-based technologies. The formose reaction, a classical chemical process that spontaneously polymerizes formaldehyde into a variety of sugars under alkaline conditions, lacks relevance due to its lack of control and low selectivity [1,2].

Here, we focus on the development of a fully enzymatic approach for the selective synthesis of functionalized sugars from formaldehyde. Building on our previous results demonstrating the formation of erythrulose [3], we now aim to improve the efficiency, specificity, and product range of this route. For this, we systematically compare, engineer and apply enzymes from various classes capable of catalyzing C1-to-C_n sugar formation, including glycolaldehyde synthase (GALS), carboxylases, aldolases and formolase variants. These enzymes enable the assembly of C2-C4 sugar intermediates and their subsequent elongation and functionalization.

With this we seek to establish a robust platform for the synthesis of rare or industrially relevant sugars from formaldehyde. This work contributes to the advancement of sustainable bioprocesses for C1-based sugar production and supports the broader transition to a circular bioeconomy.

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[2] Irina V. Delidovich, Alexandr N. Simonov, ChemSusChem 7(7), 1838, (2014)
[3] Samed Güner, Vanessa Wegat, Green Chemistry 23(17), 6583, (2021)

Poster 17

Effects of microwave-assisted deep eutectic solvent pretreatment on enzymatic digestibility of rice straw

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[c]Department of Chemical and Environmental Engineering, Faculty of Engineering, University of Nottingham, University Park, Nottingham NG7 2RD, UK

Lignocellulosic biomass (LCB), such as agricultural residue rich in cellulose and hemicellulose, can serve as a feedstock for bioethanol production due to its environmental benefits. Deep eutectic solvents (DESs) are attractive for lignocellulosic biomass deconstruction because of their easy synthesis, reusability, inexpensive and eco-friendliness. The present study investigated the efficiency of two DES types for rice straw pretreatment under microwave conditions: choline chloride:glycerol (ChCl:Gly) and choline chloride:formic acid (ChCl:FA). DES pretreatment was performed under microwave conditions (100-140 °C and 5-15 min) at 10% solids loading and constant power 200W. After pretreatment, the samples were characterized, and enzymatic digestibility was investigated at 50 °C for 72 h using Cellic® CTec3 HS (6 filter paper unit (FPU) g^{-1} cellulose) and 10% solids loading. Untreated rice straw consists of cellulose (41.8%), hemicellulose (24.9%), lignin (17.0%) and ash (15.0%). The cellulose content increased to 59.8% and 59.2% after ChCl:Gly and ChCl:FA pretreatment, respectively, while hemicellulose decreased to 15.6% and 10.1% after ChCl:Gly and ChCl:FA pretreatment, respectively. Lignin content decreased to 8.2% after ChCl:Gly pretreatment compared to 9.6% after ChCl:FA pretreatment. Ash content (20.4%) obtained after ChCl:FA pretreatment was higher than 20.4% obtained after ChCl:Gly pretreatment. The cellulosic and hemicellulose fractions from ChCl:Gly pretreatment were effectively hydrolyzed with glucose and xylose yield of 86.0% and 68.4%, respectively, compared to glucose and xylose yield of 58.2% and 62.8%, after ChCl:FA pretreatment. ChCl:Gly pretreatment enriched cellulosic content and preserved hemicellulose fraction, achieving a higher yield of fermentable sugars than ChCl:FA pretreatment; hence, it can potentially support a biorefinery.

Poster 18

Development of a targeted colon delivery system for antimicrobial peptides using natural polymers in green plants

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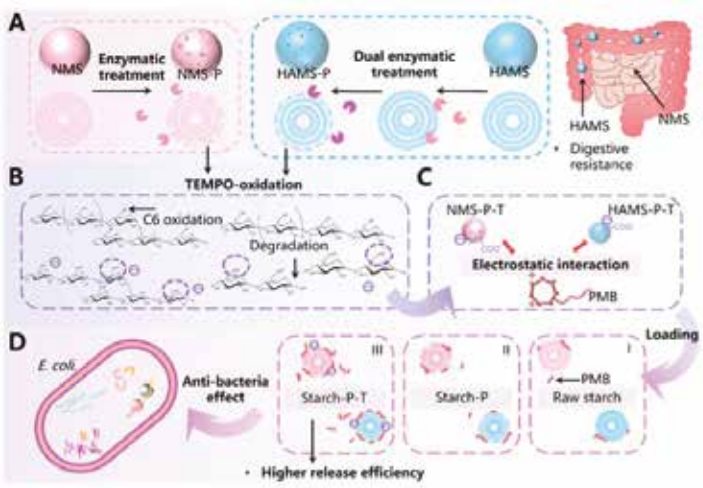

Starch, a naturally occurring polymer abundant in green plants, has high drug delivery potential [1]. The study aims to synthesize and develop enzyme-responsive porous starch microcarriers for targeting antimicrobial drug delivery. To achieve this, we modified normal starch (NMS) and high-amylose maize starch (HAMS) through enzymatic treatment and oxidation to create a porous structure of starch. Using 2,2,6,6-tetramethyl-1-piperidinyloxy (TEMPO), the oxidation process introduced negative charges to the porous starch, enhancing drug adsorption capacity. The modified starch was then loaded with positively charged antimicrobial peptides Polymyxin B (PMB) to study their absorption, release, and antibacterial activity. We hypothesize that the modified starch will allow high loading of drugs, and the digestive resistance HAMs will allow the drug to reach the colon.

Our results showed that HAMS had smaller pores than NMS after enzymatic treatment, though both showed similar changes in relative crystallinity. The drug loading results showed that oxidation significantly increased the adsorption capacity to 80% through electrostatic interaction. HAMS, with its smaller pores and digestive resistance, demonstrated better performance in the slow release of PMB, extending the antibacterial effect against *Escherichia coli*. Porous HAMS proved to be effective as a colon drug delivery system for antibacterial active substances.

