EBIC Environmental Biotechnology Innovation Centre

8-9 July 2025

Early Career Researcher Conference

Engineering Biology for Environmental Sustainability

Conference Programme

Venue

The University of Edinburgh

Pentland Suite, John McIntyre Conference Centre, University of Edinburgh, EH16 5AY

Day 1 | Tuesday 8 July 2025

9:00 – 10:00	**Welcome and Registration**
Opening session	
10:00	**Opening Remarks** Prof Frederic Coulon, Director, Environmental Biotechnology Innovation Centre.
10:20	**Keynote** **Liz Fletcher**, Director of Business Engagement and Operations, IbioIC, UK. Mapping the journey from lab bench to marketplace for (environmental) biotechnologies.
11:05	**Poster session & Tea/Coffee Break**
Session 1 - Engineering tools & traceability	
11:25	**Muhammad Yasir Akbar, Newcastle University.** Deciphering *Picosynechococcus pcc 7002* genome to identify neutral sites for synthetic barcode integration.
11:45	**Dr Marcos Valenzuela Ortega, The University of Edinburgh.** Engineering microbes to transform PET plastic into nylon precursors.
12:05	**Dr Rachel Samson, Cranfield University.** Advancing Water Safety: Insights into Coliphage Viromics Across Drinking Water Treatment Using Nanopore Sequencing.
12:25	**Dr Amanda Hopes, University of East Anglia.** Generating mutant strains for the EBIC: developing standardised cloning and transformation systems for a wide range of species and applications.
12:45	Q&A / Session Wrap-up.
12:50 -13:50	**Lunch Break**
Session 2 - Bioremediation and biodegradation	
13:50	**Dr Prabhakar Srivastava, Bangor University.** Harnessing catalytic potential of marine bacteria for bioremediation of recalcitrant organic pollutants.
14:10	**Dr Anil Kumar, University of Nottingham.** Towards sustainable resource recovery through integrated bioleaching and electrodialysis.

14:30	**Dr Yasmin Meeda, Cranfield University.** Engineering biology for metaldehyde biodegradation in drinking water using *Sphingobium sp* and *Acinetobacter sp.*
14:50	**Hairong Ma, Bangor University.** Discovery and engineering of microbial carboxylesterase for potential applications in polyester recycling.
14:10	Q&A / Session Wrap-up.
15:15 - 16:00	**Poster Session & Tea/Coffee Break**
Session 3 – Engineering biology for metal-contaminated wastes	
16:00	**Dr Maria Magliulo, Natural History Museum.** Exploring microbial diversity in mine waste: a roadmap for bioengineering technologies.
16:20	**Dr Natalie Byrd, The University of Manchester.** Hydrogenase Mediated Biosynthesis of Catalytically Active Cu Nanoparticles.
16:40	**Christine Paul Vazhathara, University of Nottingham.** Bioelectrochemical Recovery of Platinum Group Metals from Spent Car.
17:05	Q&A / Session Wrap-up.
17:05	**Keynote** **Dayal Saran**, Vice-President Research, Allonia, USA. From Lab to Field: Overcoming Deployment Barriers and Leading Safe, Scalable Biological Solutions for a Cleaner Future
17:50	**Networking Drinks Reception**
19:00	**Conference Dinner**

Day 2 | Wednesday 9 July 2025

Day 2 - Welcome and opening	
09:00	**Keyote** **Beatrix Ellis**, CEO, GitLife, UK. Securing Investment and Building Resilience from Pre-Seed to Series A in UK Bio Startups
9:45 -10:00	**Poster Session & Tea/Coffee break**
Session 4 - Biocatalysis and bioengineering	
10:00	**Gwion Williams, Bangor University.** Mining the plastisphere: diverse cold-active enzymes from seawater metagenomes.
10:20	**Dr Tejasvi Shivakumar** Cell-free synthetic biology for sustainable biomanufacturing.
10:40	**Kawinharsun Dhodduraj, Cranfield University** Sustainable production of 2,3-butanediol using renewable feedstock.
11:00	Q&A / Session Wrap-up.
11:05 -11:30	**Poster Session & Tea/Coffee break**
Session 5 - Water and waste management & resource recovery	
11:30	**Dr Dominic Quinn, University of Glasgow.** Validated molecular quantification of intact pathogens following propidium monoazide treatment in drinking water.
11:50	**Dr Kyle Parker, The University of Edinburgh.** Suitability & Feasibility of Synthetic Biology in the UK Water Sector.
12:10	**Dr Fabien Cholet, University of Glasgow** Effect of temperature on microbial assembly and activity in Granular Activated Carbon drinking water biofilters.
12:30	**Dr Danting Chen, University College London** Material/Substance Flow Analysis of biomass ash in the United Kingdom.
12:50	Q&A / Session Wrap-up.

12:55	**Science Creates – Engineering Biology Accelerator** **Dr Lucy McGowan,** Innovation Manager, Science Creates.
13:00	**Closing Remarks & Presentation Awards sponsored by the Environmental Biotechnology Network (EBNet)** Prof Frederic Coulon, Director, Environmental Biotechnology Innovation Centre Em. Prof Sonia Heaven, The University of Southampton, EBNet.
13:25 -14:25	**Lunch**
Skills Development for Early Career Researchers	
14:25 - 16:25	**Workshop** The why, how, and impact of research commercialisation **Lissa Herron**, Deputy Director & Head of Enterprise, Converge.
16:25 – Main Conference Close – thank you all for joining us!	
16:30 – 17:30	**EBIC ECR Challenge** **Proposed by EBIC Operational Board (Prof. Bruce Jefferson & Em Prof. Sonia Heaven)** Group challenge session for **EBIC funded ECR only**. *From Laboratory to Applied Environmental Solutions: Development of Protocols and a Testing Facility for Environmental Biotechnologies.*

Poster Presentations

ID	Name	Poster Title
#1	**Dr Hannah Adams** University of Essex	Engineering Hydrocarbon Biodegradation Pathways.
#2	**Amulyasai Bakshi** University of Nottingham	Enzymatic degradation of rubber with latex clearing proteins
#3	**Dr Christopher Egan-Morriss** University of Manchester	Biorecovery of Platinum group metals as nanocatalysts
#4	**Dr Andrea Gallio** University of Bristol	Sensing heme: a systems approach to understanding heme-regulated cellular function
#5	**Miss Rachael Giles** Cranfield University	Identifying opportunities for biological coagulant recovery in drinking water and wastewater treatment processes
#6	**Magdalena Howe** Brunel University of London	Exploring plastic degradation amongst Acinetobacter species
#7	**Manuel Lera Ramirez** University College London	OpenCloning: a credible Open-Source alternative to SnapGene and Benchling that supports automation and integration with research software
#8	**Harry Maguire** University of East Anglia	Development of high-throughput systems for environmental bacterial mutant construction
#9	**Cathal O'Reilly** University of Manchester	Utilising ML and AI tools to understand difficult-to-engineer enzymes
#10	**Dr Giuliano Pechar** University of York	Engineering plant-mediated metal solubilisation in the rhizosphere.
#11	**Mrs Naja'atu Shehu Hadi** Cranfield University	Bioengineering of Plastic-Degrading Bacterial Biofilms for Enhanced Microplastic Removal in Wastewater Treatment Systems.
#12	**Dr Tatiana Spatola Rossi** Heriot-Watt University	Metabolic engineering in Pseudomonas putida for the production of rhamnolipids
#13	**Luke Moore** Glasgow University	Identifying highly active nitrifiers in the environment with Raman-activated cell sorting.
#14	**Miriam Watafua** Heriot-Watt University	Soil Remediation: Biochar as a Carrier for Acinetobacter calcoaceticus in Hydrocarbon Degradation
#15	**Dr Joe Weaver** Newcastle University	Agent-Based Models as predictive, strategic, and exploratory tools for engineering biology
#16	**Dr Jinxin Xie** University of Manchester	Biorecovery of gold nanoparticles from industrial wastewaters by Shewanella oneidensis

Abstracts – Session 1

Muhammad Yasir Akbar

Interdisciplinary Computing and Complex Biosystems (ICOS) Research Group, School of Computing, Newcastle University.

