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Book of abstracts

Contents

Abstracts Plenary Lectures

Markus Herrgard

As the Chief Technology Officer at BioInnovation Institute (BII), Markus is responsible for shaping and executing BII's broad science and technology strategy, with a focus on digital technologies and data. BII is a leading life science incubator that supports startups and researchers in bringing their science to life by developing products that improve human or planetary health. Previously, he held a professorship in data-driven design and engineering of cell factories at DTU Biosustain, and acted as director of data science and automation, amongst others. With over 20 years of experience in innovation, data science, and technology development in life science, he has passion for operating at the intersection of life science and engineering. He has led and contributed to multiple projects and initiatives that leverage bioinformatics, cell biology, and metagenomics to address challenges and opportunities in biotechnology, medicine, and sustainability. He has have also built and mentored teams of talented scientists and engineers, and established and fostered partnerships with academic and industry stakeholders.

Title of the lecture:
Bring Science to Life: Scaling Biotechnology Innovation for Human and Planetary Health

iGEM team presentation

Camile van Harmelen & Anirudhan Puvvada

BCoated: Tailored Coatings for Tomorrow’s Crops

Agriculture is changing fast, and farmers everywhere are feeling the heat. Every crop faces different issues, from abiotic stressors like drought to biotic stressors such as pests. Traditional breeding for resilience takes years; a quicker solution is needed. Seed coatings are commonly used for uniform seed size, germination, and delivery of active compounds, but they could reduce the severity of many more problems. Therefore, we developed a modular material without microplastics to create a platform for all seed coating applications. Desired properties can be selected before production, such as altered water holding capacity or biodegradability, but also added active components or proteins. During fermentation, the functionalised bacterial cellulose (BC) is made, which can be applied directly to seeds. This way, BCoated is creating a fast, farmer-friendly support for crops: Customizable bacterial cellulose (BC) coatings that protect seeds and boost resilience, tailored to meet the challenges of today’s and tomorrow's fields.

Vera Meyer

Vera Meyer studied biotechnology at the Sofia University (Bulgaria) and the TUB (Technische Universität Berlin, Germany). After obtaining a PhD degree (2001) and habilitation (2008) at the TUB, she worked in the Netherlands as Assistant Professor at Leiden University (2008-2011). She has been visiting scientist at the Imperial College London (2003) and at Leiden University (2005-2006). In 2011, she became Full Professor of Applied and Molecular Microbiology at the TUB. As a scientist, she tries to decode and understand nature's genetic principles that define growth, product formation, survival and physiology of fungal systems. Here research fields include the optimization of protein and metabolite formation in fungal cell factories with the help of systems and synthetic biology tools, production of bioactive substances using fungal cell factories and the development of new antifungal agents and strategies. Recently she entered the field of material sciences exploiting mushroom-forming fungi as sustainable resource for innovative biomaterials. For more details see: www.tu.berlin/mikrobiologie/ Vera Meyer also works as a visual artist, using the pseudonym V. meer. Inspired by her scientific work with fungi, she puts a strong emphasis on sculpting and creating objects from chance finds like forest mushrooms, decaying wood and scrap metal. Through her art work she wants to enhance the awareness for fungi and their potential in biotechnology and for a sustainable bioeconomy in general.

Title of the lecture:
Building with Fungi: Paths into a new material future

Luísa Cruz

Luísa is the Co-Founder and CTO of MicroHarvest, a German biotech using proprietary biomass fermentation to produce sustainable protein ingredients at industrial scale. With a background in biotechnology and a passion for translating science into real-world impact, she has led the technical development of MicroHarvest's proprietary fermentation platform from the ground up - from lab to industrial scale. Under her technical leadership, MicroHarvest has achieved significant milestones including the BloombergNEF Pioneers Award and is now preparing to launch its first 15kT industrial production facility.

Title of the lecture:
A vision and a Business Plan: What Startups Teach Us About Food's Future

Abstracts for Oral Presentation

Upstream process development for cell-tolerant direct capture of monoclonal antibodies

Stefan Kint[1], Ivo Tjalma[2], Marcel Ottens[2], Marieke Klijn[2], Dirk Martens[1], Michel Eppink[1] and René Wijffels[1]
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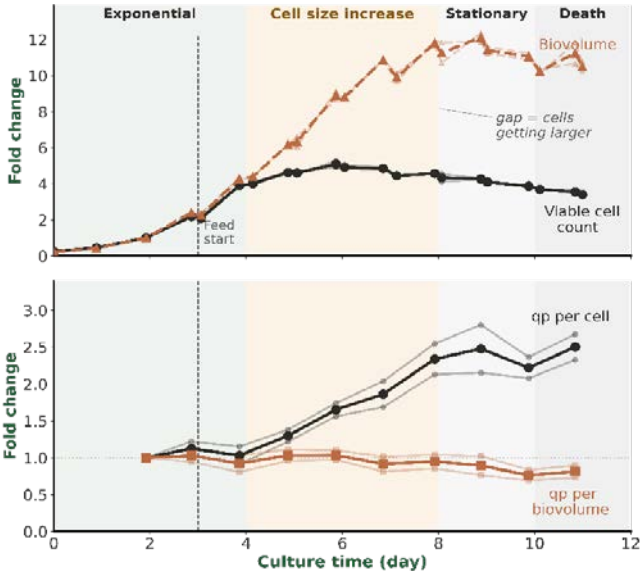
Abstract

Continuous antibody manufacturing may remove clarification unit operations by loading whole CHO culture broth directly onto a cell-tolerant Protein A capture column. In this direct-capture technique, cells pass through the column while antibody is captured and later eluted. This could simplify the process, but it also changes the role of upstream processing. The capture column is now exposed to the biological and physicochemical state of the culture rather than to clarified harvest.