Reference

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Poster 19

Building a global, scalable R&D pipeline for microbial biofertiliser development

Lucas Levassor, Søren D. Petersen, Gloria Muñoz Fernández, Parvathy Krishnan, Yumiko Sakuragi, Lars Jelsbak, Rasmus J. N. Frandsen

The global transition toward sustainable agriculture demands alternatives to synthetic fertilizers, which contribute to soil degradation and pollution, while nutrient runoff drives eutrophication of aquatic ecosystems, algal blooms, and fish mortality [1], [2]. Microbial biofertilizers offer a promising solution by improving nutrient availability (e.g., via nitrogen fixation, phosphorus and potassium solubilization), promoting plant health, and enhancing resilience under stress conditions [1]. However, their discovery and development remain slow, fragmented, and difficult to scale; a key bottleneck is our limited understanding of the biology of biofertilizers, which hampers the translation from small-scale lab findings into reproducible, field-ready products across diverse environments.

To address this gap, we are developing a standardized pipeline that combines laboratory automation with systematic data capture. The pipeline integrates high-throughput assays for phosphate solubilization, nitrogen fixation, and potassium solubilization with mechanistic studies of plant-microbe interactions, mode-of-action studies, scalable biofertilizer production workflows, biosafety assessment, and field trials. All data are recorded in standardized formats to ensure reproducibility and alignment with FAIR principles [3]. Importantly, through our international partnerships, we also aim to evaluate candidate biofertilizers under diverse environmental and agricultural conditions, strengthening the global applicability of our findings.

Our immediate focus is on establishing these workflows across the full development chain, from discovery to application. In the longer term, the accumulated datasets will provide the foundation for predictive models that can prioritize strains for testing. The vision is to enable the adoption of sustainable and affordable crop productivity worldwide by increasing the use of biofertilizers at all farm scales, reducing reliance on costly and environmentally harmful chemical fertilizers.

By linking automation, standardization, data sharing, and global collaboration, this pipeline aims to accelerate the translation of microbial diversity into practical agricultural solutions and support innovation in the bioeconomy.

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Poster 20

Investigating enzyme kinetics by quantifying trace amounts of methanol and formaldehyde with the chromotropic acid method

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Introduction: Methanol and formaldehyde are involved in many enzymatic reactions. Pectin methyl esterases (PMEs) can remove methylations on galacturonic acid residues in pectins, releasing methanol. Glucuronoyl esterases (GEs) may release methanol by hydrolysis of methylated 4-O-methyl-D-glucuronic acid (Me-MeGlcA)-lignin esters. The methanol, generated by the activities of PMEs and GEs, may be oxidized to formaldehyde by alcohol oxidases or alcohol dehydrogenases. Quantification of methanol and formaldehyde could serve as direct indicators of several enzymatic activities, including those mentioned above. However, it is challenging to measure methanol and formaldehyde with sufficiently high sensitivity in enzymatic assays. Thus, there is a demand for simple methods that allow sensitive and accurate quantification of these small volatile compounds.

Objective(s): The aim of this work is to investigate the applicability of the chromotropic acid method for the quantification of methanol and formaldehyde in enzyme assays.

Methods and Results:
The chromotropic acid method is a highly sensitive colorimetric method that can detect formaldehyde directly and methanol indirectly via oxidation to formaldehyde. Under high concentrations of sulfuric acid, formaldehyde reacts with chromotropic acid to produce a purple chromogen with absorbance maximum at 570-580 nm. We have found that the chromotropic acid method is applicable for quantification of methanol released by PME and GE when acting on methylated pectin and 4-O-methyl-D-glucopyranosyluronate (Me-MeGlcA), respectively. The methanol, released in the enzymatic reactions, was first oxidized to formaldehyde via alcohol oxidase. To stabilize formaldehyde in the solution, formaldehyde was trapped with sodium bisulphite, which forms a stable non-volatile adduct (sodium hydroxymethanesulfonate) before it was quantified by the chromotropic acid method.

By this procedure, it was possible to quantify methanol, released by PME and GE, quickly and with very high sensitivity.

Conclusion:
The chromotropic acid method is applicable for quantification of both methanol and formaldehyde in enzyme assays. Due to its simplicity, high sensitivity, and accuracy, the chromotropic acid method provides a highly efficient tool for investigating enzymatic reactions and studying enzyme kinetics.

Poster 21

It's Not All About the Newest Technology

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Innovation is often measured by how new or advanced a technology is. Yet, in practice, the success of innovation depends less on novelty and more on relevance, usability, and adoption. This presentation explores the often-overlooked reality that the newest technology is not always what users need or want.

Focusing on the Australian context, specifically in the aquaculture and agriculture sectors, we reflect on case studies that illustrate both the challenges and successes of technology adoption. These include the Australian Plant Phenomics Network, which offers data collection tools for plant research; the Grains Research and Development Corporation's strategic investments in grower-driven innovation; and the evolving practices of the Great Barrier Reef's sea cucumber industry, where traditional practices meets modern sustainability goals.

Through these examples, we examine how user engagement, contextual understanding, and co-design can bridge the gap between development and adoption. We also highlight what is working well, and how these lessons can inform more effective, inclusive, and sustainable bioeconomy solutions.

While grounded in Australia, the insights shared are globally relevant. The principles of aligning innovation with user needs, valuing simplicity over complexity, and fostering trust and collaboration apply across sectors and geographies. Whether in agriculture, aquaculture, or beyond, this presentation invites a rethinking of how we define and deliver impactful innovation.

