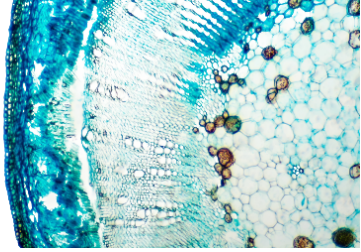
EBIC Environmental Biotechnology Innovation Centre



Early Career Researcher Conference

Engineering Biology for Environmental Solutions

16 - 17 September 2026 | Southampton, UK

Conference Programme

Venue

National Oceanography Centre

European Way, Southampton, SO14 3ZH

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Reason for visiting NOC: Conference

Dates: 16 - 17 September

Host: NOC Events

Location: NOC

Day 1 | Wednesday 16 September 2026

9:00 - 10:00	**Welcome and Registration**
Opening Session	
10:00	**Opening Remarks** **Professor Frederic Coulon** Director, Environmental Biotechnology Innovation Centre (EBIC)
10:20	**Keynote** **Francesca Dawson-Pell** Senior Policy Advisor Department for Business, Innovation, Science & Trade (UK Gov).
11:00 -11:25	**Tea/Coffee break/Poster session**
Session 1 – Environmental Bioremediation & Water Treatment	
11:25	**Mahsa Baniasadi – Cranfield University** Integrated Biological, Physical, and Chemical Approaches for Betaine Extraction from Salt-Stressed Algal Biomass
11:45	**Heni Wang – Cranfield University** Rapid and low-cost PFOA detection in drinking water by coupling engineered aptamers with DNA amplification
12:05	**Evieva F. Ogbara – Liverpool John Moores University** Re-evaluating Biochar-Based Remediation: Disentangling Sorption and Biodegradation Controls on PAH Attenuation in Soil Systems
12:25	**Yasmin Meeda – Cranfield University** Engineering biology for metaldehyde biodegradation in drinking water using *Acinetobacter sp*.

12:45	Q&A/ Session Wrap-up
12:50 - 13:50	**Lunch break**
Session 2 – Synthetic Biology & Engineering Biology Platforms	
13:50	**Amanda Hopes – University of East Anglia** Generating mutant strains for EBIC: Progress on development of a standardised cloning and transformation system to generate markerless mutants for a broad range of species and applications
14:10	**Daniel Evans - UK National Measurement Laboratory at LGC** Digital PCR methods to support tracking of engineered organisms in environments
14:30	**Joshua Loh – Newcastle University** BaNeX-guided identification and validation of neutral genomic integration sites for stable engineering biology applications
14:50	**Prabhakar L. Srivastava – Bangor University** Neutral Site-Driven Genome Engineering of *Alcanivorax borkumensis* to Expand Substrate Scope for Enhanced Bioremediation
15:10	Q&A/ Session Wrap-up
Flash Talks	
15:15	**James Bowbrick Smith – University of Surrey** Biorecovery of Gold Nanoparticles from Industrial Waste: Life Cycle and Techno-Economic Assessment of Scale-Up Pathways

15:20	**Josephine Giard – Heriot-Watt University** Adaption to climate change in the rhizosphere across the millennia
15:25	**Monika Steinke – University of Essex** In search of novel marine oil-degrading bacteria
15:30	**Natalio Krasnogor – Newcastle University** Informatics infrastructure in support of barcoding
15:35	**Oxford Nanopore**
15:40	**GENEWIZ**
Tea/Coffee break/Poster session (15:45 – 16:00)	
16:00 - 17:00	**Panel Discussion** Biocontainment Techniques and the Safe Use of Engineering Biology for Environmental Applications
Networking /Poster session (17:00)	
Dinner (19:00 - onwards)	

Day 2 | Thursday 17 September 2026

Day 2 - Welcome and opening	
09:00	**Keynote** **James Allen - Co-Founder & CSO twig** Why are there still so few commercialised Engineering Biology products?
Session 3 – Biofilms, Microbial Communities & Environmental Systems	
9:40	**Maria Magliulo – Natural History Museum** From Attachment to Adaptation: Exploring Biofilm Formation of *Acidithiobacillus ferrooxidans* on Pyrite
10:00	**James Croxford – University of Glasgow** Dynamics of SynBio and SynComs in environmental biofilms
10:20	**Zachary Thompson – Newcastle University** Spatio-temporal analysis of activated sludge emissions
10:40	**Lyuboslava Harkova – University of Southampton** Engineering biofilms for improved bioremediation
11:00	Q&A / Session Wrap-up
Flash Talks	
11:05	**Hannah Adams – University of Essex** Polycyclic aromatic hydrocarbon degradation pathways in *Cycloclasticus Sp.* TK8
11:10	**Yasir Akbar – Newcastle University** BaNeX: Bacterial Neutral sites prediction using multi-Omics: A Comprehensive Computational Framework for Predicting Neutral Integration Sites in Bacterial Genomes

11:15	**Giuliano Sting Pechar – University of York** Engineering plant-mediated nickel solubilisation in the rhizosphere
11:20	**Zahra Khomarbaghi – Durham University** Intracellular Metal Buffering as a Design Principle for Engineering Robust Microbial Cell Factories
11:25	**Muhammad Ejaz – Qatar University** Metagenomic and Biotechnological Characterization of Spore-Forming Bacteria from Arid Soils of Qatar
11:30	**Carla Spatola Rossi – Cranfield University** Origami paper microfluidic device for the detection of viable bacteria in water
Tea/Coffee break/Poster session 11:35 – 11:50	
Session 4 – Metals, Mining & Resource Recovery Biotechnology	
11:50	**Alex Marks – University of York** Engineering Temperate Biomass Hyperaccumulators: Understanding the Biological Mechanisms of Nickel Tolerance and Accumulation
12:10	**Anjali Vijay Prajapati – Swaminarayan University, Gujarat** Fungal-based biosorption: An eco-friendly strategy for heavy metal removal from contaminated water
12:30	**Elizabeth A. Watton – The University of Manchester** Understanding metal homeostasis in the metal-reducing bacterium *Shewanella oneidensis* towards enhanced metal biorecovery
12:50	Q&A / Session Wrap-up

Lunch break (13:00-14:00)	
Session 5 – Sustainable Biotechnology & Environmental Adaptation	
14:00	**Joseph Pennycook – University of Bristol** Evaluation of a photosynthetic chassis organism in response to long-term ecological challenges
14:20	**Maira Anam – Newcastle University** Impact of fluid flow on microbial community development in pilot-scale MEC
14:40	**Nick Dawson – Cranfield University** Microbial Interactions in Vermifilter Sanitation
15:00	**Magdalena A Howe – University of Southampton** Mining For Novel Plastic Degrading Enzymes in the Human Gut Microbiome
15:20	Q&A / Session Wrap-up
Tea/Coffee break (15:25 – 15:40)	
15:40- 15:50	Awards for best presentation
15:50 -16:00	**Closing Remarks** Prof. Frederic Coulon, EBIC Director
16:00	**Conference close – thank you all for joining us!**