This project asks whether upstream process development can define and control the harvest-state requirements for direct capture. The work focuses on three classes of column-relevant harvest variables: particle-related properties, including viable biomass, size distribution, aggregates and debris; dissolved components, including mAb product, host cell proteins, and metabolites; and physicochemical properties, including pH, osmolality, conductivity and viscosity. These variables will be linked to capture-relevant outcomes such as pressure development, breakthrough, dynamic binding capacity, recovery and fouling.

The first biological focus is cell size dynamics in CHO fed-batch culture. Preliminary fed-batch data show that viable cell density alone can become an incomplete process metric when cell size changes. It was found that cell count plateaus while viable biovolume continues to increase. Productivities expressed per cell and per biovolume can therefore lead to different interpretations of the same culture state. This matters for feeding strategy, productivity analysis and the biomass load presented to direct capture. Cell size may also co-vary with aggregation, viability decline and lysis-related impurity release.



The research strategy is to quantify the phenotype across CHO cell platforms, perturb candidate triggers such as amino acid balance, organic acids, osmolality and feed timing, test reversibility and cell-cycle involvement, and translate the resulting culture-state map into upstream control targets for column-compatible fed-batch and perfusion operations. The intended output is an upstream framework that connects CHO culture physiology to direct-capture process design.

Single-domain antibodies as versatile tools in biotechnology: from lead-discovery out of large libraries to numerous applications

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Abstract

Antibodies are key proteins of the adaptive immune system which recognize and bind specific molecular targets with high selectivity. Due to this selectivity, antibodies have become indispensable tools in research as well as in technological and clinical applications. Conventional full-length antibodies consist of two heavy and two light protein chains, resulting in a relatively large and complex structure. While highly effective, this complexity makes them costly to produce, sensitive to harsh conditions, and challenging to engineer into different formats.

Single-domain antibodies (sdAbs) are small antibody fragments derived from heavy-chain-only antibodies naturally found in camelids such as llamas. At roughly one-tenth the size of a conventional antibody, sdAbs consist of only a single protein domain, yet retain full antigen-binding capacity. They are highly stable, can be produced as recombinant proteins in common microbial expression systems such as *E.coli* or yeast, and can be readily re-engineered or chemically modified, for example by conjugation of fluorescent dyes, radioactive labels, enzymes, oligonucleotides, or other proteins (1). This modularity makes sdAbs highly adaptable scaffolds for a wide range of applications, from research tools to material and surface engineering, diagnostics and therapeutics (2).

In this presentation, I will give an overview of how sdAbs are generated - from the conventional route of llama immunization to newer, animal-free approaches using synthetic libraries and AI-guided computational methods. Furthermore, examples of sdAbs applied across different areas of biotechnology will be discussed: from molecular and cellular imaging in the lab to clinical applications such as lateral flow assays and *in-vivo* (tumor) imaging, and applications beyond the biomedical field, such as food and detergents. Together, these examples illustrate the broad applicability of sdAbs to the field of biotechnology.

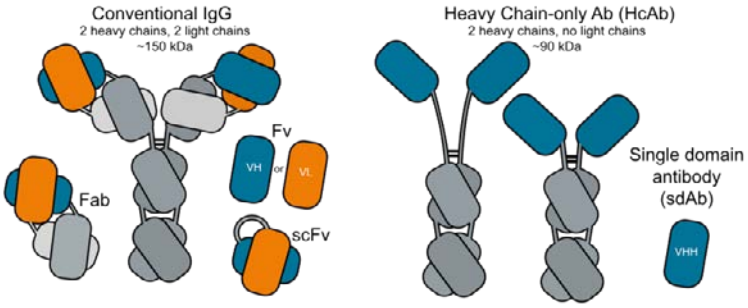

Figure: Size differences of antibody formats. A conventional antibody (Ab) composed of two heavy chains and two light chains which need each other for stability (left). A heavy-chain-only antibody (HcAb) lacks light chains but remains stable (middle). A sdAb is the isolated binding domain of a heavy-chain-only Ab (right).

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Small-scale bioreactor cultivation of HEK293-based suspension cells increases extracellular vesicle yield

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Abstract

Purpose - Extracellular vesicles (EVs) are increasingly explored as natural vehicles for drug delivery and gene therapy approaches. However, reproducible yield and scalability of EV production still pose major challenges in the clinical translation of EV-based therapies. In this study, we sought to quantify and characterize EVs released by suspension-cultured HEK293 cells (Expi293F cells) grown in shaker flasks or small-scale bioreactors, to investigate how the culturing environment affects EV production yield.

Methods - Expi293F cells were cultivated (N=3) in either shaker flasks or a bioreactor system and total cell density, viability, and size were monitored. Supernatants were drawn daily post-inoculation, and samples were analyzed for EV quantity, size, morphology, and CD63 expression.

Results - No differences were observed in terms of total cell density, viability and cell size between both cultivation settings. However, cultivation of Expi293F cells in the bioreactor environment significantly increased EV yield by 3-fold compared to shaker flask cultivation ($p < 0.01$). Other parameters such as average nanoparticle size, EV morphology and CD63 expression remained comparable between both cultivation methods.

Conclusion - These results demonstrate that Expi293F-derived EV yield can be increased by culturing cells in a scalable bioreactor system. These findings pave the way towards the production of therapeutic-based EVs in a scalable and reproducible manner suitable for future (pre-)clinical applications.

Keywords: Suspension Cell Culture, Bioprocessing, Bioreactor, Extracellular Vesicles, Scalability

Machine Learning-Guided Pathway Optimization Case Study: *p-Coumaric Acid Production in S. cerevisiae*

Joep Schmitz, dsm-firmenich

Developing better production strains often requires testing thousands, or even millions, of possible genetic combinations. This quickly becomes a bottleneck, as building and evaluating strains is time-consuming and expensive. In this talk, I will show how machine learning can help guide strain engineering and accelerate the search for improved designs. Using p-coumaric acid production in *Saccharomyces cerevisiae* as a case study, we combined high-throughput strain construction, automated screening, genome sequencing, and iterative machine learning models to identify promising pathway designs. The approach delivered a four-fold improvement in production performance while testing only a tiny fraction of all possible variants. I will share key lessons on how balancing exploration and exploitation can improve outcomes and discuss the broader potential of AI-driven strain development for industrial biotechnology.