Deciphering *picosynechococcus pcc 7002* genome to identify neutral sites for synthetic barcode integration.

Keywords: Cyanobacteria; Neutral Sites; Synthetic Barcodes

Picosynechococcus pcc 7002 model cyanobacteria can be engineered for a variety of environmental applications. The spread of engineered organisms into the environment should be monitored so taking biosecurity measures is critical. The focus of biosecurity is now shifting from containment to traceability. To track engineered organisms and ensure biosecurity, they must be tagged using synthetic DNA barcodes. To avoid any effect on the normal functioning of the organism the barcodes must be integrated into a neutral site. For this purpose, we focus on three approaches to finding the best neutral sites. The first approach is to use intergenic regions, as they are non-coding regions. Despite their non-coding nature, care must be taken as they may contain several regulatory elements. To avoid the regulatory element, a longer intergenic region was targeted having no regulatory elements. Expression at the final region was also observed to confirm no sign of any activity. Next, we focused on pseudogenes as most pseudogenes are under relaxed selective pressure indicating neutrality so they can be good candidates. The last approach was to study transcriptome to find any gene that is silent or shows low expression across multiple conditions, further filtered by protein-protein interaction. By executing these methods, multiple candidate regions were prioritized from the whole genome.

Dr Marcos Valenzuela Ortega

The University of Edinburgh.

Engineering microbes to transform PET plastic into nylon precursors.

Keywords: synthetic Biology; Plastic Waste; Metabolic Engineering

Engineered E. coli converted PET plastic waste into adipic acid, a key nylon precursor, in a one-pot process. This microorganism was engineered to express 8 enzymes for a new-to-nature metabolic pathway converting terephthalatic acid into adipic acid. Enhanced gene expression and enzyme activity improved pathway flux, while cell immobilization in alginate stabilized the limiting enzyme BcER. Pairing pathway enzymes with hydrogen gas and a Pd catalyst enabled conversion from metabolic intermediates. These advances allowed direct adipic acid production from both industrial and consumer PET-derived terephthalate.

Dr Rachel P Samson

Faculty of Engineering and Science, Cranfield Water Science Institute, Cranfield University.

Advancing Water Safety: Insights into Coliphage Viromics Across Drinking Water Treatment Using Nanopore Sequencing.

Keywords: Coliphages; Nanopore Sequencing; Virome

Environmental monitoring of drinking water treatment plants (DWTPs) is vital for ensuring water safety and sustainability. While bacterial indicators are routinely used, viral indicators such as somatic

coliphages offer a more relevant signal for tracking viral and treatment performance. This study used Oxford Nanopore-based metagenomic sequencing to explore coliphage diversity across multiple DWTPs. Samples collected from raw intake through to post-disinfection stages were processed using optimized viral enrichment and end-repair workflows. Nanopore sequencing enabled real-time profiling of coliphage communities, allowing assessment of taxonomic diversity, alpha and beta diversity, and changes in abundance across treatment stages. The data revealed clear shifts in coliphage composition during treatment and allowed reconstruction of metagenome-assembled genomes (MAGs), providing further insight into coliphage ecology and potential lineages. These findings highlight the potential of nanopore-enabled coliphage monitoring as a practical and scalable tool in environmental biotechnology. This approach supports more responsive microbial risk assessment and enhances our understanding of viral dynamics in engineered water systems. Ultimately, this work contributes to the development of sustainable water quality monitoring strategies that align with net zero goals and circular economy principles.

Dr Amanda Hopes

University of East Anglia.

Generating mutant strains for the EBIC: developing standardised cloning and transformation systems for a wide range of species and applications.

Keywords: Mutants; Cloning; Transformation

Working across themes 2 and 3, we are the main hub for creating constructs and mutant strains for EBIC members, this includes manipulation of dozens of bacterial species for applications such as wastewater management, biotechnology and bioremediation. Using synthetic biology we have created and tested backbone constructs for use with Golden-gate cloning, compatible with a high-throughput, standardised strategy, to allow production of a large number of constructs and mutants. Our cloning strategy uses suicide plasmids, designed for use in a wide range of species and includes multiple antibiotic resistance options, an oriT for conjugation and SacB with a range of promoters to generate markerless strains. We are optimising or developing transformation systems for our strains, with an emphasis on electro transformation, including for new or understudied species. Constructs are being used to knockout and alter genes, as well as to insert new sequences, cassettes and barcodes into 'landing pads' within the genome. Suitable landing pads including neutral sites and pseudogenes are being tested for all species. This presentation aims to update EBIC members on our progress, including genetic tractability of species, progress with high-throughput cloning, testing of landing pads, and creation of mutant strains.

Abstracts – Session 2

Dr Prabhakar Srivastava

School of Environmental and Natural Sciences, Bangor University.

Harnessing catalytic potential of marine bacteria for bioremediation of recalcitrant organic pollutants.

Keywords: Bioremediation; Alkane monooxygenase; Hydrocarbons

Over 700 - 800 million tons of hydrocarbons are spilled in the oceans each year through combination of natural seeps, accidental releases from the petrochemical industry, and the biological activity of cyanobacteria, causing extensive damage to the marine ecosystem. In an attempt to contribute towards a solution, we have isolated alkane monooxygenase (ALKB1), primary enzyme responsible for oxidation of aliphatic hydrocarbons from marine bacterium *Alcanivorax borkumensis* SK2 known to degrade linear and branched hydrocarbons (C6-C24). Functional characterization of AbALKB1 revealed that, it accepts the small chain length substrate (upto C7) more efficiently and shows very little activity with longer alkanes. To improve the substrate scope towards larger chain length of AbALKB1, we constructed a homology model using AlKB1 from *Fontimonas thermophila* as a template and identified active site residues which could have significant impact on chain length determination and performed site-directed mutagenesis. AbALKB1 W60A showed preference towards higher alkane (C10-12) whereas L311A showed more preference for C8, indicating the importance of W60 and L311 in chain length determination. These engineered variants with broad substrate specificity will be incorporated into the genome of *Alcanivorax borkumensis* using genetic engineering approach, making it more effective at removing hydrocarbons from the environment.