Poster Presentations

ID	Name	Poster Title
#1	**James Bowbrick Smith** University of Surrey	Biorecovery of Gold Nanoparticles from Industrial Waste: Life Cycle and Techno-Economic Assessment of Scale-Up Pathways
#2	**Josephine Giard** Heriot-Watt University	Adaption to climate change in the rhizosphere across the millennia
#3	**Tatiana Spatola Rossi** Heriot-Watt University	Recombinant expression of rhamnolipid synthesis genes in Pseudomonas putida for biosurfactant production
#4	**Yasir Akbar** Newcastle University	BaNeX: Bacterial Neutral sites prediction using multi-Omics: A Comprehensive Computational Framework for Predicting Neutral Integration Sites in Bacterial Genomes
#5	**Hannah Adams** University of Essex	Polycyclic aromatic hydrocarbon degradation pathways in *Cycloclasticus Sp.* TK8
#6	**Juwon Samuel Afolayan** Nottingham Trent University	Engineered Mycelial Scaffolds with Tuneable Ultraviolet Protection, Wettability, Thermal Stability, and Spatial Mechanics
#7	**Yexin Feng** University of Southampton	Chemical-free production and in-situ product recovery (ISPR) of value-added chemicals from mixed culture anaerobic fermentation of organic waste streams
#8	**Yu Wang** Cranfield University	Understanding the CO2 impacts on mycelium: implications for circular bio-based materials
#9	**Giuliano Sting Pechar** University of York	Engineering plant-mediated nickel solubilisation in the rhizosphere
#10	**Somaya Ahmed** University of Southampton	Optimization of the Biotreatment of GTL Process Water Using *Pseudomonas aeruginosa* Immobilized in PVA Hydrogel
#11	**Zahra Khomarbaghi** Durham University	Intracellular Metal Buffering as a Design Principle for Engineering Robust Microbial Cell Factories

#12	**Merin Thyagu Pereira** University of Westminster	Engineering *Geobacillus* for High-Temperature Plastic (PET) Degradation via Fusion of PETase and MHETase Enzymes
#13	**Harry Maguire** University of East Anglia	Development of transformation systems for engineering a range of diverse environmental bacteria
#14	**Haydon Ross** University of Nottingham	Enzymatic Degradation of Polyethylene
#15	**Mohammed Rehmanji** University of Oxford	High-throughput phenotyping to engineer carbonate biominerals using *Sporosarcina pasteurii* system
#16	**Monika Steinke** University of Essex	In search of novel marine oil-degrading bacteria
#17	**Muhammad Ejaz** Qatar University	Metagenomic and Biotechnological Characterization of Spore-Forming Bacteria from Arid Soils of Qatar
#18	**Katharine Davis** University of York	Assessing ability of plants and microbes to establish vegetative cover and remove rare earth elements from African mine tailings and soils
#19	**Rebecca Morton** Heriot-Watt University	Bioinoculation of Plants using Plant-Growth Promoting Bacteria to Alleviate the Impact of Drought Stress.
#20	**Carla Spatola Rossi** Cranfield University	Origami paper microfluidic device for the detection of viable bacteria in water
#21	**Hamid Rehman** Yildiz Technical University	From Black Mass to Battery-Grade Metals: A Bioleaching Approach for Spent Lithium-Ion Battery Recycling

Abstracts – Session 1

Mahsa Baniasadi

Cranfield University, UK

Integrated Biological, Physical, and Chemical Approaches for Betaine Extraction from Salt-Stressed Algal Biomass.

Two high salinity resistant algal strains *Chlorella vulgaris* and *Spirulina platensis* were adapted to be grown at high salinity in order to bioaccumulate higher amount of betaine. A large scale set-up was developed for cultivation and harvesting of algal biomass. Series of process were applied for extraction betaine. Bioactive material extraction starts with microwave digestion to increase biomass porosity, followed by enzyme digestion and sonication to rupture biomass cell. Solvent extraction was further applied for precipitation and purification of proteins. As the last stage of purification ion exchange resins (Dowex 50W and Amberlite IR-120) were used to selectively adsorb betaine. Betain was recovered with crystallisation method after eluting betaine from Amberlite ion exchange resin. Betaine is a valuable product for the market, with several application in pharmaceutical and food industry. Pathways for betaine accumulation in algae and mechanisms to adapt to high salinity were investigated for further application of synthetic biology to improve process economy.

Heni Wang

Cranfield University, UK

Rapid and low-cost PFOA detection in drinking water by coupling engineered aptamers with DNA amplification.

Keywords: Biosensing, water quality monitoring, PFOA

Rapid and cost-effective monitoring of per- and polyfluoroalkyl substances (PFAS) remains a critical challenge in sustainable water management, given the stringent safety limit (500 ng/L set by EU). Conventional mass spectroscopy-based detection is expensive and rely on centralized facilities, highlighting the need for field-deployable sensors. Among the engineering biology-based rapid sensing approaches, aptamers are promising for PFAS detection due to their high specificity, stability and adaptability for individual PFAS.

In this study, aptamers were used to detect perfluorooctanoic acid (PFOA), coupled with isothermal DNA amplification for signal enhancement. Filtered water samples spiked with PFOA (0-200 µg/L) were added to a 20 µL reaction mixture containing aptamer, DNA polymerase, template DNA, fluorophore, and primer, followed by incubation at 30 °C. Upon aptamer-PFOA interaction, a blocked primer is released, initiating DNA amplification. This produced a linear fluorescence response over 0-40 µg/L, with a detection limit of ~1 µg/L. The assay enabled selective detection of PFOA over PFOS within 30 minutes in a single-pot reaction, with fluorescence or colorimetric readouts.

This platform shows a promising low-cost portable solution for PFAS monitoring, with ongoing work focused on enhancing specificity/sensitivity through additional peptide-based recognition elements and integrating the system into easy-readout platforms for real-world applications.

Evieva F. Ogbara

Liverpool John Moores University, UK

Re-evaluating Biochar-Based Remediation: Disentangling Sorption and Biodegradation Controls on PAH Attenuation in Soil Systems.

Keywords: Biochar sorption, soil PAH remediation, microbial ecology & environmental biotechnology

Biochar is widely promoted for polycyclic aromatic hydrocarbon (PAH) remediation in soils; however, the relative roles of sorption-driven sequestration and microbial degradation remain unclear. This study investigates the fate of naphthalene in biochar-amended soils using FTIR spectroscopy, GC–MS, and 16S rRNA microbial profiling to distinguish physicochemical redistribution from biological transformation. Biochar amendment increased soil pH from 5–6 to 7–8, accompanied by shifts in microbial communities, including enrichment of Actinobacteria and Firmicutes and reduced relative abundance of reported PAH-degrading genera such as Burkholderia, *Novosphingobium*, and *Comamonas*. GC–MS and FTIR analyses indicated reduced extractable naphthalene, consistent with sorption and sequestration within biochar–soil matrices as dominant attenuation processes. Collectively, the results indicate that apparent reductions in extractable PAH concentrations in biochar-amended soils may be strongly influenced by physicochemical immobilisation processes, with limited evidence of enhanced microbial mineralisation under the conditions studied. These findings emphasise the importance of distinguishing between contaminant removal and true degradation when evaluating biochar-based remediation strategies and highlight the need for integrated chemical–biological approaches in environmental biotechnology assessments. This study aligns with UN Sustainable Development Goals 6, 12, 13, and 15.

Yasmin Meeda

Cranfield University, UK

Engineering biology for metaldehyde biodegradation in drinking water using *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 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. *Acinetobacter calcoaceticus E1* has 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 approach can then be scaled to see the potential for use in water treatment.

Abstracts – Session 2

Amanda Hopes

University of East Anglia, UK

Generating mutant strains for EBIC: Progress on development of a standardised cloning and transformation system to generate markerless mutants for a broad range of species and applications.

Keywords: Golden-gate cloning, mutant generation, engineering biology

As the central hub for generating mutant strains, we work with multiple groups across the consortium and dozens of species to create strains for a wide range of applications including bioremediation, wastewater management and biotechnology. Therefore, we need a high throughput, standardised cloning system and transformation method that can be applied to a broad range of species.

Our cloning strategy uses custom made, Golden-gate compatible suicide plasmids and includes multiple options for antibiotics, origins of replication for cloning, and promoters to drive sacB for counterselection to generate unmarked strains. Plasmid construction with our backbones appears to be highly efficient with ~90% cloning success rate and is compatible with high throughput production. We have created unmarked mutants for Gram negative, Gram positive and acid-fast bacteria.

Many of our strains do not have established transformation systems, therefore, we have developed a standardised transformation protocol that tests different parameters and conditions for each species. We are trialling a plasmid cocktail to test transformation, with multiple origins of replication at once, using Cultivarium's POSSUM kit.