Assessing the stability of using growth-coupled fumarate as a substrate for malate production during circadian cycles in *Synechocystis*

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Abstract

Cyanobacterial CO_2 conversion holds great promise towards sustainability while challenges remain. One of them is the instability of production. When production imposes a fitness burden on the cell, revertants that eliminate it via spontaneous mutations ultimately take over the population by impairing the overall productivity. A strategy to overcome this instability is via growth-coupled production. In the cyanobacterium *Synechocystis* sp. PCC6803, this has been explored for the stable production of both acetate [1] and fumarate [2]. However, native candidates for growth-coupled production are somewhat limited. The product range of this strategy could be expanded by the concept of relief production, in which a growth-coupled metabolite is consumed, leading to a fitness benefit by relieving a rate limiting bottleneck in a metabolic pathway.

In the cyanobacterium *Synechocystis* sp. PCC6803 it has been proposed that the relief product malate can be produced stably from the growth-coupled product fumarate, when the enzymes responsible for recycling malate (ME and Mdh) are knocked out. Pioneering experiments suggested that such constructs would be stable even when higher production levels of malate would be achieved via the overexpression of fumarase (FumC) [3]. Here, we use tightly controlled turbidostats where we cultivate during many generations with a small propagation bottle neck (5%), while growth rate is applied as the selection pressure. Results obtained show stable production in both the *ΔmeΔmdh* and *ΔmeΔmdhΔNSI::fumC* strains for over 200 generations.

We are now also testing this relief production in fluctuating environments. In circadian cycles, light availability varies throughout the day. By redirection of the energy generation flux during the dark periods, malate production can also be achieved. Results show that by rewiring metabolism, a relief compound such as malate, can be produced during a full day-night cycle. This production is increased during day and night by overexpression of FumC. Our results show that this is a promising strategy to extend the list of alternative compounds to be stably produced and maximize production in settings that rely directly on the exposure to sun light.

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Examining the reversibility of the soluble- and membrane-bound transhydrogenases in *Escherichia coli*.

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Microbial cell factories (MCF) have the potential to produce chemicals sustainably. Their efficiency often relies on proper regulation of the ratios between oxidized and reduced cofactors, with NAD(H) and NADP(H) being the most important. In *E. coli*, the ratio between the oxidized and reduced forms can be modulated by the soluble and membrane-bound transhydrogenases, SthA and PntAB, respectively. Sauer et al [1] postulated that both have distinct roles in metabolism: SthA converts excess NADPH to NADH, whereas PntAB catalyzes the opposite reaction. As the opposite reaction is thermodynamically unfavourable, PntAB uses the proton motive force across the cell membrane to transfer electrons from NADH to $NADP^+$. In the literature, however, there is conflicting evidence about whether both enzymes are reversible *in vivo* [2], [3]. Therefore, we systematically examined the directions in which the transhydrogenases can operate using growth-coupled selection strains. Both enzymes were overexpressed in NADPH- and $NADP^+$-auxotrophic strains to test their ability to produce NADPH and $NADP^+$, respectively. While other reports suggested reversibility of SthA, we did not observe this under the conditions tested. To our surprise, PntAB did catalyze the reverse reaction, even though this is thermodynamically very challenging, but it is in line with limited other reports [3], [4].

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Nitroreductase-triggered Indazole Formation

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Purpose: Biocatalysis has made a substantial contribution to the development of more sustainable synthetic pathways by employing mild reaction conditions and water as a solvent.[1] However, many relevant compound classes, including privileged groups in drug design, remain inaccessible using enzymatic pathways. In this context, the development of an enzymatic route to indazoles remains an unmet challenge.

Methods: Here, we present a nitroreductase-triggered indazole formation, in which 2-nitrobenzylamine derivatives are converted to reactive nitrosobenzylamine intermediates that spontaneously cyclize and aromatize to indazoles.[2] Two nitroreductases (NRs), NfsA and BaNTR1 from *Bacillus amyloliquefaciens* and *Escherichia coli*, respectively, were found to accept a broad range of 2-nitrobenzylamine derivatives. We established an enzymatic cascade reaction involving imine reductase and glucose dehydrogenase-based NADPH regeneration. All analytical-scale reactions were analysed using GC-FID. Identity was confirmed using GC-MS, HRMS and NMR. Preparative-scale reactions were performed on 20 mg and 50 mg scales.

Results: Using our NR-triggered synthetic route we achieved up to 99% conversion for 17 substrates (**Figure 1A**). In the case of *N*-substitution, 2*H*-indazoles were formed, whereas other derivatives led to 1*H*-indazoles. The synthetic utility of nitroreductase-triggered indazole formation was demonstrated through successful coupling with an imine reductase (IRED15) in a sequential cascade reaction, enabling the production of 2*H*-indazoles from inexpensive 2-nitrobenzaldehydes and amines (**Figure 1B**). All reactions were scaled up to the preparative level, achieving isolated yields ranging from 52% to 99%.

Conclusions: We present the first enzymatic route to 1*H*- and 2*H*-indazoles. Using an enzymatic cascade reaction, we have developed a versatile and synthetically useful NR-triggered indazole formation process that provides these valuable compounds from cheap, readily available starting materials.