Dr Anil Kumar

Food Water Waste Research Group, University of Nottingham

Towards sustainable resource recovery through integrated bioleaching and electrodialysis.

Keywords: Resource Recovery; Integrated Bioleaching; Critical Minerals

Global demand for critical minerals is anticipated to surge by 2040 or 2050, driven by the ongoing shift towards clean energy transition. Secondary metallic waste streams have been viewed as a valuable resource, owing to critical elements in quantities exceeding those found in ores. This demands recycling for resource recovery, which is integral to a circular economy and sustainable development. Microbial biotechnological processes, such as bioleaching and bio-oxidation, leverage nature-based solutions and are preferred over traditional recycling methods. While commercially used for ores, their applications to secondary resources remain primarily limited to laboratory and pilot-scale efforts, thus requiring innovative interventions. This study employs integrated bioleaching and electrodialysis to recover critical and rare earth minerals from various waste streams, including foundry wastes and spent car catalysts. Different microorganisms, such as acidophiles and heterotrophic bacteria, were employed in the process. Preliminary screening indicated that *Acidithiobacillus ferrooxidans* facilitated the solubilization of 35%, 28%, and 14% of Sr, Mg, and Ce, respectively, in the anode compartment. Meanwhile, 22% of Sr and 18% of Ce were mobilized to the cathode compartment at 100 g/L pulp density. The findings are encouraging, paving the way for innovative and sustainable resource recovery practices.

Dr Yasmin Meeda

Faculty of Engineering and Science, Cranfield Water Science Institute, Cranfield University.

Engineering biology for metaldehyde biodegradation in drinking water using *Sphingobium sp* and *Acinetobacter sp*.

Contaminated soil and water resources, particularly from persistent agrochemical pollutants, present a growing environmental challenge. These pollutants, such as pesticides and molluscicides, can remain in the environment for extended periods, leading to long-term contamination of ecosystems. The risks are widespread, affecting soil health, water quality, and biodiversity. In addition to impacting agricultural productivity, these pollutants can leach into waterways, harming aquatic life, disrupting ecosystems, and posing risks to human health. The need for effective management and remediation strategies is critical to mitigate these environmental threats and ensure the sustainability of natural resources. This study explores the potential use of synthetic biology to enhance the natural biodegradation capabilities of two environmental bacterial isolates for the breakdown of metaldehyde. Metaldehyde is a widely used compound found in slug pellets, which has recently been banned in the UK due to its environmental persistence and risks to water quality. *Sphingobium sp* MEH and *Acinetobacter calcoaceticus* E1 have metaldehyde-degrading enzymes found on plasmids, which are a product of convergent evolution. Without a selective pressure (no metaldehyde), these enzymes can be ejected from the cell and the biodegrading capability will be lost. Here, we use engineering biology as an approach to optimise these pathways by integrating the enzymes into the bacterial genome or by overexpressing them to improve the degradation efficiency.

Comparative analysis of engineered strains and wild-type (WT) bacteria under different metaldehyde concentrations have been assessed to determine the effectiveness of these genetic modifications. This proof-of-concept study highlights the potential for using synthetic biology to enhance bioremediation solutions for emerging contaminants. This research is part of a broad interdisciplinary collaboration through the Environmental Biotechnology Innovation Centre (EBIC), and involves innovative technologies, and systemic approaches. This approach can then be scaled to see the potential for use in water treatment.

Hairong Ma

Centre for Environmental Biotechnology, School of Environmental and Natural Sciences, Bangor University, Bangor.

Discovery and engineering of microbial carboxylesterase for potential applications in polyester recycling.

Enzyme-based depolymerization of plastics, including polyesters, has emerged as a promising approach for plastic waste recycling and reducing environmental plastic pollution. Currently, most of the known polyester-degrading enzymes are represented by a few natural and engineered PETases from the carboxylesterase family V.

To identify novel groups of polyesterases, we selected 25 proteins from the carboxylesterase family IV, which share 22 % to 80 % sequence identity to the metagenomic thermophilic polyesterase IS12. All purified proteins were found to be active against chromogenic para-nitrophenyl esters with a preference for short acyl chains. Screening for polyesterase activity using emulsified polyesters demonstrated the presence of hydrolytic activity against bis(benzoyloxyethyl) terephthalate (3PET), polycaprolactone (PCL), and polylactic acid (PLA) in all tested proteins.

Biochemical characterization of four selected polyesterases revealed high thermostability in CBA10055, whereas the mesophilic GEN0105 exhibited higher polyesterase activity. Two ancestral variants of GEN0105 showed higher thermostability and activity against PCL and PLA, but reduced activity with amorphous PET. Furthermore, six established PETases were found to be highly active against PCL and PLA. Thus, our results indicate that polyesterase activity is widespread in the family IV carboxylesterases, and that most polyesterases are promiscuous being able to degrade different polyesters.

Abstracts – Session 3

Dr Maria Magliulo

Natural History Museum.

Exploring microbial diversity in mine waste: a roadmap for bioengineering technologies.

Keywords: Biomining; Microbial Diversity; Bioengineering

Exploring the 16S rRNA microbial diversity in naturally occurring bioleaching consortia and mine waste environments could be a powerful tool for advancing microbial biotechnology. These extreme ecosystems host a wide array of microorganisms with specialized functions, including metal solubilization, acid tolerance, and biofilm formation—traits highly relevant to bioengineering applications. In this study, microbial communities from a naturally occurring bioleaching consortium, mine tailings, and enrichments obtained from mine tailings were analysed using 16S rRNA gene analysis. By characterizing these communities, we aim to gain insights into microbial interactions,

metabolic capabilities, as well as abundances and presence/absence of specific taxa, that can inform the design of synthetic consortia. The results obtained so far from the bioleaching consortium highlight the dominance of bacterial and one archaeal species such as *Leptospirillum, Acidithiobacillus* and *Ferroplasma*; these organisms form a functionally resilient microbial network, facilitating the oxidation of chalcopyrite and mobilization of copper under autotrophic conditions. This type of microbial interactions can help understanding microbial adaptation and interspecies interactions in environments considered extreme due to a combination of physiochemical stressors, including highly acidic conditions: their ability to survive and contribute to metal solubilization under such conditions highlights their biotechnological potential.

Dr Natalie Byrd

Department of Earth and Environmental Sciences, The University of Manchester.

Hydrogenase Mediated Biosynthesis of Catalytically Active Cu Nanoparticles.