We are currently using our strategy to knockout genes, test 'landing pads' for gene insertion, and introduce heterologous gene cassettes and barcodes for multiple species and projects across EBIC.

Daniel Evans

UK National Measurement Laboratory at LGC, UK

Digital PCR methods to support tracking of engineered organisms in environments.

Keywords: Digital PCR, engineered cells, biosecurity

The application of engineered cells offers a valuable tool in a variety of potential functions, including bio-remediations where modified organisms may be deployed into ecosystems to restore environments. However, adoption of these technologies for environmental purposes is limited due to regulations and a lack of traceability systems to ensure safety. The application of synthetic genomic barcodes (SGBs) to allow for identification and tracking of engineered cells offers an avenue to improve biosecurity and increase trust.

A key hurdle to the use of SGBs is the detection and monitoring of the SGBs once modified organisms are released to the environment and well as the stability of the SGB through multiple generations after environmental exposure.

Utilising digital PCR, an absolute quantification approach, we sought to develop a framework to support development of engineered cells and SBGs. This allowed us to identify and quantify the presence of SGBs

and their retention within the engineered cells. This technique can be further applied for monitoring functional modifications at trace level detection, allowing evaluation of real-world performance and biosecurity of engineered cells for environments. The incorporation of such an approach alongside SGBs should aid in overcoming regulatory hurdles in applying engineering biology in environments.

Joshua Loh

Newcastle University, UK

BaNeX-guided identification and validation of neutral genomic integration sites for stable engineering biology applications.

Stable genomic integration is essential for engineering robust microbial chassis, but experimentally validated neutral sites for genomic insertion remain limited for many non-model organisms. BaNeX is a reproducible prediction framework designed to identify candidate neutral sites by combining genome annotation with filtering based on genomic context and multi-omics features. Its goal is to prioritise loci that are unlikely to disrupt host fitness, function or phenotype following DNA insertion.

This work presents a cross-species validation strategy for BaNeX-predicted neutral sites in three biotechnologically relevant microbial hosts: *Corynebacterium glutamicum*, *Alcanivorax borkumensis* and *Picosynechococcus* PCC 11901. Validation is centred on the integration of DNA barcodes and reporter constructs to assess insertion stability, fitness effects and expression behaviour across loci. Preliminary work in *C. glutamicum* indicates that BaNeX-selected neutral sites can support stable barcode integration with minimal impact on host phenotype. In contrast, barcode insertion in *A. borkumensis* at a non-BaNeX gene knockout locus resulted in unstable barcodes, highlighting the importance of rational neutral-site selection. Work in *Picosynechococcus* PCC 11901 is ongoing and will extend this framework to a cyanobacterial chassis. Together, these results benchmark BaNeX predictions and support more reliable genome engineering across diverse microbial hosts.

Prabhakar L. Srivastava

Bangor University

Neutral Site-Driven Genome Engineering of *Alcanivorax borkumensis* to Expand Substrate Scope for Enhanced Bioremediation.

Keywords: Genome engineering, hydrocarbon, bioremediation

Hydrocarbon pollution in marine environments is a major global concern, with an estimated 700-800 million tons released annually through natural seeps, petrochemical discharges, and biological activity, causing long-term ecological damage. To address this, we aim to engineer the marine hydrocarbon-degrading bacterium *Alcanivorax borkumensis* SK2 to enhance its bioremediation capacity via targeted genome modification. *A. borkumensis* degrades linear and branched hydrocarbons (C6-C24), with alkane monooxygenases (AbAlkB1) and cytochrome P450 enzymes catalysing the initial oxidation of aliphatic substrates. To identify suitable genomic loci for engineering, we performed transcriptomic analysis of *A. borkumensis* grown on hexadecane (C16) and pyruvate. This enabled the selection of lowly expressed, non-essential genes as candidate neutral integration sites, as well as promoters associated with high expression under hydrocarbon growth conditions. These neutral sites provide a platform for stable insertion of heterologous constructs. By replacing them with genes encoding engineered AlkB1 variants, dehalogenases, surfactant biosynthesis pathways, and other enzymes under diverse promoter systems, we aim to optimize expression and expand substrate scope, including recalcitrant fluorinated

compounds. Overall, this work establishes a modular genome-scale engineering strategy in *A. borkumensis*, enabling the development of strains with enhanced and broadened hydrocarbon degradation capabilities for improved bioremediation performance.

Abstracts – Session 3

Maria Magliulo

Natural History Museum, UK

From Attachment to Adaptation: Exploring Biofilm Formation of *Acidithiobacillus ferrooxidans* on Pyrite.

Keywords: Biofilm, bioleaching, proteomics

Bioleaching, the process that uses microorganisms to recover metals from metal sulfide ores, is an interfacial process, and biofilm formation is crucial to establish and maintain contact with the ore. In this study, we used SEM images and quantitative proteomics to resolve the progression of *Acidithiobacillus ferrooxidans* from early stage (10-day) to long-term (38-day) biofilm formation on pyrite. SEM images showed initial extracellular polymeric substances formation during the early stage, suggesting that early metabolic activities are devoted to the establishment of biofilm structures. These structures are consolidated at 38 days, showing bacterial cells embedded in a more complex biofilm structure. Global proteome analysis revealed that growth on pyrite mineral was characterized by a reduction of proteins involved in DNA replication and protein translation. In contrast, proteins associated with membrane structure, lipid metabolism, transport systems, and cellular homeostasis were more abundant in mineral-grown cells. We also observed increase abundance of metal efflux systems, proton pumps and stress response proteins, indicating sustained adaptation to metal-rich, acidic and oxidative conditions at the mineral interface. Our results indicates that growth on pyrite focuses on maintenance of cellular structures and stress resilience, with cells reallocating resources from proliferation to adaptation and survival to extreme environments.

James Croxford

University of Glasgow, UK

Dynamics of SynBio and SynComs in environmental biofilms.

Keywords: Synthetic biology, natural communities, environmental biofilms

Synthetic biology (SynBio) offers tools to engineer microorganisms for environmental applications. However, how engineered strains and synthetic communities (SynComs) establish and persist within natural microbial communities after scale-up remains poorly understood. A review undertaken within this project highlights the limited nature of studies deploying GMO strains in real-world community contexts.

Initial work used E. coli BL21 carrying a c-di-GMP overproduction construct to characterise growth and biofilm formation across a nutrient gradient. A dual-plasmid GMO strain failed to grow below 2x R2A, despite WT BL21 growing down to 0.125x R2A, demonstrating that even minimal genetic load substantially reduces fitness under nutrient limitation. Preliminary experiments in river water showed no detectable planktonic growth of the WT or GMO strain. However, nutrient supplementation increased biofilm formation across WT, GMO, and native community samples, indicating that nutrient availability is a key determinant of GMO deployability.

Future work will extend beyond this E. coli model to environmental isolates with chromosomally-integrated constructs, testing strains and SynComs across environmental matrices including river water

and wastewater, with increasing genetic load through addition of PET-degradation genes. This work aims to link genetic load, nutrient context, and community composition to SynBio performance in realistic environmental settings.

Zachary Thompson

Newcastle University, UK

Spatio-temporal analysis of activated sludge emissions.

Keywords: Greenhouse gases, activated sludge, bio-informatics

This presentation shows spatio-temporal analysis of emissions from activated sludge (AS) and primary settlement tanks (PSTs) coupled to bio-informatics. Work conducted at a carbonaceous plant found a low AS N_2O emission factor (EF) of 0.0154% kg N2O-N / kg influent N with sporadic peaks, a shifting microbial community, and positive correlations between temperature and CH_4 emissions. This EF reflects low ammonia-oxidiser counts and peaks may stem from transient facultative denitrification. CH_4-producers, but not consumers, were consistently detected. CH4 emissions varied four-fold spatially in both processes, decreased along the AS lanes due to stripping and discrepancies between parallel lanes which may reflect diffuser fouling. Overall, both temporal and spatial factors should be considered to reduce bias while flow and concentration measures should always be coupled, particularly in ventilated PSTs. Analysis of spatio-temporal data coupled to bio-informatics at a nitrifying AS process is ongoing, aiming to link gene expression to GHG transformations. AS microcosms will explore carbon transformations including if significant methanogenesis occurs in aerobic AS along with the effect of shock loads of nitrite and nitrate.