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Recycling mixed plastic materials by selective enzymatic hydrolysis

Daan M. van Vliet[1], Jurgen J. Mateman[1], Rick H.A.M. van de Vondervoort[1,], Antoine P.H.A. Moers[1], Lucas Collazo[2], Ana Mencher[2], Marc W.T. Werten[1], Shanmugam Thiyagarajan[1], Arno Cordes[3], Christian Sonnendecker[4], Eggo U. Thoden van Velzen[1], Rosa Doménech-Mata[2], Juan Antonio Tamayo-Ramos[2,], Mattijs K. Julsing[1], Tom A. Ewing[1]

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Abstract

Enzymatic back-to-monomer recycling allows polyesters, such as polyethylene terephthalate (PET) to be broken down to their constituent monomers under mild reaction conditions. These monomers can subsequently be processed into new polymer, enabling closed-loop recycling. The high selectivity of enzymatic catalysis makes it an interesting technology to apply to complex, mixed plastic waste streams that cannot be processed by mechanical recycling. Here, we will discuss the development of an efficient enzymatic process for the recycling of PET-PE multilayer trays[1]. Polyester hydrolase enzymes were produced in *Pichia pastoris.* Then, they were used to selectively hydrolyze the PET layer of PET-PE (PE = polyethylene) trays, giving depolymerization degrees of ≥94%. The resulting terephthalic acid monomer was isolated and successfully repolymerized into PET. Meanwhile, following a mild alkaline treatment to remove residual PET, the PE layer was mechanically recycled into films with mechanical properties similar to virgin low-density PE. These results demonstrate the potential of enzymatic processes to be employed in the recycling of complex, mixed plastic waste streams. In future, this may be extended to other mixed materials and post-consumer waste streams containing large amounts of (amorphous) PET. Current efforts focusing on enzymatic recycling of mixed streams containing renewable, biobased polyesters will also be briefly addressed.

References: D.M. van Vliet et al. (2025), ACS Sus Chem Eng, **13**, 8212-8219

AI-Guided Rational Design For Improvement of Protein Solubility

Matias Brezina-Borges[1,2], Caterina Martin[1], Hugo van Beek[1], Marcelo Masman[1], Marco Fraaije[1,2]and Nikola Lončar[1]

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Abstract

Many enzymes of biotechnological interest are membrane-embedded or carry solvent-exposed hydrophobic patches that drive nonspecific association with membranes or hydrophobic cellular structures. These enzymes can often be expressed, extracted, and purified, but only with the aid of detergents, which complicates downstream processing, characterization, crystallization, and industrial application.

To overcome this limitation, we developed an AI-guided computational workflow aimed at decoupling catalytic function from membrane association by rationally redesigning enzyme surfaces. As a proof-of-concept, we applied this pipeline to T3G1, a bacterial heme-dependent peroxygenase identified by GECCO Biotech **[1]** that features a broad substrate scope for hydroxylation and epoxidation, but requires detergent for downstream processing. Our workflow mapped surface hydrophobic patches and used SolubleMPNN for sequence redesign, the protein language model ESM-IF and a solubility predictor were used to evaluate and filter the capacity of the newly generated mutants to fit into the original structure without compromising solubility. Experimental screening of the computationally designed library revealed that all 88 tested mutants successfully bypassed the wild-type detergent requirement, exhibiting fully soluble peroxygenase activity. Ultimately, this robust AI-driven strategy successfully generates active, detergent-free biocatalysts, unlocking the structural and industrial potential of previously difficult to work membrane-associated enzymes.

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Acknowledgement

Floris Foijer
Groningen University

Single cel genomics to quantify heterogeneity in cancer towards better treatment stratification

pDNA-PEI complex size in transient transfection – Viral titer yield increases through PAT-based process monitoring

Carl C.L. Schuurmans[1], Jort J. Altenburg[2], Ganesh Ramesh[2], Zsolt Sebestyen[2]

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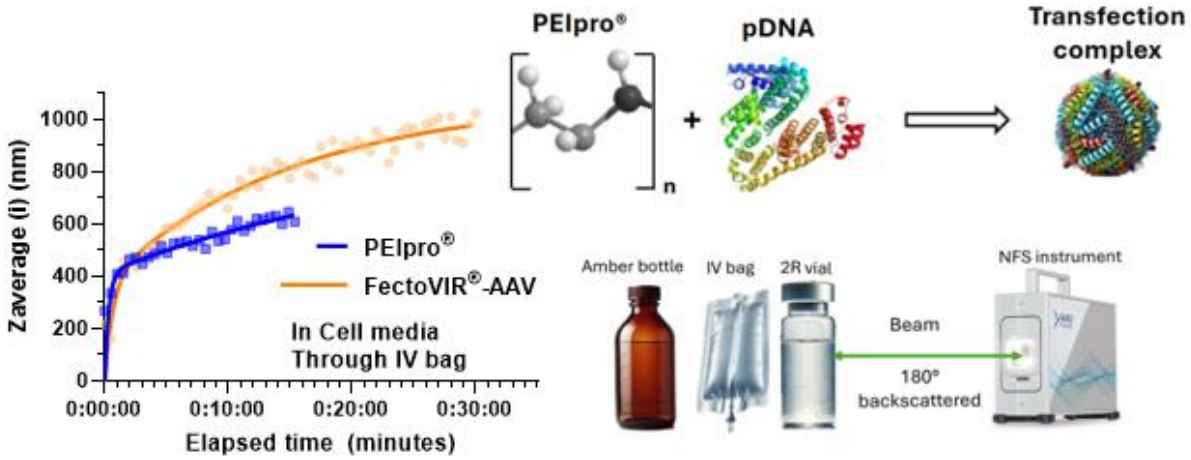
Abstract

Transient transfection using pDNA-PEI complexes is a cornerstone technology in viral vector manufacturing for cell and gene therapy, yet scale-up remains challenging due to yield issues stemming from the narrow optimal range of transfection complex sizes and the dynamic nature of complexation kinetics. In this study, we demonstrate how real-time monitoring of pDNA-PEI complex growth using Spatially Resolved Dynamic Light Scattering (SR-DLS) provides critical process insights for improved transient transfection control. The NanoFlowSizer platform enabled continuous, non-invasive monitoring of nanoparticle size evolution in both static and flow conditions across multiple process-relevant containers, including glass vials, Falcon tubes, disposable bottles, and single-use bags.