Keywords: Bioreduction; Copper Nanoparticles; *Shewanella oneidensis*

Shewanella oneidensis MR-1 can biosynthesise cell-supported Cu-nanoparticles (CuNPs), via the bioreduction of aqueous Cu(II), with excellent catalytic activity for click chemistry reactions. However, enzymatic mechanisms underpinning Cu(II) bioreduction were unclear. Here, the oxidation of hydrogen as electron donor was essential for Cu(II) bioreduction by *S. oneidensis* and hydrogenase deletion mutants were used to demonstrate the critical role of the periplasmic [NiFe] hydrogenase, HyaB. Wild type (WT) cultured cells coupled hydrogen oxidation to biosynthesis of CuNPs comprising Cu(0)/Cu(I) within the periplasm (identified using XRD and TEM with SAED, EDS, EELS); ΔhyaB mutants did not produce CuNPs. *S. oneidensis* biosynthesised CuNPs were catalytically active for the cycloaddition of methyl azidoacetate and 1-hexyne, confirming the potential for microbial revalorisation of Cu(II)-containing wastewaters, by forming catalytically active nanomaterials. The identification of a hydrogenase (conventionally considered sensitive to Cu), as a key mediator for Cu(II) reduction in *S. oneidensis* is an important first step in the development of industrial bioprocesses for Cu(II) recovery and CuNP synthesis, offering a template for scalable improvements using engineering biology. Interestingly, we also report that c-type cytochromes, critical for reduction of other metals, were unable to fully reduce Cu(II) from solution despite being capable of Cu(II) reduction under in vitro conditions.

Christine Paul Vazhathara

Faculty of Engineering, University of Nottingham.

Bioelectrochemical Recovery of Platinum Group Metals from Spent Car Catalysts.

Keywords: Sustainable Metal Recovery; Bioelectrochemical Process; Bioelectrochemical Process

As the demand for platinum group metals (PGMs) rises, sustainable recovery methods from spent car catalysts (SCC) become critical, given the environmental and energy burdens of traditional extraction techniques. This study explores a bioelectrochemical approach using *Cupriavidus metallidurans* CH34 in microbial fuel cells (MFCs) to recover PGMs while generating electricity.

Batch culture experiments showed that *C. metallidurans* CH34 tolerated high concentrations of SCC, up to 100,000 ppm (10% w/v). Viable cell counts, protein assays, and gluconate utilisation (HPLC) confirmed sustained growth in the presence of catalyst particles. MFC performance varied with catalyst concentration: without SCC (0 ppm), the voltage reached 0.37V; with 10,000 ppm, it increased to 0.43V, suggesting enhanced electron transfer. However, higher concentrations of SCC caused a decrease in performance, with voltages of 0.28V at 50,000 ppm and 0.17V at 100,000 ppm, indicating inhibitory effects.

To uncover the genetic mechanisms driving PGM recovery, transcriptomic and proteomic analyses will identify genes and pathways activated by metal exposure. These insights will help understand how *C. metallidurans* CH34 adapts to metal stress and optimises electron transfer. Finally, a life cycle assessment (LCA) will evaluate the environmental impact of MFC-based PGM recovery, supporting more sustainable and efficient recovery strategies.

Abstracts – Session 4

Gwion Williams

School of Environmental & Natural Sciences, Bangor University.

Mining the plastisphere: diverse cold-active enzymes from seawater metagenomes.

Keywords: Biotechnology; Plastics; Biocatalysis

Awareness of plastics as pollutants is widespread in public and scientific contexts, but our understanding of microbial life growing on environmental plastics (the "plastisphere"), in addition to their catalytic toolbox, remains limited. We additionally know that significant fractions of plastic pollution enter marine systems; thus seawater microbial communities are of particular relevance in characterising plastics-associated communities, and may contain biotechnologically useful biocatalysts allowing their persistence in the xenobiotic environment of polymers & their additives.

We proposed that by investigating the marine plastisphere we could understand biofilm colonisation dynamics, hypothesising that putative plastic/additive metabolising genera would become enriched, and subsequently we could mine the plastisphere to discover enzymes of relevance for biotechnology, including plastics biodegradation.

To this end, we incubated four polymer types in seawater and extracted metagenomic DNA over 16-weeks. Initial 16S sequencing enabled assessment of longitudinal community changes, and informed selection of a representative sample set for metagenomic sequencing. The sequence assemblies were mined for hydrolases and oxidoreductases enriched in samples, resulting in 13 soluble enzymes after synthesis. The kinetic parameters of these biocatalysts were characterised with model substrates and plastics via spectrophotometry, chromatography; and potential plastic degradation was assayed using HPLC product analysis and FTIR surface modification analysis.

Dr Tejasvi Shivakumar

Imperial College Centre for Synthetic Biology, Imperial College London.

Cell-free synthetic biology for sustainable biomanufacturing.

Keywords: Yeast; Cell-free Synthetic Biology; Biomanufacturing

Cell-free protein synthesis (CFPS) is a versatile platform enabling decentralised and sustainable biomanufacturing, particularly in extreme and low-resource environments. By eliminating the need for live cells, CFPS accelerates the production of protein therapeutics and reduces reliance on cold-chain supply. While bacterial systems are widely used, they lack post-translational modifications, whereas mammalian systems offer superior functionality but suffer from high cost and low yield. Yeast-based CFPS offers a middle ground, combining efficient protein synthesis with eukaryotic processing capabilities.

This study presents the development and optimisation of a novel yeast CFPS platform based on the industrially relevant *Kluyveromyces lactis*. A semi-automated design-of experiments (DoE) approach was used to refine reaction conditions, significantly enhancing protein yields. We developed an extract preparation workflow and demonstrated the use of lactose as a cost-effective carbon and energy source. The optimised *K. lactis* CFPS system achieved a four-fold improvement in erythropoietin (EPO) synthesis, reaching 54 nM.

By integrating rational optimisation with renewable feedstocks, yeast-based CFPS provides a scalable and energy-efficient alternative to traditional fermentation. Notably, *K. lactis* thrives on cheese whey, a dairy industry by-product, further reinforcing its sustainability. This work paves the way for environmentally conscious biomanufacturing, with applications ranging from biosensors to biopharmaceutical production.

Kawinharsun Dhodduraj

Faculty of Engineering and Science, Cranfield University.

Sustainable production of 2,3-butanediol using renewable feedstock.

Keywords: Waste Valorization; Biorefinary; 2, 3-butanediol

The dependence on fossil fuels for production of fuels and chemicals significantly contributing to environmental damage, and climate change. As a result, there is growing interest in renewable feedstocks, with lignocellulosic biomass (LCB) emerging as a promising alternative.

Sugar beet pulp (SBP), a major waste stream of the sugar industry typically used as animal feed or disposed of in landfills. It is an underutilized LCB with rich in fermentable sugars - comprising ~25% cellulose, 33% hemicellulose (arabinose-rich), and 26% pectin (galacturonic acid-rich). Its low lignin content (3-8%)makes it especially suitable for bioconversion, yet traditional pretreatment methods uses harsh chemicals and/or energy demanding.

Our study focuses on developing an environmentally friendly pretreatment strategy to efficiently extract sugars from SBP and produce 2,3-butanediol (BDO), a high-value platform chemical with applications in fuels, cosmetics, and pharmaceuticals. Since most industrial microbes are unable to utilize sugars such as arabinose and galacturonic acid, pectin-rich biomass is often excluded from biorefinery pipelines. We aim to overcome this limitation through targeted metabolic engineering to enhance sugar assimilation, knockout byproduct formation and fermentation process optimization to boost BDO production metrics. This approach supports the sustainable valorization of agro-industrial residues and advances the responsible resource management and circular bioeconomy.

Abstracts – Session 5

Dr Dominic Quinn

James Watt School of Engineering, University of Glasgow.