Poster 22

Leaf-cutting ant inspired biomass conversion using enzyme driven Fenton chemistry

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Acromyrmex leaf-cutting ants maintain an intricate symbiosis with the basidiomycete fungus *Leucocoprinus gongylophorus*. The ants cultivate underground fungal gardens by supplying freshly cut plant material, which the fungus degrades to produce nutrient-rich gongylidia that the ants eat to sustain the colony. To prepare the plant biomass, the ants deposit their fecal fluid onto chewed leaf fragments before spreading these pellets across the garden. Upon contact, the material darkens, a process linked to oxidative chemistry facilitated by enzymes present in the fecal fluid. Proteomic analyses have shown that this fluid is enriched with oxidative enzymes of both ant and fungal origin [1]. These enzymes, together with cofactors such as aryl alcohols and iron, drive Fenton reactions that explain the observed blackening and the rapid breakdown of otherwise recalcitrant plant polymers. Fenton chemistry involves the generation of hydroxyl radicals from the reaction of hydrogen peroxide with ferrous iron (Fe^{2}). These radicals are highly reactive and capable of cleaving a broad range of chemical bonds, leading to the non-specific degradation of lignocellulose.

Our project aims to explore whether this natural system can be replicated *in vitro* to achieve more efficient plant biomass conversion. From the proteomic dataset of *Acromyrmex* fecal fluid, we selected 10 proteins for heterologous expression in *Komagataella phaffii*, focusing on their individual activity profiles and potential synergistic effects in sustaining Fenton reactions. We targeted two functional enzyme groups: (i) hydrogen peroxide generating enzymes and (ii) enzymes that recycle ferric iron (Fe^{3+}). We successfully expressed two fungal aryl alcohol oxidases from the AA3_2 and AA7 families. These enzymes generate hydrogen peroxide, which reacts with free iron to drive Fenton chemistry. Secondly, an ant-derived glucose oxidase (AA3_2) oxidize a range of mono- and disaccharides with reducing ends with the direct use of either ferric iron as an electron acceptor or rely on quinone-mediated electron transfer to regenerate ferrous iron, thereby sustaining the Fenton cycle. Together, the coupling of enzymatic hydrogen peroxide production, iron redox cycling, and inorganic Fenton reactions creates a highly effective oxidative system. Remarkably, leaf-cutting ants compartmentalize and regulate this chemistry within their gardens, preventing self-damage while enabling efficient biomass deconstruction. This natural strategy provides an inspiring blueprint for developing advanced biotechnologies for sustainable plant biomass conversion.

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Poster 23

Valorization Of Market Waste In Bioelectricity Production, And Subsequent Fertilizer Production

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Sustainable Solid waste management is a global challenge urgently seeking redress, as the planet struggles with the subsequent effects – climate change, pests and diseases and other socio-economic pressures. This challenge is conspicuously pronounced in developing countries like Kenya, whose solid waste management systems are at embryonic stage and are struggling to contend with the ever increasing quantities.
This study explored the possibility of using organic market waste from Nairobi's CBD in production of bioelectricity, and using the resultant (exhausted) material as organic fertilizer.

The fruit waste was obtained from open air grocery markets in Nairobi city. It was miniaturized in a blender and, together with goat rumen from a slaughter house, placed in the anodic chamber of an H-shaped one-liter double-chamber microbial fuel cell equipped with carbon graphite electrodes, a saturated sodium chloride salt bridge and distilled water in the cathodic chamber. The system was connected to a multi-meter and the voltage and current therein produced monitored for 22 days. The anodic contents were, then, removed, dried and incorporated into soil where potted maize and beans were allowed to grow. The growth of the plants was monitored, and compared with those that were planted without the fertilizer.
The results obtained showed that the fruit mixture gave an average voltage of and average current of. The power and power density obtained was in the range of 3.047 to 4.038 μW and 572.4 to 758.5 respectively.

The Compost and vermicast obtained at the anode showed favorable characteristics of a fertilizer for both the micro and macro nutrients, as the values for the N, P, K, Mg, Mn, Cu, Fe and Zn for the compost were obtained as 8.9 ± 0.1, 32.4 ± 1.4, 0.003 ± 0.0004, 1.3 ± 0.2, 1.8 ± 0.22, ND, 0.17 ± 0.08, 4.85 ± 0.08 and ND g/kg respectively, while those of the vermicast were obtained as: 87.0 ± 3.8, 7.6 ± 0.07, 18.0 ± 0.23, 7.1 ± 0.11, 97.4 ± 11.9, 16.74 ± 0.022, 6.61 ± 0.11, 0.62 ± 0.03 and 0.13 ± 0.0001 g/kg respectively.
When the yield, height, number of leaves and roots as well as the biochemical composition of the leaves of maize and beans grown using vermicompost and vermicast were investigated in the growth of maize and beans, it was noted that the yield was higher than that of the soil without the fertilizer. The vermicompost, generally, has a greater advantage over commercial fertilizer as it is highly degradable and results to organic and, therefore, healthier crops.

The study has shown that organic waste in Kenya can undergo a closed loop – from the farm through production of electricity back to the farm. Thus in this study, multiple solutions have been obtained – sustainable solid waste management (with the consequent results including improved human health and climate change mitigation), generation of clean fuel and appropriate food security solutions. We recommend that the generated power be stored in an appropriate battery and be used for to supply energy needs for appropriate systems and also that the viability of the vermicompost be assessed with other crops.

Keywords: Bioelectricity; Fruit Waste; Organic fertilizer; Vermicompost; Vermicast

Poster 24

Harnessing simulation-based statistical modelling to optimize agroforestry systems for a sustainable bioeconomy in sub-saharan Africa

Presenting Author: **Fred Nyamitago Monari**

The bioeconomy in Sub-Saharan Africa will be at a fulcrum where agriculture, sustainability and data driven technologies meet. This intended study will aim at applying simulation based statistical modelling to determine the performance and optimal way to practice agroforestry and specifically in regard to small holder farms in Kenya. As a holistic approach to land management, it is likely that agroforestry will be a highly effective tool in improving food security, biodiversity conservation, and promoting healthy soils as well as increasing household income- important facets of a stable bioeconomic system [1].