Complexation kinetics were investigated for a variety of transfection reagents from most established vendors, with formulations in both PBS and serum-free cell culture media. All products show distinct growth profiles upon mixing with pDNA and typically show reproducible two-phase particle formation behavior. Inline measurements further showed that peristaltic pumping had no significant impact on particle size under tested conditions, supporting the feasibility of real-time process monitoring in scalable GMP-compatible workflows. In addition to monitoring existing transient transfection workflows for viral vectors, we also investigate the use of SR-DLS in monitoring a variety of complex size stabilizing products that have recently entered the market. Taken together, these findings highlight pDNA-PEI complex size as a critical process parameter and demonstrate the value of SR-DLS-based monitoring for process optimization, scale-up, and enhanced transfection robustness in advanced therapy medicinal products manufacturing.



Exploring a native microalgae-virus interaction for biotechnological innovation

Amendola, S.[1*]; Julia Bevervanco[1]; Richard Kormelink[2]; Dirk Martens[1]; Maria Barbosa[1]; Sarah D'Adamo[1]

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Abstract

Microalgae are a promising platform for industrial biotechnology due to their metabolic versatility and sustainability, as they can use light and CO_2 to produce a diverse range of valuable compounds[1]. While microalgae-infecting viruses are commonly viewed as harmful pathogens that devastate production cultures, they hold great potential for driving innovation in microalgae biotechnology. In fact, viruses are highly specialized infective agents, capable of modulating their host's cellular and metabolic pathways to redirect cellular resources toward their own replication, making them powerful "natural engineers"[2].

Recently, a virus specific to the green marine microalga *Tetraselmis striata* was discovered[3], offering the opportunity to study the infection dynamics of an algal virus in an industrially relevant species. Our study investigates the molecular mechanisms of this viral infection, aiming to understand how microalgal viruses rearrange host metabolism and hijack cellular resources during infection.

To characterize this host-virus dual system, an infection pipeline was developed combining flow cytometry for infection monitoring and plaque assay for viral quantification. This enabled a synchronized, high virus-to-cell infection, allowing observation of the entire viral life cycle with high temporal resolution. Dual transcriptomic profiling of both *T. striata* and its virus throughout the infection cycle provided insights into the molecular strategies employed by the virus to modulate host metabolism, as well as the host's response to infection. Together, these findings shed light on the dynamics governing this microalgae-virus system, diving into the largely untapped potential of microalgal viruses as innovative tools for microalgae cell factory development.

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Acknowledgments

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Emerging Microalgae Bioprocessing for more Sustainable, Affordable and Nutritious Foods

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Abstract

Microalgae offer a promising, resource-efficient alternative for sustainable food production, yet their industrial adoption requires optimized bioprocessing and downstream technologies. By leveraging polyextremophilic microalgae such as *Galdieria sulphuraria*, we establish selective, robust cultivation environments that lower both CAPEX and OPEX while facilitating circular residue upcycling. Process intensification using nanosecond pulsed electric field (nsPEF) stimulation enhances microalgal biomass productivity by up to 20%. Downstream, high-moisture extrusion incorporating up to 50% yellow fermented microalgae yields meat substitutes with superior B and E vitamin profiles compared to soy isolates, while the microalgal biomass exhibits high mineral bioaccessibility and iron bioavailability. Industrial collaborations demonstrate that integrating extremophilic bioprocessing with novel technologies provides a scalable, economically viable pathway toward more sustainable food production.

Abstract ECB2026

Biotechnological production of bacterial cellulose from industrial side streams: a promising avenue to replace polystyrene

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Yearly, the world produces polystyrene equal to the volume of Manhattan, and this global production is expected to rise to 17.5 million metric tons by 2030. This fossil-based material is difficult to recycle and takes over 500 years to decompose. Foamlab B.V. produces bacterial nanocellulose (BNC) through fermentation and functionalizes it into high-quality foams for insulation purposes that can replace fossil-fuel-based plastics like polystyrene. However, current production methods rely on pure sugar as the primary feedstock. This not only limits the circularity of the final product but also constrains yield optimization. Transitioning to industrial waste streams as feedstocks offers a promising path to both increase yield and enhance sustainability. However, BNC-producing bacterial strains are typically not adapted to the complexity and variability of industrial side streams, which needs to be addressed. To bridge this gap, the collaboration between Foamlab and the HAN BioCentre leverages HAN's expertise in side-stream fermentation to complement Foamlab's production capabilities. The objective of this project is to develop a high-performance, biobased, and fully compostable BNC foam from industrial side streams—offering a circular and functionally superior alternative to polystyrene. This private-public partnership will deliver a fully biobased, biodegradable, sustainable and functionally superior alternative to polystyrene for years to come.

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Built to Last: Self-repair in Living Mycelium Materials

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Abstract

Mycelium-based materials are emerging as a promising sustainable alternative to conventional synthetic materials. In addition, Engineered Living Materials (ELMs) offer new possibilities for material functionalities, such as adaptive growth or self-repair. In this research, we investigate the production, mechanical properties, and self-repair capacity of a mycelium-based living material.

A mycelium-based material can be either a pure mycelium material or a mycelium-bound composite, where the fungal hyphae infiltrate and bind a lignocellulosic substrate. In our ELM, the hyphae function as the structural component of the material, whereas co-cultivated bacteria are engineered to carry out programmable functions. The fungus, *Schizophyllum commune,* can grow over non-nutritive environments (such as plastic or air) which is an important feature for self-repair. When growing blocks of *S. commune* composite, two blocks can adhere to each other through fungal growth, creating a biological bond or glue between the blocks. Additionally, *E. coli* can co-migrate with the fungal hyphae over a non-nutritive environment to cover a distance of at least 3 mm, demonstrating the potential transport and redistribution of the engineered functionality in an ELM.