Validated molecular quantification of intact pathogens following propidium monoazide treatment in drinking water.

Keywords: Propidium Monoazide; Drinking Water; Opportunistic Pathogens

Quantifying pathogens in drinking water is challenging, with standard culture-based methods being time-consuming and not always reflective of large-volume or real-time conditions. Molecular techniques offer faster alternatives but can overestimate pathogen levels by quantifying extracellular DNA (eDNA) or DNA from dead cells. Propidium monoazide (PMA) helps address this by making eDNA unamplifiable following light exposure. However, its regulatory acceptance is limited due to a lack of validation in real-world settings.

Here we develop and validate a PMA-based method using GFP-labelled Pseudomonas aeruginosa in both pure cultures and in a filtered drinking water background. Kill gradients (ethanol and chlorine) were applied to compare total DNA to intracellular DNA (PMA-treated) using digital droplet PCR, with results cross-verified by plate culture and flow cytometry. Total DNA levels remained unchanged despite significant drops in viable cell counts, while PMA-treated samples showed a 99.9% and 99.7% reduction in detected DNA at high ethanol and chlorine concentrations, respectively. Molecular quantification following PMA treatment found cell numbers were not significantly different (ANOVA p-values > 0.05) from intact cell counts across both ethanol and chlorine gradients, indicating accurate quantification of intact pathogens post-PMA treatment. This validated approach may support improved molecular monitoring in drinking water systems.

Dr Kyle Parker

School of Biological Sciences, University of Edinburgh.

Suitability & Feasibility of Synthetic Biology in the UK Water Sector.

Keywords: Responsible Research; Social Dimensions; Science & Technology Studies

The Environmental Biotechnology Innovation Centre (EBIC) is an interdisciplinary, BBSRC-funded UKRI mission hub which aims to apply synthetic biology tools to environmental problems, bringing together expertise from both the life and social sciences.

In addition to its technical programme, the EBIC hub also has a strong emphasis on responsible research and innovation in environmental biotechnological applications. As researchers and innovators striving to mitigate environmental pollution and counteract climate change, we must scrutinise the efficacy and appropriateness of synthetic biology-based solutions within the broader climate change mitigation and adaptation strategies. It is imperative to question how synthetic biology can effectively address environmental challenges without inadvertently creating new challenges or amplifying existing social and political disparities.

To that end, our work explores the social, ethical, and environmental implications of environmental biotechnology. This encompasses considerations of feasibility, benefits, consequences, implementation factors, and societal impacts, and the diversity of possible futures for environmental biotechnological deployments. We will present ongoing work studying potential uses for engineering biology tools in the water treatment applications. Our work analyses the suitability and feasibility of incorporating these developing technologies into

existing large-scale, critical infrastructure, and how this might shape the future of the UK's water system.

Dr Fabien Cholet

James Watt School of Engineering, University of Glasgow.

Effect of temperature on microbial assembly and activity in Granular Activated Carbon drinking water biofilters.

Keywords: Biofiltration; Microbiome; Drinking water

Biofiltration is a sustainable drinking-water treatment method that relies on microbial processes to remove contaminants. However, reduced winter temperatures may slow microbial metabolism and affect performance. To investigate the impact of temperature on drinking-water biofiltration, an 11-month experiment was conducted using slow (3H EBCT) granular activated carbon (GAC) columns at 10°C and 20°C. Total organic carbon (TOC) and pathogen concentrations were measured in influent and effluent. Results showed minimal differences in TOC removal between the two temperatures, with only slight improvement at 20°C at eight time points, and no effect on pathogen removal ($p.value<0.05$). A subsequent batch experiment tested the response of the microbial communities developed on the 10°C (GAC-10) and 20°C degrees (GAC-20) biofilters. Both were incubated at 6, 10 and 20 degrees, and their capacity to degrade organic carbon in the same influent water was measured after 8, 24, 48, and 72 hours. The GAC-10 community was temperature-flexible, with no significant impact of incubation temperature on organic carbon degradation whereas the GAC-20 temperature-sensitive, degrading up to 90% less organic carbon at 6 and 10°C compared to 20°C. This study suggests that low temperatures may not limit drinking-water biofiltration as cold-tolerant microbial communities can be selected on GAC biofilters.

Dr Danting Chen

Department of Civil, Environmental and Geomatic Engineering (CEGE), University College London (UCL)

Material/Substance Flow Analysis of biomass ash in the United Kingdom.

Keywords: Combustion Residue; Heavy Metals; Circular Economy

Understanding of the availability of biomass ash is critical for developing its circularity, and has not been investigated in the UK. Material/Substance Flow Analysis (MFA/SFA) of biomass ash in the UK was conducted using the ash generation and management flows in 2021, and its element composition based on collection of literature data. The results showed a total of 831kt biomass ash generated in 2021, 88% of which was wood ash. Wood bottom ash was mainly disposed of in landfill, while wood fly ash was dominantly recovered as block materials. Most agricultural and other biowaste ashes were found to be downcycled in land. UK biomass ashes were calculated to contain a total of 126 kt Ca, 47 kt Si, 41 kt K, 19 kt P, 12 kt Al and 7.9 kt Fe. Biomass ashes also contain toxic elements, whose fate and management must be considered in any utilisation scenario, e.g., 551 t Ba, 190 t Sr, 179 t Zn, 103 t Cu, 57 t of As, 49 t Ni, 46 Cr and 28 t of Pb. Since circularity of biomass ash is poor under current management practice, this study suggests opportunities for improving resource management.

Abstracts – Posters

Dr Hannah Adams

School of Life Sciences, University of Essex.

Engineering Hydrocarbon Biodegradation Pathways.

Keywords: Hydrocarbons; Biodegradation; Protein Expression/Characterisation

There are several steps in aerobic hydrocarbon biodegradation pathways, which covert hydrocarbons into various products, such as alcohols, aldehydes and fatty acids, before eventually being completely mineralized to carbon dioxide and water. This complex series of reactions is catalysed by an array of different protein interactions in hydrocarbon-degrading bacteria, such as *Alcanivorax spp*. and *Cycloclasticus spp*.
Our aim is to use transcriptomic and proteomic approaches to identify genes and proteins which are upregulated in these, and other marine bacteria in the presence of particular hydrocarbons, pinpointing key proteins involved in their biodegradation. Once identified, mutations can be engineered to test the importance of these proteins within the pathway, where the ability to degrade hydrocarbons may be removed in the case of an essential gene, and the protein it codes for, being 'knocked out'. Using recombinant protein expression methods on these essential proteins, we can probe their activity against different hydrocarbons, or intermediate degradation products, to confirm exact enzyme function and specificity. Structure-function relationships can be further studied using techniques such as X-ray Crystallography or Cryo-Electron Microscopy, where the structure of the proteins can be examined in detail.

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Enzymatic degradation of rubber with latex clearing proteins.