Lyuboslava Harkova

University of Southampton, UK

Engineering biofilms for improved bioremediation.

Keywords: biofilms, plastic degradation, pollutants removal

Millions of tons of plastic waste are generated annually with current recycling rates insufficient to meet the demands, resulting in large proportions of microplastic pollution in the environment. Bioremediation provides a sustainable approach to tackle this global issue. However, current strategies rely on the modifications of single microorganisms for production and purification of enzymes, which is costly and nonrecyclable. A solution for improving bioremediation is utilising the natural ability of microbes to form communities which can facilitate not only the enzyme production, but also its targeted delivery. Utilising approaches for protein expression both from plasmids and chromosomally inserted genes, we demonstrate that engineering biofilms by manipulating second messenger levels can improve plastic degradation. Additionally, we show that enhanced biofilm levels can be used for capturing antibiotics, which are commonly found in wastewater and contribute to another global issue - the antimicrobial resistance. Biofilms increase microbial tolerance to stresses present in the environment and further investigation of such synthetic communities has the potential to enhance the bioremediation of environmental pollutants.

Abstracts – Session 4

Alex Marks

University of York, UK

Engineering Temperate Biomass Hyperaccumulators: Understanding the Biological Mechanisms of Nickel Tolerance and Accumulation.

Keywords: Metals, plants, remediation

Intensifying global industrialization and the rapid transition to green energy have driven an unprecedented demand for transition metals. However, conventional mining and processing methods cause severe environmental pollution. Phytomining and phytoremediation offer transformative, nature-based solutions for landscape restoration and the circular recovery of technology-critical elements. Nickel (Ni) presents a unique challenge: while it is an essential micronutrient for plant metabolism, it induces acute phytotoxicity at elevated concentrations through mis-metalation and oxidative stress.

This study employs high-throughput RNA-Seq and comparative bioinformatics to map the complex transcriptional landscapes of Ni stress in the model organism Arabidopsis thaliana and high-biomass Salix (willow) cultivars selected for divergent Ni-tolerance phenotypes. Using differential expression analysis (DESeq2) and Gene Ontology (GO) enrichment, we characterize the spatial coordination of nickel homeostasis. Our analysis focuses on identifying key differentially expressed genes (DEGs), including candidate transporters such as IRT1, and evaluating the metabolic role of chelators like nicotianamine in sequestering free Ni ions.

Results identify distinct transcriptomic signatures between root and aerial tissues, highlighting key biological processes involved in metal homeostasis and stress response. These findings contribute to the development of high-biomass, temperate Ni-hyperaccumulators for environmental decontamination and an additional, sustainable, supply of Ni for the clean energy transition.

Anjali Vijay Prajapati

Swaminarayan University, Gujarat, India

Fungal-based biosorption: An eco-friendly strategy for heavy metal removal from contaminated water.

Keywords: Fungal biosorbent, industrial effluent, sustainable remediation

Fungal-based adsorbents are gaining widespread attention as an eco-friendly and cost-effective solution for removing heavy metals (HMs), particularly in dilute solutions where synthetic resins are ineffective. The goal of this study was to develop a fungal biosorbent for the removal of HMs from wastewater. For this, *Curvularia lunata*, AD6 strain was isolated from a municipal solid waste and evaluated for its capacity to remove various HMs in non-competitive and competitive systems where the removal efficiency order was Cr > Pb > Cd > Ni > Cu in 2 h. The maximum metal removal capacity were ranged from 3.83 to 6.24 mg/g under optimized conditions. The role of various functional groups and surface chemistry of the fungal biosorbent was determined by FTIR and SEM. Furthermore, the thermodynamic parameters proved that the biosorption process was endothermic, spontaneous and feasible. The adsorption equilibrium isotherms and kinetic modelling studies were significant proven a multi stage physisorption and chemisorption. The biosorbent showed a significant removal of Ni and Cu when

applied to the electroplating industrial effluent and metallic leachate in a laboratory scale up study. These findings indicated that the fungal sorbent AD6 possesses potential efficiency for the removal of various HMs from contaminated water.

Elizabeth A. Watton

The University of Manchester, UK

Understanding metal homeostasis in the metal-reducing bacterium *Shewanella oneidensis* towards enhanced metal biorecovery.

Keywords: Environmental biotechnology, intracellular metal homeostasis, metal biorecovery

The growing demand for critical metals in clean energy technologies poses significant challenges due to their scarcity and environmental damage caused by their extraction. The use of bacteria to biorecover metals from unconventional resources, such as electronic waste, offers green solutions to these challenges whilst promoting a circular economy by producing high-value metallic nanoparticles. Metal-reducing bacterium *Shewanella oneidensis* can recover a range of waste metals and deposit these as intracellular nanoparticles. However, the mechanisms for these reactions and metal homeostasis for this organism is not fully understood. The toxicity of electronic waste feedstocks also poses a challenge for biorecovery approaches, with metal toxicity limiting metal biorecovery capacity. To enhance the selective biorecovery of critical metals by *S. oneidensis*, we are investigating the genes and pathways underlying metal tolerance, with a focus on copper and gold. We have drawn together findings generated from TraDIS-Xpress transposon mutagenesis experiments, transcriptomic studies and cell culture-based assays to predict systems for subsequent characterisation. Our work on metal biorecovery optimisation will be presented alongside key insights into natural metal tolerance processes that have informed our molecular engineering strategies for environmental biotechnology applications.

Abstracts – Session 5

Joseph Pennycook

University of Bristol, UK

Evaluation of a photosynthetic chassis organism in response to long-term ecological challenges.

Keywords: Cyanobacteria, ecology, evolution

Photosynthetic microbes are exciting tools for engineering biologists, able to channel sunlight and CO2 into the production of valuable organic materials or into waste treatment and environmental restoration processes. Rapidly growing organisms such as the cyanobacterium *Synechococcus sp*. PCC11901 are especially promising. However, ecological stress factors such as competition, predation, and nutrient limitation could interfere with the effective function of these organisms in complex natural environments or in industrial settings where maintaining optimal, sterile conditions may not be viable. For long-term projects, ecological context will be particularly important, since selection over time could lead to the loss or change of engineered traits. Using a novel culture system, we have grown *Synechococcus sp*. PCC11901 for 14 weeks within environments highlighting the contrast between laboratory and natural conditions on a range of biotic and abiotic axes. We found distinct changes to the growth rate, pigmentation, and biofilm morphology of cultures depending on the environment, and we are using whole-genome sequencing with replicate populations to explore the extent to which evolution in these systems is stochastic or predictable. Evaluating the long-term performance of engineered organisms in the correct ecological context will be essential to fulfilling the potential of photosynthetic microbes in engineering biology.

Maira Anam

Newcastle University, UK

Impact of fluid flow on microbial community development in pilot-scale MEC.

Microbial electrolysis cells (MEC) are bioelectrochemical reactors that exploit electrochemically active bacteria to convert organic matter into value-added by-products by applying potential. This technology offers a promising approach for resource recovery and wastewater treatment. Despite the promising results with lab-scale systems, pilot-scale MEC struggles to reproduce the same production rate at large volume, as much is unknown about real-world complexities. This study attempts to reduce the start-up period of MEC and improve the overall system efficiency by accelerating biofilm formation. In this study, three pilot-scale MEC (1m3) fed with sludge liquor were operated under different stirring conditions: static, 200 rpm, and 600 rpm, to understand the impact of stirring conditions on biofilm formation at the pilot scale. The diversity of biofilm composition was further analysed through high-throughput sequencing, comparing microbial communities on electrode surfaces facing and opposite the stirring motor. The result from this study will show how stirring impacts fluid flow around the anode, ultimately governing the substrate availability to biofilm by preventing mass transfer limitations. These findings highlight the complex interplay between stirring-induced hydrodynamics and biofilm growth, emphasising the need for further pilot-scale studies to optimise operating conditions and bridge the gap between laboratory and real-world MEC applications.