Next, pure mycelium sheets were produced in monoculture or in co-culture with bacteria *E. coli* or *Pseudomonas putida*. Mechanical testing showed that monoculture sheets are stronger than co-cultures, while the elasticity remained unchanged. To assess self-repair, a cut was made in the mycelium sheet. Both mono- and co-culture sheets demonstrate self-repair when wet, and both fungal and bacterial cells are present in the repaired region. The repaired material retained mechanical properties comparable to undamaged material. And, although dried sheets normally do not self-repair, the addition of moisture enabled repair regardless of whether the damage occurred before or after drying. Together, these results show that mycelium-based living materials have the potential to self-repair after damage and can retain their strength and functionality.

Acknowledgements
The FUNGATERIA project has received funding from the European Union's HORIZON-EIC-2021-PATHFINDER CHALLENGES programme under grant agreement No. 101071145.

Abstracts for Poster Presentation

P01

Exploring a native microalgae-virus interaction for biotechnological innovation

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Abstract

Microalgae are a promising platform for industrial biotechnology due to their metabolic versatility and sustainability, as they can use light and CO_2 to produce a diverse range of valuable compounds[1]. While microalgae-infecting viruses are commonly viewed as harmful pathogens that devastate production cultures, they hold great potential for driving innovation in microalgae biotechnology. In fact, viruses are highly specialized infective agents, capable of modulating their host's cellular and metabolic pathways to redirect cellular resources toward their own replication, making them powerful "natural engineers"[2].

Recently, a virus specific to the green marine microalga *Tetraselmis striata* was discovered[3], offering the opportunity to study the infection dynamics of an algal virus in an industrially relevant species. Our study investigates the molecular mechanisms of this viral infection, aiming to understand how microalgal viruses rearrange host metabolism and hijack cellular resources during infection.

To characterize this host-virus dual system, an infection pipeline was developed combining flow cytometry for infection monitoring and plaque assay for viral quantification. This enabled a synchronized, high virus-to-cell infection, allowing observation of the entire viral life cycle with high temporal resolution. Dual transcriptomic profiling of both *T. striata* and its virus throughout the infection cycle provided insights into the molecular strategies employed by the virus to modulate host metabolism, as well as the host's response to infection. Together, these findings shed light on the dynamics governing this microalgae-virus system, diving into the largely untapped potential of microalgal viruses as innovative tools for microalgae cell factory development.

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Acknowledgments

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P02

Single-domain antibodies as versatile tools in biotechnology: from lead-discovery out of large libraries to numerous applications

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Abstract

Antibodies are key proteins of the adaptive immune system which recognize and bind specific molecular targets with high selectivity. Due to this selectivity, antibodies have become indispensable tools in research as well as in technological and clinical applications. Conventional full-length antibodies consist of two heavy and two light protein chains, resulting in a relatively large and complex structure. While highly effective, this complexity makes them costly to produce, sensitive to harsh conditions, and challenging to engineer into different formats.

Single-domain antibodies (sdAbs) are small antibody fragments derived from heavy-chain-only antibodies naturally found in camelids such as llamas. At roughly one-tenth the size of a conventional antibody, sdAbs consist of only a single protein domain, yet retain full antigen-binding capacity. They are highly stable, can be produced as recombinant proteins in common microbial expression systems such as *E.coli* or yeast, and can be readily re-engineered or chemically modified, for example by conjugation of fluorescent dyes, radioactive labels, enzymes, oligonucleotides, or other proteins (1). This modularity makes sdAbs highly adaptable scaffolds for a wide range of applications, from research tools to material and surface engineering, diagnostics and therapeutics (2).

In this presentation, I will give an overview of how sdAbs are generated - from the conventional route of llama immunization to newer, animal-free approaches using synthetic libraries and AI-guided computational methods. Furthermore, examples of sdAbs applied across different areas of biotechnology will be discussed: from molecular and cellular imaging in the lab to clinical applications such as lateral flow assays and *in-vivo* (tumor) imaging, and applications beyond the biomedical field, such as food and detergents. Together, these examples illustrate the broad applicability of sdAbs to the field of biotechnology.

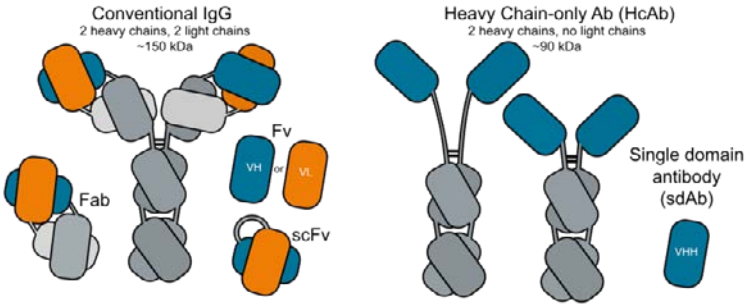

Figure: Size differences of antibody formats. A conventional antibody (Ab) composed of two heavy chains and two light chains which need each other for stability (left). A heavy-chain-only antibody (HcAb) lacks light chains but remains stable (middle). A sdAb is the isolated binding domain of a heavy-chain-only Ab (right).