Keywords: Biocatalysis; Directed Evolution; Waste Re-Valorisation

Rubber, a commonly used material in everyday objects, generate huge waste globally. Current waste management methods are energy consuming and cause secondary pollution. This can be overcome by using enzymes which are sourced from renewable and biodegradable feedstock and are energy efficient. Enzymes called latex clearing proteins (Lcp) were shown to degrade various polyisoprene rubbers by oxidation, producing functionalised isoprene oligomers, which can potentially be re-valorised. However, the activity of the wild-type Lcp is too low for industrial applications possibly because of the limited interaction between the enzyme and polymer chains. Organic solvents could improve the contact between rubber and Lcp, but those have a detrimental impact on the enzyme.
This research aims to engineer Lcp towards increasing enzyme activity in water-solvent biphasic mixtures. Previous modelling data was used to identify amino acid residues (A159, R394, R395), predicted to impact the enzyme stability in solvents.
Initial results from testing 31 mutants in 10% tetradecane showed that A159F and R395L have 35.8% and 64.4% increase in oligomer formation, respectively, compared to the wild type. This result is promising, suggesting that the methodology developed has potential to test mutants on synthetic rubbers, offering a practical solution to dealing with rubber waste.

Dr Christopher Egan-Morriss

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Biorecovery of Platinum group metals as nanocatalysts.

Keywords: PGMs; Biorecovery; Catalysis

The platinum group metals (PGM) are highly important catalysts and are critical materials across many industries but are associated with high economic and environmental costs due to limited availability, toxicity, and energy-intensive extraction methods. Our research utilises metal-reducing bacteria, such as *Geobacter sulfurreducens* and *Shewanella oneidensis*, for the sustainable biorecovery of PGMs as catalytically active nanoparticles from industrial waste streams. Our goal is to develop a scalable, low energy, and chemically benign biotechnology to fabricate high-performance nanocatalysts from waste, advancing the metals circular economy.
This work utilised *G. sulfurreducens* to biosynthesise palladium nanoparticles (bio-Pd) under ambient conditions. By modulating synthesis parameters—such as solution chemistry, Pd(II) loading and the choice of electron donor—we demonstrate control over nanoparticle properties, including cellular localization, particle size, and Pd(II):Pd(0) ratios. Advanced characterization (HAADF-STEM, XRD, XPS, XAS) revealed tuneable nanostructures with catalytic activities comparable to commercial Pd catalysts in the reduction of 4-nitrophenol and Suzuki cross-coupling reactions. Co-bioreduction with secondary metals (Groups 9 - 11) enabled the biosynthesis of bimetallic bio-PdM nanoparticles with enhanced catalytic performance. The biosynthesis of mixed metal nanoparticles was influenced by redox potential and metal toxicity, highlighting key constraints in mixed-metal biorecovery that we aim to overcome using engineering biology.

Dr Andrea Gallio

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Sensing heme: a systems approach to understanding heme-regulated cellular function.

Keywords: Tetrapyrroles homeostasis; Biosensors; Heme

Heme is an essential and versatile molecule for the regulation of cellular functions and bioenergetics. The processes of heme biosynthesis, transport and degradation are responsible for the supply of heme in mitochondria and its insertion into other downstream proteins. What remains unresolved is how these processes interconnect, and the wider implications for the cell in the restoration of homeostasis in response to different perturbations. We have developed a range of fluorescent genetically encoded biosensors to quantify through Fluorescence Lifetime Imaging Microscopy (FLIM) intracellular shifts in heme bioavailability and heme loading into hemoproteins used for heme scavenging (e.g. myoglobin) or with important roles in immunoregulation (e.g. indolamine 2,3-dioxygenase). We are using these sensors in conjunction with -omics approaches, qPCR, and flow cytometry to show how changes in heme levels impact mitochondrial function, including the tricarboxylic acid cycle and oxidative phosphorylation, and engage iron storage and uptake in mammalian cell culture models. These results define a dynamic "hemome" that integrates heme homeostasis with energy metabolism and mitochondrial health. Understanding this framework provides a roadmap towards new angles for addressing diseases linked to tetrapyrrole dysregulation and can inform the development of cellular platforms with programmable responses to environmental or immunological stimuli.

Rachael Giles

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Identifying opportunities for biological coagulant recovery in drinking water and wastewater treatment processes.

Keywords: Resource recovery; Coagulation; Iron Reducing Bacteria

Coagulant dosing is essential for removing impurities in many wastewater and drinking water treatment processes. However, this is a linear process, where coagulant is only dosed once before disposal. This model is coming under increasing stress due to market volatility, increasing demand, and tightening environmental targets.

A novel method is proposed whereby iron reducing bacteria (IRB) are used to separate iron from sludge for re-use. IRB are known to already be present in wastewater sludges, and to reduce the insoluble Fe(III) present in sludge to soluble Fe(II) when the correct conditions are provided.

However, not all sludges are suitable for biological coagulant recovery. The key factors impacting the ability of IRB to reduce iron are the solid iron species present, the ageing of these species, and the sludge conditions. IRB can usually only reduce amorphous/poorly crystalline Fe(III) with minimal ageing, and will preferentially use nitrate as an electron acceptor.

By selecting sludges that match these target criteria, it is proposed that IRB can be used to separate iron from the sludge, to allow for its re-use as coagulant. This method of biological coagulant recovery and re-use will introduce circularity, therefore increasing the resilience and sustainability of the coagulation process.

Magdalena A Howe

College of Health, Medicine and Life Sciences, Department of Life Sciences, Brunel University of London

Exploring plastic degradation amongst *Acinetobacter* species.

Globally 52 million tons of plastic waste are produced every year, of which 10-20 million tons end up in the ocean. Aggregation of such litter in the environment damages ecosystems and affects human health. Currently only around 10% of plastic waste is recycled, with the remaining 90% being incinerated or buried in landfills, both of which can severely impact the environment. In recent years bacteria have been identified that encode enzymes capable of degrading a range of different plastic polymers, suggesting that bacteria may offer a sustainable solution to tackle the plastic waste problem. While the characterisation of plastic degrading and their associated enzymes is developing at pace, relatively little is known about *Acinetobacter* genus capacity in this regard. Here we explore the plastic degrading capabilities of different *Acinetobacter* species. Environmental sampling of plastic contaminated sites identified four *Acinetobacter* species (A1-4) that could degrade plastic to various degrees. The most efficient plastic degrader was A3. Subsequent analysis showed that A3 culture supernatant possessed the plastic degrading ability, indicating secretion of the functional enzyme. Furthermore, we have evidence of bacterial growth in the presence of different plastic. In addition, our data shows that A3 is able to use plastic as a sole carbon source. Taken together our study demonstrates that *Acinetobacter* spp. are capable of degrading plastic and utilising it as energy source, and that the degradation efficiency depends on the plastic type and species. Better understanding of *Acinetobacter* polymer degradation can inform further studies to enhance bacterial bioremediation for tackling plastic pollution.

Manuel Lera Ramirez

Department of Genetics, Evolution & Environment, University College London.

OpenCloning: a credible Open Source alternative to SnapGene and Benchling that supports automation and integration with research software.