Simulation-based statistical methods will be applied to build and verify statistical models of the dynamic interactions between the tree-crop combinations, soil fertility and variability in rainfall and crop yields. These models will deliver forecasts to be used when making decisions by farmers and policymakers. A future planned case study in Kisii County will be designed to give quantitative results on the effects of the agroforestry interventions, possibly indicating an increase in crop yields of 35 percent, increasing household income, and reducing exposure to climate shocks.
The relevance of this research will be directly aligned with the GBA Conference theme of on key technologies in the bioeconomy since it will highlight how statistical simulations as an emerging analytical technology, can be applied to evidence-based planning, scaling and adaptation of bioeconomic practices. It will be consistent with GBA aims of creating cross-disciplinary innovation and supporting sustainable technology in low-resource environments. Moreover, the project will also advance the international agenda of inclusion and diversity in that it aims to preserve African settings (rural areas), work on participatory types of research, cooperate with local universities, and communities. Attending the GBA Conference will give an opportunity to bring new bioeconomic models into the processes of policymaking and academic training and to develop cooperation that would be able to facilitate the economies of scale of sustainable land-use innovations in Africa.

Factor	Impact
Agroforestry Simulation	Yield ↑ 35%, Income ↑, Climate risk ↓

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Poster 25

Evaluating Biobased Value Chains Through Circular Economy Principles: The Case of Sugarcane Biomethane in São Paulo, Brazil

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Introduction: Integrating the concept of circularity into bioeconomy opportunities is essential to support robust prospective analyses, in which new biobased value chains are designed in a systemic and regenerative way, aligned with sustainable development. By incorporating circular flows of materials and energy from the early stages of biobased value chain design, it is possible to enhance environmental benefits, resource use efficiency, and the generation of socioeconomic value at the regional scale. This study proposes a sustainability assessment approach for emerging biobased value chains guided by the circular economy principles. The proposed approach seeks to inform public policies and support the development of more integrated, efficient, and regionally contextualized bioeconomy projects.

#	Circular Economy Principle	Scenario 1 – Diesel Replacement	Scenario 2 – LPG Replacement
1	Shortening Resource Flows	Circular Bioproduct Degree (Circular Demand/Potential Offer)	
		100%	100%
		Reduced volume of diesel transported	
		85,703 L	99,438 L
		GHG emissions avoided	
		227 tCO2e	264 tCO2e
2	Eliminating Waste and Pollution	Volume of fossil fuel replaced	
		7.2 million L of diesel	10,000 m^3 of LPG
		GHG emissions avoided	
		16.7 kt CO2e	37.6 kt CO2e
3	Endless Cycles, Retained/Maximized Value, and Effective Solutions	Co-benefits of using biodigested vinasse and filter cake: increased nutrient availability for sugarcane; N_2O emissions reduction of 4.7 kt CO_2e	
4	Regeneration of Nature	Benefits of biodigested residues: improved soil microbial activity; reduced eutrophication, fish mortality, soil salinization, phytotoxicity, and risks of leaching and percolation	
5	Retention of Ownership: Transactional Efficiencies	Bioproduct self-consumption rate (Dint/Opot): 100%	No internal consumption
		No need for transportation to point of use	Biomethane must be transported to external clients
6	Value Sharing	Environmental benefit transferred in the value chain: GHG reduction of 78 kg CO_2e/t sugar and 184 kg CO_2e/m^3 ethanol	GHG reduction of 3.8 t CO_2e per 1,000 m^3 LPG replaced
7	Resource Traceability	Full traceability within internal operations	Partial traceability through pipeline infrastructure

Methodology: Our methodology adapts seven key principles of the circular economy, consolidated from a review of relevant literature, to assess the sustainability impacts of two potential scenarios for sugarcane biomethane production in São Paulo, Brazil. The first scenario involves autoconsumption of the biofuel in the the farm´s agricultural activities, while the second focuses on trading to replace industrial use of LPG in nearby facilities. This approach moves beyond traditional tools by incorporating qualitative, territorial, and relational aspects of sustainability.

Results: The study presents a comparative analysis of two scenarios for biomethane use, as detailed in the table. The results highlight the potential for enhanced resource efficiency, decentralized production benefits, and the creation of shared value across regional networks. The findings indicate how circular principles can reveal indirect effects, such as gains from self-consumption and transactional gains from local or regional supply chains.

Conclusion: Using circular economy principles as a methodological framework for assessing sustainable value chains offers an innovative and complementary approach to traditional tools such as Life Cycle Assessment (LCA). This approach provides a robust tool for designing and evaluating bioeconomy projects, and its findings can influence both public policy and industry strategies toward a more integrated and resilient regional bioeconomy.

Key Words: biobased value chains, bioeconomy, circular economy, sustainability assessment, sugarcane residues, biomethane

Poster 26

Impact of lignocellulose-derived inhibitors on isobutanol production by *Corynebacterium glutamicum*

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Isobutanol is a promising precursor for biofuel production because isobutanol-derived fuels have advanced properties like high compatibility with existing engines. Various microorganisms have been engineered for the biotechnological production of isobutanol from renewable resources. However, these strains have mainly been optimized to use glucose as substrate in chemically defined medium. Complex substrates such as lignocellulosic hydrolysates contain, in addition to sugars, inhibitors such as phenolic acids, aldehydes and aliphatic acids that affect the production performance.

We aim to optimize the isobutanol production from wheat straw hydrolysate (WSH) with *Corynebacterium glutamicum* Iso [1] through systems metabolic engineering. Therefore, we characterized the impact of exemplary inhibitors on anaerobic isobutanol production in synthetic glucose medium and compared these effects to those observed in WSH medium. The underlying inhibition patterns were analyzed by HPLC, HILIC-QTOF-MS and flow cytometry analysis identifying metabolic and bioprocess engineering targets for improving the production performance on WSH.