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P03

AI-stabilized pre-fusion glycoprotein for nanoparticle vaccine against Newcastle Disease Virus

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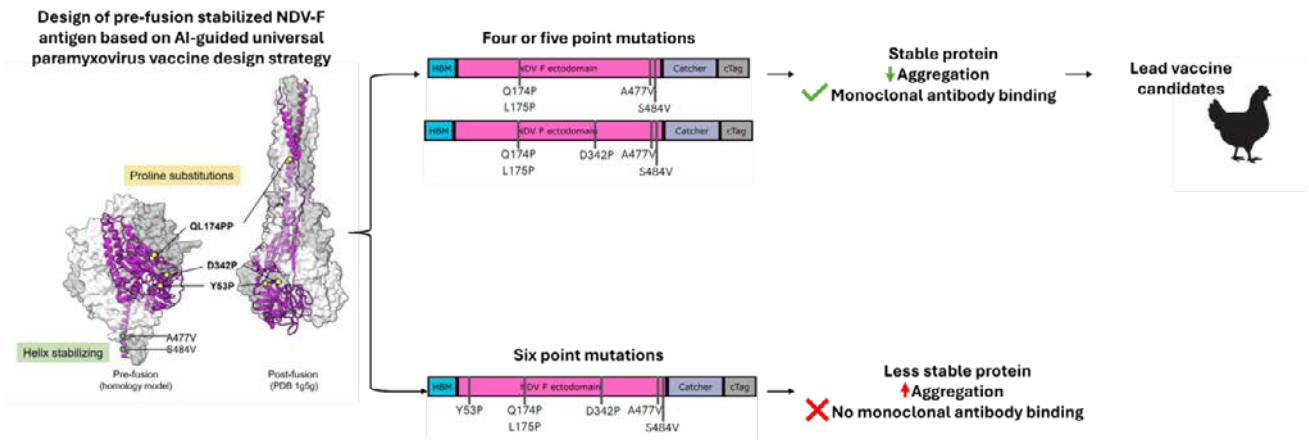
Abstract

Newcastle Disease Virus (NDV) is an infectious disease that causes severe outbreaks in poultry, resulting in high mortality rates, economic losses and trade restrictions. Although effective vaccines are available, alternative vaccine platforms are needed to improve efficacy and storage conditions and to reduce the production of egg-based vaccines. The two-component nanoparticle vaccine platform seems a promising alternative. This platform uses split Tag and Catcher peptides for antigen display on nanoparticles, enabling rapid exchange of antigens and improved immunogenicity. The NDV fusion (F) protein, a viral surface glycoprotein essential for viral entry, was selected as vaccine antigen. The NDV-F protein can exist in a metastable pre-fusion (preF) and stable post-fusion (postF) conformation. PreF is predominantly present on virus particles prior to host cell interaction, whereas postF is mainly present when the fusion process is finalized and the virus has entered the host cells. Since preF is present on mature viral particles, maintaining the vaccine antigen in this conformation is essential for vaccine development. To stabilize the NDV-F protein in preF, four NDV-F variants containing different combinations of preF-stabilizing point mutations, including proline substitutions and stem-stabilizing mutations, were designed based on an AI-guided universal paramyxovirus vaccine design strategy. All four recombinant NDV-F variants were successfully expressed, N-glycosylated, and secreted in insect cells using the baculovirus expression vector system and could be purified and efficiently coupled to the nanoparticles. Although the universal paramyxovirus vaccine design strategy proposed six preF-stabilizing mutations, incorporation of the sixth mutation (Y53P) negatively affected the protein stability. NDV-F variants containing four or five stabilizing mutations showed improved protein stability, reduced aggregation and stronger binding to NDV-F specific monoclonal antibodies, compared to the wild-type recombinant NDV-F variant. In contrast, the variant with six stabilizing mutations showed increased aggregation and loss of antibody binding. Based on these findings, two stabilized NDV-F variants were selected as lead vaccine candidates and will be evaluated in a vaccination study in chickens alongside the wild-type recombinant NDV-F variant, both displayed on nanoparticles. These results demonstrate that the AI-guided universal paramyxovirus vaccine design strategy can support rational antigen design of a distantly related virus by identifying promising stabilizing strategies. However, experimental validation remains essential, as the predicted mutations do not always result in the most optimal antigen.



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P04

From Phytoremediation to Biorefinery: Downstream Processing of *Tetradesmus obliquus* Cultivated in the Presence of Cosmetic UV Filters

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Abstract

The use of microalgae for wastewater treatment offers a sustainable approach for removing emerging contaminants (EC) while generating biomass that might be further utilized. However, the presence of persistent organic pollutants, such as some cosmetic UV filters, raises important questions about the safety and real applicability of the resulting biomass. In particular, the fate of these contaminants during further downstream processing (DSP) in a biorefinery is unknown. In this study, *Tetradesmus obliquus* was cultivated in the presence of representative UV filters commonly used in sunscreen formulations, at concentrations relevant to cosmetic wastewater. The effects of individual and combined contaminants on microalgal growth were evaluated, together with the uptake of selected UV filters by the biomass. For this, an HPLC-DAD method was developed to detect and quantify the target compounds in the culture medium and biomass extracts. Preliminary results showed that contaminant exposure influenced growth in a dose-dependent fashion, while HPLC analyses indicated that a fraction of the UV filters remained in the harvested biomass. Current work focuses on developing a DSP strategy based on sequential fractionation. The objective is to determine the distribution of UV filters among the aqueous, lipid-rich, and residual solid biomass fractions, providing key insights into their fate during biomass processing and the implications for its potential valorization within a circular bioeconomy framework.

P05

Developing of a Modular Workflow to Engineer *Xanthobacter SoF1* for Recombinant Food Protein Production from Air and Renewable Energy

Maria Bernal Cabas

Abstract:
Hydrogen-oxidizing bacteria (HOB) are a diverse group of microorganisms capable of utilizing hydrogen gas (H_2) as an energy source while fixing carbon dioxide (CO_2) via the Calvin-Benson-Bassham (CBB) cycle. This unique metabolism makes HOB highly attractive for the sustainable bioproduction of food proteins from non-arable feedstocks helping alleviate the planetary crisis. Among these, *Xanthobacter* species, particularly *Xanthobacter SoF1*, has shown potential as a highly sustainable food source due to its efficient CO_2 fixation capabilities and nutritious biomass.

However, the absence of suitable genetic tools is currently limiting its industrial exploitation. To address this limitation, engineering workflow tailored to Xanthobacter SoF1 for recombinant protein production, with potential applicability across other Xanthobacter species. This workflow streamlines strain development and genetic manipulation, enhancing the applicability of SoF1 for sustainable bioproduction. As part of this workflow, we developed a Modular Cloning Kit (SoClo) and identified optimal growth conditions using phenotype microarrays to accelerate strain development in heterotrophic conditions. The workflow's effectiveness was validated using plate screenings, flow cytometry, and activity assays.