Nick Dawson

Cranfield University, UK

Microbial Interactions in Vermifilter Sanitation.

Keywords: Vermifiltration, pathogen surveillance, bioinformatics

Earthworms are an effective biocatalyst for both wastewater and waste management. They are widely applied from household scale in the Tiger worm toilets to being the primary mechanism driving small, decentralised sewage treatment works or sludge stabilisation. They provide an incredibly effective eco-friendly solution to decentralised sanitation, reducing greenhouse gases, and allowing valuable resource recovery. However, being a relatively novel approach, much of the fundamental science is still unknown, particularly around the microbial interactions, including mechanisms to pathogen removal.

To address this, I have applied untargeted long-read metagenomics to give detailed insights into the driving processes of the vermifilter. This involves modelling the many complex microbial interactions throughout the system from the sewage input being composted, through the worms' gut to the final water effluent. Supplemented by applying standardised measures of water pollution such as COD and ammonia, reduction of sludge volume, and confirming system efficacy. Thus, providing important evidence of reduction in many pathogens, including some rarely screened for, as well as functional activities of other organisms in relation to nutrient removal. The outcome should aid in the operation or bioengineering improvements in design parameters such as earthworm selectivity and tailoring the ecosystem to promote beneficial micro-organisms.

Magdalena A Howe

University of Southampton, UK

Mining For Novel Plastic Degrading Enzymes in the Human Gut Microbiome.

Keywords: Plastic, metagenomics, gut microbiome

400 million tonnes of plastic were produced globally in 2025, with annual projections expected to increase to 590 million tonnes by 2050. Specifically, in our oceans, plastic waste is expected to increase by 11 million tonnes annually. This accumulation of plastic waste disrupts ecosystems, impacts wildlife and importantly, affects human health. Current recycling processes are inadequate because they are financially inefficient, requiring high energy consumption and reducing the plastic quality with each cycle. Enzymatic degradation is a more sustainable approach, promoting a circular economy and reducing the reliance on raw materials. Although several plastic-degrading enzymes have been discovered in environmental microorganisms, these are inefficient, prohibiting their development as part of large-scale processes. Microplastics have been found in the human gut which may enrich for bacteria with the enzymatic capacity to break them down. Here, we use metagenomic analysis to mine for novel plastic-degrading enzymes in the gut microbiome of healthy individuals and those with Inflammatory Bowel Disease, targeting a range of plastics, including those where the arsenal of enzymes is limited. The gut microbiome may represent a novel, unexplored reservoir of plastic degrading enzymes which could be repurposed and further developed to tackle the plastic waste crisis.

Abstracts – Posters

James Bowbrick Smith

University of Surrey, UK

Biorecovery of Gold Nanoparticles from Industrial Waste: Life Cycle and Techno-Economic Assessment of Scale-Up Pathways.

Keywords: Biorecovery, life cycle assessment, techno-economic analysis

Gold-containing waste is an increasingly important environmental challenge but also represents a valuable resource. The bacterium *Shewanella oneidensis* MR-1 can synthesise gold nanoparticles (AuNPs) from waste streams, offering an environmental biotechnology route for resource recovery and circular economy applications. Using authentic industrial waste sourced from Mint Innovation, high AuNP yields have been achieved at laboratory scale.

This research evaluates the pathway to industrial scale-up of this biorecovery technology using Life Cycle Assessment (LCA) and Techno-Economic Analysis (TEA). LCA is applied to compare the current laboratory process, a proposed industrial-scale biorecovery process and existing AuNP production routes. LCA results suggest the proposed industrial biorecovery process reduces global warming potential by approximately 65% relative to primary mining, while also improving over the laboratory configuration.

TEA is used to estimate a break-even selling price for biorecovered AuNPs. At high production scales, this approaches the gold commodity price and suggests AuNPs could be produced at approximately 1.6% of their nanoparticle product selling price.

Overall, this research indicates that AuNP biorecovery is both environmentally advantageous and commercially promising. Key operational factors such as anaerobic reactor conditions and continuous flow processing requirements are highlighted as areas to prioritise as the technology matures.

Josephine Giard

Heriot-Watt University, UK

Adaption to climate change in the rhizosphere across the millennia.

Keywords: Climate change, plant-growth promoting bacteria, rhizosphere

Climate change brings severe agricultural challenges as crops are exposed to increased levels of both abiotic and biotic stresses. By enriching soils with bacteria possessing plant growth-promoting (PGP) characteristics, drought resilience in plants can be improved. As partners of the TOLERATE EU project (https://tolerate-eu-project.com/), we aim to expand the scope of available PGP bacteria by expressing ancient genes from past geological times that have already experienced changing climate. To achieve this, ancient DNA metagenomes from Arctic soils, spanning approximately 8,000 to 600,000 years before present, were reassembled, annotated, and screened for genes encoding potential stress-adaptive traits. This led to the identification of >130 paleo-phasins, small polyhydroxyalkanoate granule-associated proteins. By assessing their sequence, structure and age diversity, a subset of paleo-phasins was selected. Subsequently, an E. coli chassis was engineered for their over-expression resulting in the

production and purification of two paleo-phasins at scale as well as greater solvent stress tolerance in the phasin-producing E. coli. Additionally, three *Pseudomonas* strains were engineered to constitutively express paleo-phasins increasing their osmotic as well as their solvent stress tolerance. We are currently assessing how the engineered *Pseudomonas* strains compare to their wild-type counterparts during bioaugmentation studies seeking to identify bacteria suitable for agricultural applications.

Yasir Akbar

Newcastle University, UK

BaNeX: Bacterial Neutral sites prediction using multi-Omics: A Comprehensive Computational Framework for Predicting Neutral Integration Sites in Bacterial Genomes.

Keywords: Neutral sites, Genomic safe harbors, Integration sites

The identification of genomic loci that enable safe and stable integration remains a central challenge in bacterial genome engineering. The existing tools are very limited in number and in scope, focus primarily on single type of neutral site and application. A coherent and standardized pipeline is therefore needed. Here, we present BaNeX, a modular containerized pipeline for comprehensive identification candidate integration sites in bacterial genomes. BaNeX integrates multiple complementary modules, which provide good balance between neutrality and stability. The intergenic module identifies regions based on gene orientation and applies stringent filtering to remove sections with regulatory elements and regions with functional evidence from multi-omics data. Expanding beyond conventional approaches, the genic module identifies candidate loci within coding regions that are less likely to disrupt host physiology, including genes with low expression levels, low protein–protein interaction (PPI) connectivity, pseudogenization and absence of important topological domains or annotated essentiality. A dedicated insertion module evaluates all candidates using features such as GC content, repeats etc. to "compatibilise" loci selection with recombineering tools. Each module generates structured reporting files with all results and ranked sites according to calculated scores. BaNeX provides a standardized and scalable framework for microbial neutral site selection and is currently undergoing external validation and database extension.

Hannah Adams

University of Essex, UK

Polycyclic aromatic hydrocarbon degradation pathways in *Cycloclasticus Sp.* TK8.

Keywords: Hydrocarbons, degradation, cycloclasticus

Polycyclic aromatic hydrocarbons (PAHs) are widespread in the environment and are carcinogenic compounds which tend to accumulate in food chains due to their low bioavailability and poor biodegradability.