The isobutanol production was hardly affected by furfural, formate, ferulate and vanillate. Vanillin increased the isobutanol yield by approx. 9 % to 0.50 ± 0.01 C-mol$_{iBuOH}$ C-mol$_{Glc}^{-1}$ while reducing isobutyrate formation. Acetate reduced the glucose uptake rate by more than 60 % to 0.10 ± 0.00 g_{Glc} g_{CDW}^{-1} h^{-1} and the isobutanol yield by approx. 25 % to 0.34 ± 0.01 C-mol$_{iBuOH}$ C-mol$_{Glc+Ac}^{-1}$ compared to the culture with glucose only. The product yields and glucose uptake rates in early fermentations with synthetic acetate-glucose medium are similar to those with WSH. We assume that acetic acid uncouples the proton membrane gradient and thereby inhibits the NADH transhydrogenase. This leads to an accumulation of NADH which inhibits glycolysis. At the same time, the inhibited NADH transhydrogenase causes a shortage of NADPH for the isobutanol pathway. Therefore, the effect of acetate on the isobutanol production was compared with the effect of the known protonophore carbonyl cyanide m-chlorophenyl hydrazine (CCCP). CCCP reduced glucose uptake by 33 % compared to the culture with glucose only. This indicates that the inhibition of acetate can be partly attributed to the uncoupling effect. Thus, the membrane potential of *C. glutamicum* during isobutanol production was analyzed with the carbocyanine dye 3,3′-diethyloxacarbocyanine iodide (DiOC$_2$(3)) by flow cytometry. Finally, the metabolic effect of acetate, CCCP and WSH was analyzed more deeply by intracellular metabolome analysis showing significant differences in metabolite pools related to glycolysis, TCA, isobutanol, purine, pyrimidine and amino acid pathways compared to the culture with glucose only.

This work highlights the significant impact of acetate on anaerobic isobutanol production revealing opportunities for further strain optimization such as the construction of a transhydrogenase-independent strain.

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Poster 27

Engineering *Corynebacterium glutamicum* for 7'-deoxysedoheptulose (7dSh) production

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Modern agricultural production heavily relies on the use of artificial chemicals like fertilisers, herbicides, and fungicides, which can have detrimental effects on the environment and human health. Therefore, replacing such chemicals with more environmentally friendly bioactive compounds is one important strategy to minimise the environmental impact of the agricultural industry.

The unusual sugar 7'-deoxysedoheptulose (7dSh) was first discovered in the soil bacterium *Streptomyces setonensis* [1] and has become a promising candidate for agricultural applications due to its herbicidal properties. Like the controversial broad-spectrum herbicide glyphosate, 7dSh acts as an inhibitor of the shikimate pathway, which is only present in photoautotrophic organisms such as plants, bacteria and fungi [2]. Recently, the 7dSh biosynthesis pathway was characterised in the cyanobacterium *Synechococcus elongatus* [3], opening the door for biotechnological production of 7dSh.However, 7dSh is not yet commercially available, as its chemoenzymatic synthesis is expensive and inefficient. Therefore, this work aims to enable the biotechnological production of 7dSh through metabolic engineering of *Corynebacterium glutamicum*.

For this goal, a synthetic 7dSh production pathway is designed based on the cyanobacterial biosynthesis starting from 5'-deoxyadenosine (5dAdo) and implemented into *C. glutamicum*. Furthermore, the replacement of the phosphorylase-phosphatase steps of the pathway with a nucleosidase is explored to avoid the phosphorylated intermediate 5'-deoxyribose-1-phosphate (5dR-1P) and thus minimise loss through native salvage pathways. The precursor availability is also improved through the overexpression of native radical S-adenosyl-L-methionine (SAM) enzymes and the inactivation of salvage pathways. Lastly, *C. glutamicum* production strains are ultimately optimised for the utilisation of biogenic waste for large-scale fermentation-based production of 7dSh, thereby reducing production costs and improving sustainability.

Overall, for the optimisation of metabolic flux distributions and the maximisation of 7dSh production, tools from the fields of metabolic engineering, synthetic biology and systems biology are employed, supported by mass-spectrometry-based metabolome analyses.

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Poster 28

Production of Biomass and Bioactive Metabolites by *Phanerodontia* sp. in Different Culture Media

Lorena Resende Oliveira[1,2], Noelle Cruz Faustino dos Santos[3], Ariany Rosa Gonçalves[2], Rodrigo Silva de Oliveira[2], David Henriques da Matta[4], Vanessa Gisele Pasqualotto Severino[3], Marcio Vinicius de C. Barros Côrtes[2,*], Marta Cristina Corsi de Filippi[2,*]

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This study investigated the potential of *Phanerodontia* sp. BRM 62389, a ligninolytic fungus from the Phanerochaetaceae family, as a producer of bioactive metabolites with antifungal activity against rice phytopathogens of agricultural relevance. Different cultivation conditions were evaluated, including four liquid culture media (PD, YES, YPD, and minimal medium) and fermentation periods of up to 8 days, focusing on biomass production, pH variation, dissolved oxygen consumption, and bioactivity of the fermentative extracts. Chemical characterization by thin-layer chromatography (TLC) indicated the presence of alkaloids and terpenoids in the active extracts. Genomic analysis identified 31 biosynthetic gene clusters (BGCs), including NRPS-like, terpene, and polyketide clusters, confirming the biosynthetic potential of the fungus. Overall, the findings support the use of *Phanerodontia* sp. as a fungal biofactory to produce bioactive compounds with promising applications as biofungicides in sustainable agriculture.

Figure 1. Qualitative analysis for the detection of alkaloids in extracts of *Phanerodontia* sp. BRM 62389. On the left, chromatographic profile obtained by Thin Layer Chromatography (TLC) using Dragendorff's reagent for visualization.

Figure 2. Preliminary detection of compounds from the terpenoid and sterol classes in extracts obtained from *Phanerodontia* sp. BRM 62389 cultivated in PD and YPD media under control conditions and after 5 days of fermentation. (A) Salkowski test: the formation of a brownish-red band at the chloroform/H_2SO_4 interface indicates the presence of terpenoids. (B) Liebermann-Burchard test: a pinkish-red coloration confirms terpenoids, while the development of a green confirms sterols.