OpenCloning is an Open-Source web application to plan and document cloning and genome engineering. It allows researchers to design a cloning strategy through an intuitive web interface or programmatically, and provides a standardised data model to represent cloning strategies. Researchers can:

•Import plasmid sequences from repositories like AddGene and genome sequences from NCBI using gene names or genome coordinates.
•Plan cloning and design primers using common techniques (Gibson, golden gate, Gateway, etc.).
•Plan strain and cell line engineering via CRISPR and homologous recombination, which is not supported by commercial software.
•Automate repetitive cloning and primer design using templates, web forms or scripts.
•Archive the entire cloning strategy as a json file.

Unlike commercial alternatives, OpenCloning uses the first ever Open Data Model to represent cloning strategies, and supports integration with research software. For instance, we already have a working integration with an Electronic Lab Notebook.
You can access OpenCloning for free online at or run your own instance locally.

Try it: https://opencloning.org/
Demo video: https://github.com/manulera/OpenCloning/blob/master/demo_video.md

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Harry Maguire

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Development of high-throughput systems for environmental bacterial mutant construction.

Keywords: Efficient; Genetic; Manipulation.

A range of bacteria have beneficial environmental and bio-industrial potentials. However, genetic modification is required to utilise these, and currently many of these novel species have not been modified due to an absence of standardised protocols.

Our target is to develop a system for generating unmarked, stable bacterial mutants in a high-throughput and cost-efficient manner. This will utilise chromosomal integration and a negative selection marker. The initial plasmid consists of an antibiotic resistance, a sacB cassette, an origin of replication and transfer, and a mScarlett cassette flanked by 2 BsaI sites. Using Golden Gate cloning, specific homology sequences are integrated into the backbone plasmid, which is then used for homologous recombination.

Transformation of the plasmid into the host cells have been achieved using electroporation or conjugation. Multiple conditions are continually tested to develop a workflow of transformation into different species. A range of modified backbones, with different antibiotic resistance markers and sacB promoters have been developed. Bioinformatics work is being integrated into this project, with focus on software to identify pseudogenes and neutral sites in species. This project aims to provide a platform for genetic manipulation in a range of species, including species that have never been genetically modified.

Luke Moore

University of Glasgow.

Identifying highly active nitrifiers in the environment with Raman-activated cell sorting.

Keywords: Nitrification; Raman Activated Cell Sorting; Ammonia Oxidising Microbes .

A minority of environmental microorganisms are entirely responsible for nitrification – the oxidation of ammonia to nitrite and then to nitrate. It is important to understand nitrification to optimise wastewater treatment and to minimise harmful nitrogen release to the environment by human activities. DNA data is not a good indicator of nitrification rates and small sub-populations of nitrifiers may be responsible for the majority of nitrification gene RNA transcripts (Cholet et al., 2024).

To validate a method to identify active nitrifiers, we investigate stable isotope probing (SIP) coupled to Raman spectroscopy and single cell sorting, to separate active and inactive nitrifiers (Lyu et al., 2020). Cell sorting will be followed by single-cell metabolic activity analysis (Saito et al., 2021) and it could isolate nitrifier subpopulations responsible for driving nitrification in the environment.

As a proof of concept, an ammonia oxidising bacterium (Nitrosomonas ATCC 19718) and an ammonia oxidising archaeon from agricultural soil will be used to validate the approach – first to determine if a Raman shift is detectable in nitrifiers that incorporate carbon-13; after which labelled cells will be sorted. The approach will be applied directly to environmental samples combined with microcosm experiments to determine which microbial groups drive environmental nitrification.

Cathal O'Reilly

Scrutton Lab, University of Manchester.

Utilising ML and AI tools to understand difficult-to-engineer enzymes.

Monoterpenes are industrially important chemicals in increasing demand for their broad applications in fragrance, pharmaceuticals, and biofuels. Yet current production methods are often energy-intensive and environmentally harmful. Enzymatic synthesis using monoterpene synthases (mTSs) offers a more sustainable alternative, but these enzymes are notoriously difficult to engineer due to a weak and complex sequence-function relationship. To address this, we developed a structure-based statistical framework that applies machine learning to better understand and predict mTS function. Our model can accurately distinguish between enzymes that produce linear versus cyclic monoterpenes. As the position of specific residues is important for monoterpene synthesis, we created an algorithm to identify structurally conserved residues across and between different mTSs, uncovering motifs essential for both general catalysis and specific cyclization steps. Ongoing work uses these tools to guide the rational design of mTSs, making engineering the challenging enzymes more predictable and practically useful. This integrated workflow provides insights into terpene synthases that were previously inaccessible, and offers a generalizable strategy for probing and engineering other poorly understood enzyme families.

Dr Giuliano Sting Pechar

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Engineering plant-mediated metal solubilisation in the rhizosphere.

Keywords: Phytoremediation; Phytomining; Genetic Engenineering

Metals like platinum group metals, noble metals, and nickel are essential for developing technologies; however, their mining has significant environmental impacts, including high carbon emissions and pollution. Concentrations of valuable metals in these wastes are generally too low for economic extraction through traditional mining. Combining phytoremediation (environmental cleanup using plants) with phytomining (metal recovery from plants) could restore damaged land and recover these valuable technology-critical metals.

Metal uptake by plants is limited by their solubilisation into metals ions the rhizosphere. Biotechnological advances, such as genetic engineering and synthetic biology, offer enormous opportunities to enhance the natural capabilities of plants involved in metal recovery processes.

Cyanide has been shown to selectively solubilise our metals of interest in the rhizosphere. This work will focus on enhancing metal uptake by engineering the cyanide biosynthetic pathway in Arabidopsis root hairs. The pathway comprises two multifunctional cytochromes P450, and a beta-glucosidase, to produce a cyanoglycoside which is stored in the vacuoles. As they grow, root hairs can be damaged through physical and chemical interactions with the environment, and via root herbivory. Upon damage, the cyanoglycoside is enzymatically cleaved, releasing the cyanide into the rhizosphere for the specific solubilisation of target metals for plant uptake.

Naja'atu Shehu Hadi

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Bioengineering of Plastic-Degrading Bacterial Biofilms for Enhanced Microplastic Removal in Wastewater Treatment Systems.

Keywords: Plastic Degrading-Bacteria; Biofilms; Wastewater Treatment

Microplastics are not fully removed from conventional wastewater treatment, with large quantities retained in sludge and subsequently reintroduced into the environment through land application. Although these particles act as microbial attachment sites, influencing biofilm dynamics and nutrient cycling, they also disrupt ecosystems and soil health. Wastewater treatment plants (WWTPs) serve as vital control points for microplastic capture, yet significant particles persist in effluents and biosolids. This research aims to isolate and characterise plastic-degrading bacteria from wastewater, examine and compare bioaugmentation strategies to enhance degradation, and evaluate the stability and performance of biofilm-forming bacteria under simulated WWTP conditions. Using bioaugmentation with naturally occurring plastic-degrading bacterial strains, this study seeks to enhance microbial adhesion, depolymerase activity, and long-term biofilm resilience in competitive environments. By addressing operational inefficiencies in microbial degradation pathways, this work supports the development of a scalable and environmentally compatible bioremediation strategy to reduce microplastic loads in treated water and sludge within WWTPs. A critical literature review was conducted using Scopus and Web of Science, incorporating targeted keywords, Boolean operators, and strict inclusion criteria. Preliminary findings show variable degradation efficiencies across bacterial strains, gaps in biofilm stability metrics, and limited real-world WWTP data. Key insights guide bioaugmentation optimizations and highlight future research priorities.