Bacteria play an important role in the removal of PAHs from polluted environments (oil spills for example). In marine environments in particular, *Cycloclasticus* is one of the most prevalent PAH-degrading bacterial

genera. However, little is known regarding the degradation mechanisms for PAHs by *Cycloclasticus* strains.

We have used a combination of LC-MS/MS shotgun proteomics and transcriptomics to identify proteins involved in aerobic PAH degradation during growth on naphthalene and phenanthrene of *Cycloclastics Sp* TK8 (DSM 27168).

These results will help to elucidate the pathways of PAH-degradation, an essential first step in developing bioremediation strategies for these harmful chemicals.

Juwon Samuel Afolayan

Nottingham Trent University, UK

Engineered Mycelial Scaffolds with Tuneable Ultraviolet Protection, Wettability, Thermal Stability, and Spatial Mechanics

Keywords: Biomaterial, multifunctionality, spatial mechanics

This study presents a comprehensive demonstration of Mucorales-derived fungal systems as tuneable, multifunctional scaffolds for sustainable material applications. Using *Mucor rouxii* and *Rhizopus oryzae*, we addressed structural and mechanical inhomogeneity across the mycelial mat, a persistent bottleneck in applications of mycelium-based materials. We developed a spatial evaluation system to map localized variations in thickness, strength, elasticity, and stiffness, revealing that radial growth produces regions of differing hyphal maturity and mechanical behavior. These insights informed the optimization of post-growth processing strategies, and we found that conventional freezing at -44 °C followed by freeze-drying is the most effective method for preserving a consolidated, mechanically consistent structure (compared with commonly employed preparation routes). The engineered mycelial scaffolds were subsequently functionalized with titania (TiO2) nanoparticles, yielding uniform mineral integration. This functionalization delayed thermal degradation by approximately 100 °C, significantly increased surface hydrophobicity (water contact angles > 130°), and enhanced UV-B blocking by up to 70% relative to native mycelia. Comparative studies with melanin-rich fungi, including *Aspergillus niger*, demonstrated further enhancement of ultraviolet shielding, highlighting routes for future optimization. Overall, this work establishes a foundational framework for tuning biological growth, spatial heterogeneity, and post-growth processing to engineer high-performance, biodegradable materials for smart coatings and protective applications.

Yexin Feng

University of Southampton, UK

Chemical-free production and in-situ product recovery (ISPR) of value-added chemicals from mixed culture anaerobic fermentation of organic waste streams.

Keywords: Anaerobic Fermentation, In-situ Product Recovery, Electrochemical Membrane System

Mixed-culture anaerobic fermentation generates a variety of products from organic waste streams, including fatty acids and ammonia. Effective recovery of fatty acids and ammonia usually requires large amounts of mineral-based chemicals for pH adjustment. This study investigates the use of an electrochemical membrane system to achieve pH adjustment and ion migration for simultaneous, continuous recovery of fatty acids and ammonia, minimising or negating the need for additional chemicals.

Initial experiments using synthetic ammonium acetate solutions in both anode and cathode chambers demonstrated that pH reduction in anode from 6.8 to 4.2 and pH increase in cathode from 6.8 to 9.8 was achievable in a batch process. Simultaneously, 69% of the ammonia originally in the anode migrated to the cathode, and 41% of the fatty acids originally in the cathode migrated to the anode, further facilitating recovery.

Future research will extend the system to complex fermentation broths and integrate membrane technology for selective recovery of medium-chain fatty acids, with the intention of recycling short-chain fatty acids back to the fermenter to promote chain elongation and achieve continuous medium-chain fatty acid production, separation, and recovery.

Yu Wang

Cranfield University, UK

Understanding the CO2 impacts on mycelium: implications for circular bio-based materials.

Keywords: Mycelium-based materials, Co2 concentrations, growth rate

The development of mycelium-based materials has emerged as a promising pathway toward biodegradable, sustainable, and low-carbon alternatives across a range of applications. However, recent research still lacks a fundamental understanding of how environmental conditions affect the growth patterns of the fungi, which may influence the performance of the final products. In this study, we systematically investigated the effects of the CO2 levels on the development of aerial hyphae in various fungal species. We quantified the influence of CO2 concentration on the radial growth rates, water content of the mycelium mats, dry weight of the biomass, and the consistency of the thickness. Our results showed that rising the CO2 level resulted in a faster colonization of some tested fungal species during the cultivation, whilst other species was not sensitive to CO2 concentrations and had overlapped growth curves. The water content of mycelium mats of most tested species was not affected by different CO2 concentrations. In addition, high CO2 conditions promoted more homogeneous development of mycelium mats. This work provides valuable insights into how CO2 concentrations influence the growth rate of different fungal species and can inform future research aiming at optimising fungal colonisation on various substrates.

Giuliano Sting Pechar

University of York, UK

Engineering plant-mediated nickel solubilisation in the rhizosphere.

Keywords: Phytoremediation, phytomining, genetic engineering

Metals such as nickel, are essential for developing technologies; however, their mining has significant environmental impacts, and their concentrations are generally low for economic extraction through traditional mining. Plant based remediation and recovery approaches could restore lands and recover technology critical metals, with genetic engineering and synthetic biology presenting timely opportunities to enhance these natural capabilities.

Metal uptake by plants is limited by the solubilisation into metals ions. Cyanide has been shown to selectively solubilise metals in the rhizosphere. This work focuses on enhancing metal uptake by engineering the cyanide biosynthetic pathway in Arabidopsis root hairs. We have generated constructs to express the two multifunctional P450 and the beta-glucosyltransferase that compose the pathway, with the aim of producing a cyanoglucoside that is stored in the vacuoles of root hair cells.

Using fluorescent tagging and confocal microscopy, we have demonstrated the root hair-specific localisation of the heterologous proteins in our Arabidopsis transgenic lines, and we are currently determining the production of hydrogen cyanide and his intermediates. We expect, upon damage, the cyanoglycoside to be enzymatically cleaved, releasing the cyanide into the rhizosphere for the solubilisation of target metals for plant uptake.

Somaya Ahmed

University of Southampton, UK

Optimization of the Biotreatment of GTL Process Water Using *Pseudomonas aeruginosa* Immobilized in PVA Hydrogel.

Keywords: Industrial wastewater, biodegradation, spouted bed bioreactor (SBBR)

Gas-to-liquid (GTL) process water is a major by-product of the Fischer-Tropsch reaction and contains high concentrations of oxygenated organics, including alcohols, aldehydes, and ketones, which contribute significantly to chemical oxygen demand (COD). This study investigates the optimisation of biotreatment of GTL process water using Pseudomonas aeruginosa immobilised in a polyvinyl alcohol (PVA) hydrogel.

Batch biodegradation experiments were conducted in a spouted-bed bioreactor, and response surface methodology was used to evaluate the effects of initial COD concentration (1000–3000 mg/L), pH (5–8), and PVA volume fraction (20–30%) on COD reduction. The optimised conditions were found at an initial COD of 2595 mg/L, pH 7.3, and PVA content of 27%, achieving a maximum COD removal of 89%, closely matching the model prediction.

Continuous operation under optimal conditions demonstrated stable performance, with COD removal increasing with aeration and responding sensitively yet recoverably to changes in liquid flow rate. These results confirm the robustness and scalability of the immobilised bioreactor system, highlighting its potential for large-scale GTL wastewater treatment applications.

Zahra Khomarbaghi

Durham University, UK

Intracellular Metal Buffering as a Design Principle for Engineering Robust Microbial Cell Factories.

Keywords: Metal homeostasis, intracellular buffering, metabolic engineering

Microbial cell factories require metals to function, with up to half of all enzymes depending on metal cofactors for activity. One mechanism by which cells control metal availability is intracellular buffering, where metabolites, eg amino acids, bind metals to create a thermodynamic competition that reduces mismetalation. However, mismatches between metal availability and cellular demand can arise from variations in feedstock composition and affect correct metalation of host or heterologously expressed enzymes.