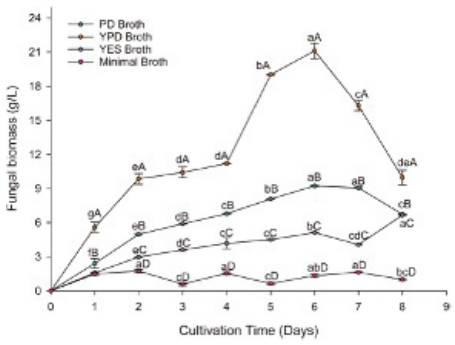

Figure 3. Biomass (g L^{-1}) of *Phanerodontia* sp. BRM 62389 produced in different culture media: BD broth (green circle), YPD (orange circle), YES (purple circle), and MM (pink circle), during 8 days of submerged bench-scale fermentation (v = 100 mL, T = 28 °C, initial pH = 5.5 ± 0.2). Means followed by the same lowercase letter (comparison among fermentation times) and uppercase letter (comparison among culture media) do not differ significantly according to Tukey's test at a 5% significance level. CV: 4.87%.
Source: Oliveira (2024).

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Poster 29

Engineering of Formate Dehydrogenases for Conversion of CO_2

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Carbon dioxide (CO_2) is one of the key drivers and biggest contributors to global warming. The ability to catalyze the conversion of CO_2 into sustainable fuels and chemicals, utilizing renewable energy sources, is critical to mitigate the irreversible climate change and environmental degradation. We are aiming at achieving robust electricity-driven biocatalysis to drive the conversions. The work involves collaborations with different members of our Pioneer Center for Accelerating P2X Materials Discovery (CAPeX) to develop scalable materials for the electricity-driven electrode systems.

A direct and green pathway to convert thermodynamically stable CO_2 into high-in-demand commodity chemicals, such as formate, formaldehyde, and methanol, is *via* cell-free multi- enzyme cascade catalysis, utilizing the reverse redox catalytic abilities of three different types of enzymes: formate dehydrogenase (FDH, EC 1.17.1.9), formaldehyde dehydrogenase (FaldDH, EC 1.2.1.46) and alcohol dehydrogenase (ADH, EC 1.1.1.1). Each step of the cascade is investigated separately before being merged into the whole pathway.

Nature has evolved two types of microbial FDHs, 'metal-dependent' and 'metal-independent' FDHs. The metal-dependent FDHs are particularly relevant to the practical/technical conversion of CO_2 as a first step in C1- based biomanufacturing from CO_2, even though they are larger, more complex, multidomain enzymes. Based on the arrangement of the gene segments and study of protein sequence alignment, the metal-dependent FDHs can be divided into six subtypes [1]. A particularly oxygen-tolerant member of the type 5 FDHs is the FDH from *Rhodobacter capsulatus* (RcFDH). These types of FDHs are high molecular weight (heterotetrametric, MW ~360 kDa), metal-dependent and NAD^+- dependent multi-domain enzymes, coordinating molybdenum (Mo) in the active site with Flavin mononucleotide (FMN) as cofactor. Recent studies of the RcFDH showed that the protein subunits connect a series of Fe-S clusters which are directly involved in the electron- transfer from FMN to Mo [2]. The metal-dependent FDHs can be expressed in *Escherichia coli*, but their structural size, fragility, and the poor electron donation capacity of NADH hinder the efficient and robust CO_2 catalysis for sustainable large- scale implementation and industrial application. To gain more insight into the catalytic function of type 5 FDHs, including understanding the significance of the subunits and the electron donor, different truncated variants were constructed. These constructs were produced in a high-throughput *E. coli* expression platform using different medias, strains and temperatures to identify their optimal expression conditions. Their catalytic activity towards CO_2 was spectrophotometrically assessed.

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Poster 30

The metabolic potential of wild Australian yeasts
Multi-omics investigations of the metabolism of non-*Saccharomyces* yeasts

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Since its domestication, *Saccharomyces cerevisiae* has become the dominant species in fermented foods, biotechnology, and the bioeconomy, favoured for its controllability, reliability, and ethanol tolerance. Yet this focus on refining domesticated strains has left the metabolic diversity, evolutionary dynamics, ecological roles, and biotechnological potential of wild yeasts largely underexplored.

Our work centres on the niche-adapted metabolic traits of wild yeasts. Isolated from Australian plants, flowers, fruits, bark, and resin, they show remarkable metabolic diversity in high-resolution metabolomics, pointing to strong biotechnological potential:

numerous microbial strains naturally produce polyols, compounds widely used as non-caloric sweeteners today, yet still predominantly sourced through chemical synthesis rather than sustainable, green fermentation [1]. Alongside ongoing multi-omics studies of polyol metabolism (metabolomics, proteomics), we are investigating the role of yeasts within microbially diverse communities (metagenomics) shaped by the ecological niches.

In line with the proposed community standards (mQACC), we are expanding the screening of our >100 clonal wild yeast isolates using a standardized and robust RP-metabolomics workflow designed for long-term comparability: Retention time alignment is ensured using N-alkylpyridinium phosphates (NAPS) as internal standards [2] and is maintained consistently even following service and maintenance interventions. Normalization based on project-specific and pooled QC samples enables robust semi-quantitative comparisons across batches and runs.

The resulting curated and searchable collection of metabolite profiles will provide a comprehensive metabolomics reference library to support fundamental investigations into yeast molecular diversity and to enable downstream applications in sustainable food systems, the bioeconomy, and biodiversity conservation.

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Poster 31

Efficient Production of n-Butanol from CO_2 via the Synthetic Acetyl-CoA Pathway

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The global demand for sustainable alternatives to traditional fossil-based fuels and chemicals has spurred considerable interest in developing novel biotechnological approaches for renewable production.

Here, we present our research focused on the production of n-butanol from CO_2 using the recently constructed Synthetic Acetyl-CoA pathway.