Dr Tatiana Spatola Rossi

Heriot-Watt University

Metabolic engineering in Pseudomonas putida for the production of rhamnolipids.

Keywords: Biosurfactants; Bioremediation; Genetic engineering

Rhamnolipids are a type of glycolipid biosurfactant, or “surface-active” compound produced by some bacteria. They have potential to replace synthetic chemical surfactants, derived from petrochemicals, in a wide variety of applications ranging from pharmaceuticals, cosmetics, detergents and in the bioremediation of soils and marine oil spills. Being biobased and biodegradable, they comprise a sustainable alternative to chemical surfactants which produce significant contamination to the environment. The major rhamnolipid producing strains are pathogenic, such as *Pseudomonas aeruginosa*. The aim of this work is to confer rhamnolipid production capacity to the non-pathogen *Pseudomonas putida* and to optimise its heterologous production via novel metabolic engineering approaches. Previous work has recombinantly expressed the rhlA and rhlB genes in *P. putida* for mono-rhamnolipid synthesis. This work aims to express all three genes (rhlA rhlB and rhlC) for di-rhamnolipid production in *P. putida*. The strain will then be further modified to increase carbon flux towards the synthesis of di-rhamnolipid precursors, namely 3-(3-hydroxyalkanoyloxy) alkanoate (HAA), and rhamnose, and to eliminate non-essential pathways with high ATP consumption or presenting precursor competition. These findings could contribute towards the effective production and use of rhamnolipids for bioremediation, and to further elucidate the metabolism of *P. putida's* metabolism, a major biotechnological chassis.

Miriam Watafua

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Soil Remediation: Biochar as a Carrier for Acinetobacter calcoaceticus in Hydrocarbon Degradation.

Keywords: Bioremediation; Biochar; *Acinetobacter calcoaceticus*

Hydrocarbon-contaminated soils spills pose serious environmental risks, impacting groundwater quality, ecosystems, and public health. In response, this study explores a novel remediation strategy combining wheat straw biochar with the hydrocarbon-degrading bacterium *Acinetobacter calcoaceticus*. Biochar, produced at 700 °C, offers a stable, porous matrix and a liming effect that enhances microbial colonization. Pre-inoculation of biochar with *A. calcoaceticus* was tested against control and single-amendment treatments over a 63-day incubation period (sampling at D0, D7, D14, D28, D42, and D63). Results demonstrated that biochar-amended soils showed sustained increases in pH and microbial diversity, with distinct community shifts observed using SEM imaging, alpha diversity indices, and NMDS ordinations. The combined treatment significantly enriched key hydrocarbon degraders (e.g. *Acinetobacter, Pseudomonas, Hydrogenophaga*) and achieved over 75% reduction in total petroleum hydrocarbons, as confirmed by GC-FID/GC-MS analysis. These findings indicate that the synergy between biochar and A. calcoaceticus creates a conducive environment for enhanced hydrocarbon degradation. This approach presents a promising, scalable solution for effective bioremediation of hydrocarbon-contaminated soils.

Dr Joseph Weaver

Environmental Engineering, Newcastle University

Agent-Based Models as predictive, strategic, and exploratory tools for engineering biology.

Keywords: Modelling; Simulation; Prediction

Safely and effectively deploying engineering biology in environmental systems faces challenges: these systems are open and complex, with highly varying communities and environments. Predicting risk, optimizing function, and experimental innovation is difficult. Microbial ecological theory addresses those challenges – bridging it with engineering biology is critical.

Agent-based models (ABMs) where organisms are discretely, spatially simulated is one bridge. I have used ABMs to link theory and function by: discerning the balance between stochastic and deterministic selection during biofilm formation; understanding how a secretion system, commonly understood as a competitive weapon, can recruit cooperative partners; and estimating time scales over which intransitive "rock-paper-scissors" networks produce dynamic coexistence which however ultimately lead to extinction.

ABMs can serve as predictive, strategic, and exploratory tools for engineering biology. Predictively, they can inform risk estimates for accidentally released organisms, with or without evolution. Strategically, they can help determine bioaugmentation dosing rates. As exploratory tools, ABMS can rapidly traverse an experimental parameter space in silico, directing resources to the most promising experiments.

ABMs are not panacea and will not, nor should not, replace, real world experiments. Challenges include validation, computational feasibility, and model accessibility. Despite these limitations, ABMs are available now and remain an underused resource.

Dr Jinxin Xie

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Biorecovery of gold nanoparticles from industrial wastewaters by Shewanella oneidensis.

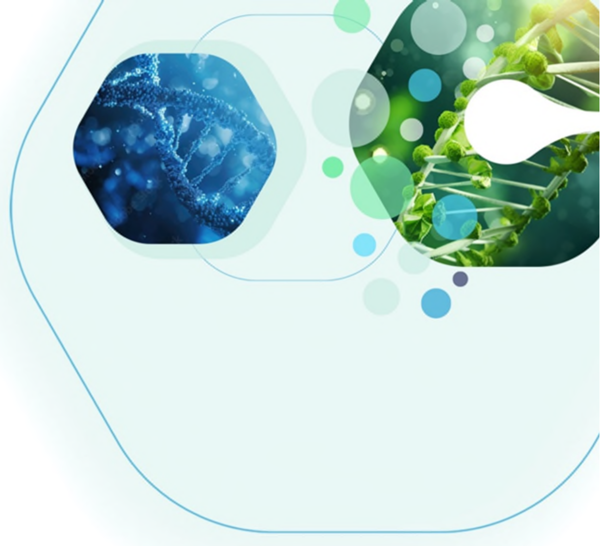
Keywords: Gold Biorecovery; Nanoparticles; *Shewanella oneidensis*

The increasing demand for precious metals, particularly gold, combined with environmental concerns over conventional recovery methods using hazardous chemicals and high energy inputs, has spurred the development of sustainable processing alternatives. This study evaluates the potential of the metal-reducing bacterium *Shewanella oneidensis* to biorecover gold from synthetic and real waste solutions via the bioreduction of Au(III) to form Au(0) nanoparticles.

The biorecovery capabilities of *S. oneidensis* was assessed across Au(III) concentrations (0.05 mM to 1 mM) using lactate and H2 as electron donors. H2 proved superior, achieving 60-100% gold removal across varying concentrations, and even at 1 mM Au(III), approximately 60% recovery efficiency was maintained with rapid kinetics.

Characterization by XRD and TEM revealed predominantly nanoscale Au(0) particles (<20 nm). Increased initial gold concentrations yielded larger nanoparticles localized at the cytoplasmic membrane when H2 was used. Hydrogenase mutant analysis underscored the key role of hyaB in H2-driven bioreduction.

Further tests with industrial gold leachates at pH ~4.5 achieved ~90% removal of 60 μM soluble Au, while acidic conditions (pH ~1.8) produced triangular and hexagonal nanoparticles with high catalytic activity. Our findings highlight *S. oneidensis* as an agent for eco-friendly gold recovery and the production of catalytically active gold nanoparticles.



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