Here, we describe an approach to engineer Escherichia coli strains with altered cytosolic metal availabilities for a range of physiologically and environmentally relevant metals (Mn, Fe, Co, Ni, Cu, Zn, Au, Pd). Our approach involves targeted genetic modifications to amino acid biosynthesis pathways that alter metabolite levels and change buffered metal availability. Using a combination of growth assays and transcriptional responses of intracellular metal sensors as functional readouts, we assess how these perturbations influence cellular responses to metal stress focusing on Ni as a model metal. Changes in metabolite levels within physiologically relevant ranges are shown significantly alter both metal tolerance and cytosolic availability. We propose that intracellular buffering represents an underexplored but tractable target for engineering and establish a framework for designing microbial chassis capable of operating robustly in variable and metal-rich environments, including the use of metal-contaminated waste streams.

Merin Thyagu Pereira

University of Westminster, UK

Engineering *Geobacillus* for High-Temperature Plastic (PET) Degradation via Fusion of PETase and MHETase Enzymes.

Keywords: PET degradation, thermophilic biotechnology, enzyme fusion

Plastics are indispensable materials due to their versatility and durability; however, these same properties contribute to their persistence in the environment and growing waste management challenges. Current end-of-life strategies—landfilling, incineration, and mechanical recycling—remain insufficient for addressing the accumulation of recalcitrant polymers. In particular, poly(ethylene terephthalate) (PET) resists degradation and fragments into microplastics, posing significant ecological and human health risks. Within the context of Engineering Biology solutions, biodegradation using recombinant strains could be a promising alternative for PET degradation.

We are exploring a thermophilic biocatalytic strategy for PET degradation through the engineering of *Geobacillus spp*. to express a fused PETase–MHETase enzyme derived from *Ideonella sakaiensis*. Operating at elevated temperatures near PET's glass transition (~70 °C) is expected to enhance polymer chain mobility and enzymatic accessibility, thereby improving hydrolysis efficiency. The performance of the engineered system is evaluated using multiple criteria, including PET weight loss, changes in surface chemistry (FTIR), metabolite production, and surface morphology (SEM).

Our findings will demonstrate the potential of *Geobacillus spp*. as a whole-cell thermophilic biocatalyst capable of simultaneous enzyme production and PET degradation, overcoming limitations associated with mesophilic systems and ex situ enzyme application.

Harry Maguire

University of East Anglia, UK

Development of transformation systems for engineering a range of diverse environmental bacteria

Keywords: Mutants, transformations, bacteria

The Environmental Biotechnology Innovation Centre (EBIC) is a multi-university consortium aiming to utilise engineered microbes for environmental solutions. As the main hub for bacterial strain production within the EBIC, our group is engineering dozens of species for biotechnological applications. Potential deployment of strains in the environment is dependent on developing markerless strains lacking antibiotic resistance cassettes.

Key to EBIC is development of high-throughput systems that can be used in an evolutionary diverse range of bacteria. We have created bespoke backbone constructs for use with Golden-Gate cloning, compatible with a high-throughput, efficient, standardised strategy. In conjunction, we have developed successful electroporation and conjugation methods for multiple species by altering parameters such as cell preparation, utilising cell weaking agents, adding enzymes to protect plasmids from endonuclease activity, and enhanced recovery of cells through supplementing recovery media with DMSO.

This has resulted in systems for genetic manipulation of 15 species, with over 25 species currently in the pipeline for testing. This platform provides optimised systems for transforming any new bacterial species which will aid not just their use in biotechnology but understanding their role in the environment and biogeochemical cycles. This work will be beneficial to the wider bacterial genomics community.

Haydon Ross

University of Nottingham, UK

Enzymatic Degradation of Polyethylene.

Keywords: Biorecycling, biocatalysis, polyethylene

Polyethylene (PE) is the most widely produced plastic globally and is highly resistant to degradation, leading to its accumulation in the environment. A major challenge in developing biocatalytic strategies for PE valorisation is the limited understanding of the enzymatic processes responsible for initiating oxidation of this chemically inert polymer. Addressing this early-stage step is critical for enabling the conversion of polyethylene into value-added chemical feedstocks, fuels, and waxes.

This work focuses on developing an integrated workflow to identify candidate enzymes capable of initiating polyethylene oxidation. Bioinformatic approaches, including structural prediction and functional annotation, were used to identify and prioritise enzymes with features consistent with hydrocarbon activation, including candidates that may have been previously overlooked using conventional annotation

methods. These candidates were subsequently evaluated through recombinant expression and systematically screened against a panel of relevant substrates to assess their potential oxidative activity and refine functional predictions.

While catalytic activity toward polyethylene itself remains under investigation, this approach establishes a strategy for linking bioinformatics-driven discovery with experimental screening to reduce large candidate pools to a tractable set of enzymes with plausible roles in early-stage polymer oxidation. These findings support the development of biocatalytic routes for converting plastic waste into useful chemical products.

Mohammed Rehmanji

University of Oxford, UK

High-throughput phenotyping to engineer carbonate biominerals using *Sporosarcina pasteurii* system.

Keywords: Biominerals, microbially induced carbonate precipitation, *Sporosarcina pasteurii*

Abstract:

Microbially induced carbonate precipitation (MICP) by *Sporosarcina pasteurii* converts dissolved inorganic carbon into calcium carbonate under ambient conditions and underpins applications in biocementation, soil stabilization, and carbon sequestration. However, controlling key determinants (carbonate polymorphism, particle size, and morphology) of material performance remains challenging. Here, we develop a high-throughput screening platform combining automated Raman spectromicroscopy, image analysis, machine learning, and response surface modelling to identify abiotic and genetic controls on carbonate biomineral formation. Carbonate precipitation experiments were conducted in 96-well plates under variable conditions. After 24 h, precipitates were imaged by microscopy and analysed using an automated Python pipeline to quantify particle abundance and morphometric descriptors. Response surface modelling identified calcium concentration as the dominant driver of total particle area in biotic system. A random-forest classifier trained on seven particle types revealed that biological mediation maintains higher morphological richness and evenness compared with abiotic precipitation. Raman spectromiscroscopy was finally used to characterise the mineralogical composition (CaCO3 polymorphism) of each particle type. Further screening of mutant libraries (86 mutants) indicates distinct alterations in morphometric parameters, displaying clear variation in mineral structures and precipitation behaviour compared to wild type wild type, which may eventually allow the identification of new genetic determinants of MICP by *S. pasteurii*. Overall, this data-driven framework enables systematic tuning of morphometric traits, providing a route toward designing application-specific, sustainable carbonate biomaterials.

Monika Steinke

University of Essex, UK

In search of novel marine oil-degrading bacteria.

Naturally occurring oil-degrading bacteria are widespread in marine environments. They play a key ecological role when degrading hydrocarbons from natural oil seeps or chronic low-level pollution. To aid in the discovery of novel marine hydrocarbon-degrading bacteria, water samples were collected from the Blackwater Estuary, West Mersea, Essex, UK. Hydrocarbon-degrading bacteria were isolated, Sanger sequenced and BLASTn queried, which suggested the presence of *Alcanivorax* sp., *Cycloclasticus* sp., *Cycloclasticus spiriliensus, Thalassolituus* sp. and *Vibrio* sp. Whole genome sequencing combined with querying BLASTn and CANT-HYD databases indicated that the isolate *Thalassolituus* sp. S6WM may possess novel properties. A phylogenetic tree will be constructed based on conserved genetic markers and this will provide insights into their taxonomic placement among known hydrocarbon-degrading taxa. Currently, the production of surfactants in *Thalassolituus* sp. is being investigated by measuring surface tension and using hydrophobic interaction chromatography. This may aid the development of targeted environmental bioremediation methodology to degrade hydrocarbon pollutants.

Muhammad Ejaz

Qatar University, Qatar

Metagenomic and Biotechnological Characterization of Spore-Forming Bacteria from Arid Soils of Qatar.