The production of n-butanol from CO_2 via formaldehyde holds significant promise for various applications. Firstly, n-butanol serves as a valuable industrial chemical with diverse uses, including as a solvent, intermediate in chemical synthesis, and additive in the manufacturing of plastics, coatings, and textiles. Furthermore, n-butanol has garnered attention as a biofuel due to its high energy density and compatibility with existing infrastructure. By harnessing formaldehyde as a precursor for n-butanol production, we not only expand the range of renewable feedstocks but also mitigate reliance on fossil resources, aligning with the global shift towards greener and more sustainable production pathways. Acetyl-CoA, a pivotal metabolite in cellular metabolism, is conventionally derived from complex carbon sources. However, the SACA pathway offers an innovative route to generate acetyl-CoA from formaldehyde, a simple and abundant feedstock. In order to improve the formation of acetyl-CoA, we will engineer glycolaldehyde synthase and acetyl-phosphate synthase. For this, we will use a combined approach based on (semi-) rational design and high-throughput methods such as microfluidics or growth coupled selection. Furthermore, we integrate this pathway with an enzyme cascade aimed at the conversion of acetyl-CoA to n-butanol. This work could contribute to the bioprocess development for renewable production of valuable chemicals and biofuels as well as to the transition towards a more sustainable and environmentally friendly bioeconomy.

Poster 32

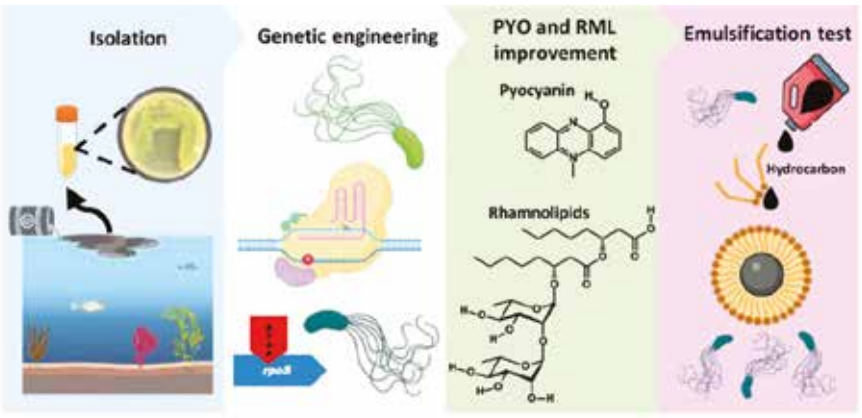
Genetic engineering of an environmental Pseudomonas (IGLPR01) by CRISPR/Cas9 to enhance PYO, RMLs production, and hydrocarbon emulsification.

Luis-Mauricio Salazar-García, Luis C. Damas-Ramos, Luisa M. Trejo-Alarcón, Daniela Rago, Linda Ahonen, Pablo Cruz-Morales, Patricia Ponce-Noyola and Cuauhtémoc Licona-Cassani

Environmental microorganisms represent a valuable but underexplored resource in the search for sustainable solutions to pressing global challenges. Among these, the mitigation of hydrocarbon impact remains a critical environmental and societal priority. Oil spills and fuel leakage continue to contaminate terrestrial and aquatic ecosystems worldwide, demanding effective and eco-friendly remediation strategies. In this context, environmental strains of *Pseudomonas aeruginosa* are of particular interest due to their natural ability to produce secondary metabolites with surfactant and redox properties, such as rhamnolipids (RMLs) and pyocyanin (PYO). These compounds can support hydrocarbon emulsification and degradation and thus hold potential for use in bioremediation processes.

My research focuses on unlocking the biotechnological potential of such environmental isolates using genetic tools. Specifically, I have worked with *P. aeruginosa* IGLPR01, a strain isolated from an oil-contaminated site in the Gulf of Mexico. To enhance its biosurfactant production, we implemented a CRISPR/Cas9-APOBEC1-UGI base editing strategy targeting the *rpoS* gene. This regulatory mutation led to a marked increase in the production of both PYO and RMLs, resulting in improved hydrocarbon emulsification in cell-free assays using gasoline. Our work demonstrates the feasibility of applying CRISPR-based genome editing in non-model, wild-type bacterial strains, which are typically less amenable to manipulation.

This study contributes to the broader goals of the bioeconomy by showing how natural microbial diversity can be harnessed through synthetic biology to produce functional molecules with real-world environmental applications. It also reinforces the need to expand biotechnological platforms beyond well-established lab strains by developing adaptable tools and frameworks for engineering new microbial chassis. Ultimately, our work supports the integration of microbial systems into sustainable technologies for pollution mitigation and circular bio-based innovation.



Poster 33

A new function among copper enzymes with implications in lignin valorization

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Lignin from *e.g.* wood and crop waste is the largest renewable source of aromatic carbon for bio-based chemicals and materials. Advancing enzymatic methods for sustainable lignin extraction, depolymerization, and functionalization is a key challenge in unlocking lignin's potential. A newly recognized class of copper-containing polyphenol oxidases found in Ascomycetes catalyze the conversion of lignin-derived guaiacyl-type phenols to the corresponding methoxy-*ortho*-quinones through sequential *ortho*-hydroxylation and two-electron oxidation reactions. Some of these enzymes can also target syringyl-type phenols and, via an unprecedented oxidative *ortho*-demethoxylation mechanism, convert these into the same methoxy-*ortho*-quinone [1]. The activity on methoxylated phenols is novel among polyphenol oxidases and the catalyzed reaction differs from canonical lignin-active oxidoreductases like laccases and peroxidases. We have named them "*ortho*-methoxyphenolases" (*o*-MPs) and proposed a new enzyme commission number (EC 1.14.18.13) [2]. Their ability to funnel the two main lignin subunits into the same product offers a potential new strategy to make lignin depolymerization mixtures more uniform and enhance their value for chemical and material applications. Unlocking the full biocatalytic potential of *o*-MPs in lignin valorization requires evaluating their activity not only on monomeric model compounds, but also on structurally more complex lignin analogues and, ultimately, on lignin polymers. Here, we examine in detail the activity of *o*-MPs on a set of lignin model dimers representing the abundant β-O-4'-linked substructures of lignin, including variations in the phenolic terminal group (guaiacyl *versus* syringyl) and oxidation at the Cα position, where we address factors such as pH and the challenge of minimizing polymerization.