Keywords: Metagenomics, arid soil microbiome, environmental biotechnology

Arid soils in Qatar host microbial communities adapted to extreme environmental conditions, making them valuable resources for environmental biotechnology and the bioeconomy. Among these microorganisms, spore-forming bacteria, particularly members of the genus Bacillus, are of special interest because of their potential applications in agriculture, environmental management, and industrial biotechnology. This study investigated the diversity, metabolic potential, and biotechnological relevance of spore-forming bacteria isolated from Qatari soils using field sampling, cultivation-based microbiology, and metagenomic analysis. Soil samples were collected from multiple regions of Qatar to capture microbial diversity across arid habitats. Spore-forming bacteria were isolated using conventional microbiological methods, while bulk soil DNA was extracted for high-throughput metagenomic sequencing. The analysis revealed diverse microbial communities, with prominent taxa including *Betaproteobacteria*, *Actinobacteria*, and *Alphaproteobacteria*. Functional annotation identified genes linked to stress tolerance, nutrient cycling, metabolic versatility, and enzyme production, indicating significant biotechnological potential. These findings highlight native Qatari soil bacteria as promising resources for sustainable agriculture, environmental sustainability, and future industrial applications, while also improving our understanding of microbial adaptation in arid ecosystems.

Katharine Davis

University of York, UK

Assessing ability of plants and microbes to establish vegetative cover and remove rare earth elements from African mine tailings and soils.

Global demand for Rare Earth Elements (REEs) is escalating, driven by their critical role in clean energy and defence technologies. However, the current supply chain is vulnerable to geopolitical control, and conventional extraction techniques have harmful impacts on the environment. This research addresses these challenges by investigating the use of plants to recover REEs from low-grade ores and mine tailings.

In this project, we will use a high biomass, sub-tropical *Eucalyptus* commonly cultivated as a sustainable woody biomass in Angola. We will conduct controlled trials to monitor the growth, biomass yield and REE accumulation in roots and aerial tissues, using methods including x-ray fluorescence and ICP-MS. In addition, we will characterise native microbial communities in soils and tailings from an REE mine site and investigate their influence on plant performance.

Ultimately, the project outcomes will provide industrial partners with a scalable, low-input strategy to mitigate environmental liability while diversifying the REE supply chain, directly supporting the UK's transition to a circular, net-zero economy. As this project is in its infancy, this poster will introduce our work with the aim of seeking advice and feedback on our experimental plans.

Rebecca Morton

Heriot-Watt University, UK

Bioinoculation of Plants using Plant-Growth Promoting Bacteria to Alleviate the Impact of Drought Stress.

Keywords: Bioaugmentation, drought, plant-growth promoting bacteria (PGPB)

Drought stress severely limits agricultural productivity, and its frequency and intensity are increasing under climate change. Engineering biology provides new opportunities to combat this challenge through the rational design and deployment of microbial bioinoculants with defined, optimisable functions. In this context, plant growth promoting bacteria (PGPB) represent a promising, engineerable platform for improving crop drought resilience.

We evaluated a panel of candidate PGPB strains—*P. fluorescens, P. putida, P. capeferrum, P. protegens,* and *M. gossypiicola*—as bioinoculants for *Hordeum vulgare* and *Arabidopsis thaliana* under drought stress. Initial seed inoculation experiments showed that *P. capeferrum* and *M. gossypiicola* significantly enhanced barley seedling growth under osmotic stress, while *P. fluorescens* and *M. gossypiicola* increased germination rates in *Arabidopsis*.

We then conducted pot scale drought experiments to assess system level robustness. Seed inoculation with *M. gossypiicola* significantly increased barley root and shoot biomass after drought, with growth promotion persisting after re watering. Comparable drought mitigation effects were observed in Arabidopsis, indicating host independent functionality.

Ongoing work applies an engineering biology framework to optimise these interactions, integrating multi omics analyses and hormone signalling perturbations to identify mechanisms conferring drought tolerance. Together, these results highlight the potential of PGPB based bioinoculants as programmable, sustainable solutions for crop resilience in water limited environments.

Carla Spatola Rossi

Cranfield University, UK

Origami paper microfluidic device for the detection of viable bacteria in water.

Keywords: Cell viability, microbial water monitoring, molecular viability testing, paper microfluidics

Microbial contamination of water remains a major environmental and public health concern, requiring monitoring tools that are rapid, portable, and capable of distinguishing viable from non-viable microorganisms. Conventional microbial detection methods often involve trade-offs between sensitivity, assay speed, specificity, multiplexing capability, cost, operational complexity, and equipment requirements, limiting their suitability for on-site detection. In this study, we address this technology gap by developing a sensing platform that combines molecular viability testing (MVT) with loop-mediated isothermal amplification (LAMP) and microfluidic paper analytical devices (µPADs). MVT was coupled with LAMP to establish a rapid isothermal viability assay. This assay was further integrated into a µPAD to create a portable platform termed 'viability-µPAD', enabling the detection of viable *Pseudomonas aeruginosa* (*P. aeruginosa*) with an LOD of 50 CFU mL^{-1} in spiked tap water within 7 hrs. The platform supported multiplexed detection of *P. aeruginosa* and *Acinetobacter baumannii* (*A. baumannii*) and demonstrated the feasibility of on-site testing using freeze-dried reagents. The viability-µPAD was further validated in real wastewater matrices for the detection of enteric bacteria and Enterobacteriaceae. This study provides a proof-of-concept for on-site, viability-specific, and rapid microbial surveillance of water systems and supports the development of accessible biosensing technologies for environmental applications.

Hamid Rehman

Yildiz Technical University, Turkey

From Black Mass to Battery-Grade Metals: A Bioleaching Approach for Spent Lithium-Ion Battery Recycling

The number of used lithium-ion batteries (LIBs) is growing fast. This makes it urgent to find sustainable ways to recover valuable metals from these batteries. Bioleaching is a promising alternative to traditional methods like smelting (pyrometallurgy) and chemical extraction (hydrometallurgy), as it uses microorganisms to extract metals from e-waste in a more environmentally friendly way. In this study, we investigated the performance of different microbial systems for recovering metals from battery waste using a one-step bioleaching process. These included sulfur-oxidizing bacteria (*Acidithiobacillus thiooxidans*), iron-oxidizing bacteria (*A. ferrooxidans*), acid-producing fungi (*Aspergillus niger*), and mixed microbial communities. Bacterial systems were operated at a pH of 2-4.5, temperatures of 28-40°C, pulp densities of 0.5-5% (w/v), inoculum levels near 10% (v/v), agitation at around 150 rpm, and leaching times of 7–21 days. Under these conditions, we achieved recoveries of 49% lithium, 73% cobalt, 87% nickel, and up to 63% manganese. At a higher pulp density of 50 g L^{-1}, spent-medium bioleaching with *A. thiooxidans* recovered up to 87% lithium, 88% nickel, and 78% cobalt within just 14 days. Adapted *A. niger* at 10 g L^{-1}

recovered up to 91% lithium, along with 72% manganese, 45% nickel, and 38% cobalt. Following leaching, a precipitation step recovered 88% of the dissolved cobalt and about 73.6% of the lithium as lithium carbonate, a usable end-product. Our results show that microbial adaptation, feedstock composition, particle size, pH, and pulp density are the key factors controlling bioleaching efficiency and metal selectivity in one-step processes. These findings demonstrate that one-step bioleaching is a practical, scalable, and eco-friendly strategy for recovering critical metals from battery waste.

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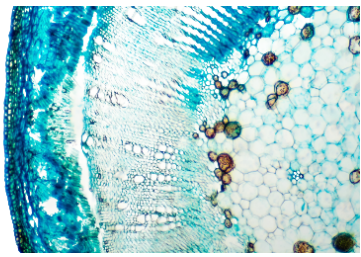

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