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Poster 34

Unspecific peroxygenases and their oxidative activity towards lignin

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Introduction: Lignin from plant biomass has the potential to be a renewable source of bulk and fine aromatic chemicals with desirable properties. To enable the precise and mild extraction of lignin, enzyme-based methods are emerging as a key technology. Unspecific peroxygenases (UPOs, EC 1.11.2.1) are heme-thiolate enzymes that are particularly abundant in lignocellulose-degrading fungi. UPOs are especially interesting for the oxyfunctionalization of lignin, as they exhibit oxidative activity toward a wide variety of functional groups present in the lignin polymer.

Objectives: The aim of this project is to investigate and understand the ability of UPOs to catalyze specific oxidative modifications on lignin or lignin derivatives, potentially increasing the reactivity and applicability of lignin derived from plant biomass.

Methods and Results: To achieve this, we heterologously expressed selected UPOs from the phyla Ascomycetes and Basidiomycetes in *Pichia pastoris*. The expressed UPOs catalyze hydroxylation, demethylation, and one-electron oxidation of lignin substructures, and UPOs from the same organisms exhibit distinct ratios of peroxidase to peroxygenase activity, along with different pH dependencies. Oxidation products from reactions on both model substrates and authentic lignin are analyzed by LC and GC-MS.

To further understand reaction preferences and substrate specificities, we will investigate the redox potentials and hydrogen peroxide consumption of individual UPOs using electrochemical methods.

Conclusion: Our initial studies provide valuable insights into the expression and purification of functional UPOs. All the expressed UPOs exhibit activity on lignin-like substrates and catalyze a variety of oxidative reactions, including hydroxylation, demethylation, and one-electron oxidation. The large variation in catalyzed reactions and pH dependency among UPOs highlights the diversity of these enzymes. A future prospect is to explore how reaction parameters, such as pH and co-substrate concentration, influence the catalyzed reactions.

Poster 35

Enhancing Transaminase Stability: Buffer Effects on SpATA in Cell-Free Systems

Juliet J Victoria, Bhu-Bhud Thongrakon, Amalie Vang Høst, Per Berglund, John M Woodley

Cell-free biocatalytic systems are powerful tools in the bioeconomy, where efficient and sustainable production of high-value chemicals is essential. By eliminating metabolic complexity, transport limitations, and undesired side reactions inherent to whole-cell biocatalysis, cell-free systems offer superior control over the reaction[1]. However, a major challenge remains: the stability of enzymes in industrial environments. Without the protective cellular membrane, enzymes are more susceptible to rapid deactivation[2]. In this study, we investigate the kinetic stability of a pyridoxal 5'-phosphate (PLP)-dependent transaminase from *Silicibacter pomeroyi* (SpATA), which is active in its dimeric form and loses activity upon dissociation. While previous research has explored the effects of light and buffer composition on SpATA stability, these studies have not addressed conditions relevant to industrial processing[3], [4]. We evaluated the effects of agitation and buffer strength (10–100 mM) in a stirred tank reactor under controlled temperature conditions on enzyme activity and structural integrity. Spectrophotometric assays and SDS-PAGE analysis revealed that while agitation had no significant impact, buffer composition strongly influenced enzyme deactivation. These findings highlight the importance of physicochemical environment in cell-free systems and provide insights for designing more robust biocatalytic platforms.

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Poster 36

The Benefits of Immobilized Sulfate-reducing Bacteria in Mining-influenced Water Treatment

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Mining activities often generate acid mine drainage (AMD), characterized by high acidity and heavy metal content. Sulfate reducing bacteria (SRB) can treat AMD by reducing sulfate, with the resultant sulfide precipitating heavy metals, potentially aiding in the recovery of rare earth elements [1, 2]. However, SRB treatment faces challenges like microbial instability from process disturbances and toxic shocks and generally requires a large process footprint if applied in a constructed wetland[3, 4]. Entrapped SRB (ESRB) technology offers an alternative by entrapping microbes in a porous hydrogel matrix, promoting biomass growth and nutrient diffusion while maintaining a stable microenvironment. This application of ESRB can increase cell density, protect against inflow shocks, enhance performance stability, and offer cost savings in a bioreactor setup. The objective of this study is to compare ESRB and non-entrapped SRB with respect to sulfate reduction performance and stability to process disturbances. The strength and lifespan of ESRB beads will also be assessed after application.

The sulfate removal ability of ESRB showed improved sulfate reduction efficiency and enhanced long-term stability compared to non-entrapped SRB across 210-day of reactor operation, particularly in response to temperature fluctuations (Figure 1). When temperature dropped from 24°C to 15°C, the ESRB's sulfate reduction rate remained stable (0.71±0.06 g SO_4^{2-}/L/day), while the non-entrapped SRB's rate was inhibited and to 0 g SO_4^{2-}/L/day. Also, compression tests confirmed that ESRB retained physical stability throughout the operation. This study supports the applicability of ESRB for AMD treatment over an extended operational period.

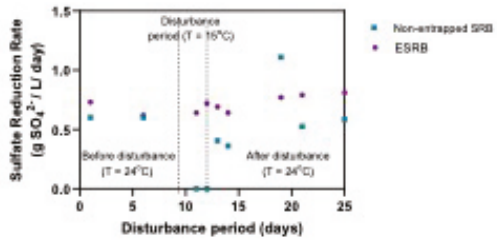

Figure 1: sulfate reduction performance of the two bioreactors affected by temperature disturbance

In addition to mining-influenced water treatment, ESRBs have the potential for valuable recovery of rare earth metals, through sulfate reduction and metal precipitation. Through their metabolic processes, SRB converts sulfate into hydrogen sulfide (H_2S) which subsequently reacts with metals, forming insoluble metal sulfides. Future work will involve larger scale testing of ESRB as well as investigating metal recovery efficiency and a comprehensive cost analysis for the viability of ESRB technology with comparison to traditional methods.

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Only participants registered before August 1 are included

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