The successful development of this toolkit establishes a robust platform for genetic manipulation of *Xanthobacter SoF1*, advancing its potential for applications in sustainable bioproduction and CO_2 fixation.

P06

Small-scale bioreactor cultivation of HEK293-based suspension cells increases extracellular vesicle (EV) yield

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Abstract

Extracellular vesicles (EVs) are increasingly explored as natural vehicles for cell and gene therapies, and drug delivery applications. However, challenges associated with yield and scalability of EV production still pose major challenges in the clinical translation of EV-based therapies. Therefore, this study aimed to quantify and characterize EVs released by Expi293F cells (suspension-grown HEK293 cells) cultivated in either shaker flasks and small-scale bioreactors with the aim of examining the influence of either culturing environment on EV production.

For this purpose, Expi293F cells were cultivated (N=3) in both shaker flask and 500 mL bioreactor system and total cell density, viability, and size were monitored. Supernatants were drawn daily post-inoculation and samples were analyzed for EV concentration, size, morphology, and CD63 expression (a putative EV marker).

The results showed that no differences were observed at the cellular level between both cultivation conditions. However, cultivation of Expi293F cells in the bioreactor environment was observed to significantly increase EV yield compared to shaker flask cultivation (~3-fold difference, $p < 0.01$). Other parameters such as average nanoparticle size, morphology and CD63 expression were comparable between cultivation conditions.

To conclude, these results demonstrate that Expi293F-derived EV yield can be increased by culturing the cells in a bioreactor setting, without changing baseline properties of the EVs. In turn, these findings pave the way for the production of therapeutic-based EVs using the small scale bioreactor as a scalable bioreactor system.

P07

Freshwater microalgae strain selection for industrial triacylglycerol production – a scale-down approach

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Abstract

Microalgae are a promising source of sustainable lipids, particularly triacylglycerols (TAGs), but large-scale production remains economically unviable and depends on strain selection. In this study, four microalgal strains were selected based on their ability to accumulate TAG: Tetradesmus obliquus wild type (wt), Tetradesmus obliquus starchless mutant 1 (slm1), Chromochloris zofingiensis, and Neochloris oleoabundans. These strains were compared on growth rate, areal fatty acid productivity, and photosynthetic parameters under diurnal light and temperature cycles and nitrogen-sufficient and nitrogen-deficient conditions. This scale-down approach integrates laboratory screening under environmental fluctuations, providing novel insight into strain performance relevant for large-scale TAG production. Under nitrogen sufficiency, T. obliquus wt and slm1 showed the highest growth, reaching 10.0 ± 0.2 (n = 2) and 9.7 ± 0.2 (n = 2) g m^{-2} day^{-1}. Under nitrogen starvation, only slm1 maintained growth at 8.4 ± 1.6 g m^{-2} day^{-1}, as productivity in other strains declined significantly. Additionally, T. obliquus slm1 reached the highest total fatty acid content with 44.7 ± 3.7%, with 38.8 ± 2.8% of TAG. Therefore, T. obliquus slm1 emerged as the highest TAG producer and reached an average areal productivity of 7.3 ± 1.1 g_{TAG} m^{-2} day^{-1} over the second week of starvation. The potential of this strain was demonstrated in a 275 L vertically stacked tubular photobioreactor, achieving an average volumetric biomass productivity of 0.53 ± 0.06 g L^{-1} day^{-1} during the growth and 0.28 ± 0.06 g L^{-1} day^{-1} during the stress phase. These values correspond to areal biomass productivities of 25.2 ± 2.8 g m^{-2} day^{-1} and 13.48 ± 3.01 g m^{-2} day^{-1}. After 21 days of stress, the lipid content reached 42.9 ± 0.9% TFA and 32.5 ± 0.5% TAG.

P08

Lemin Chen

TU Delft

Abstract

Saline wastewater, from industrial discharge to seawater intrusion, is known to be difficult to treat, as high salt concentrations destabilize the microbial communities responsible for purification. Aerobic granular sludge (AGS) is a wastewater treatment technology in which microorganisms grow in robust granules held together by self-produced extracellular polymeric substances (EPS). While salinity affects AGS performance, how microbial communities adapt their EPS matrix to maintain granule stability under salt stress remains unclear, limiting both the design of AGS systems and their potential for resource recovery from waste sludge. To study this, AGS was exposed to a stepwise seawater salinity increase (0–4%), replacing over 90% of the biomass at each step to ensure physiological adaptation was captured. Stable granulation, growth and performance were observed at each condition, showing that AGS can be a viable platform for treating saline streams up to 4% salinity. The EPS composition shifted towards glycoproteins with lower glycan diversity but higher negative charges, such as sialic acid and sulfated groups. Overall, the EPS negative charge increased by nearly 20% at the highest salinity, suggesting an adaptive response that contributes towards EPS stability under saline conditions. These shifts coincided with a dominance of the microbial community by a single organism, "*Ca*. Accumulibacter" (also known for its role in phosphate removal), which came to dominate up to 69–75% at salinities of 1% and above. Moreover, the increased production of cell-envelope building blocks under high salt stress suggested a clear adaptive strategy, while simultaneously downregulating its putative glycoprotein production. Together, these findings highlight how "*Ca*. Accumulibacter" dynamically adapts its EPS, contributing to the robustness of AGS and point to new resource recovery strategies.

P09

A Novel Halotolerant *Photobacterium halotolerans* Strain for Efficient PHA Production under Saline Conditions

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Abstract

Polyhydroxyalkanoates (PHAs) are promising bio-based alternatives to conventional petrochemical plastics because of their thermoplastic properties, biocompatibility, and biodegradability. However, their widespread industrial implementation remains constrained by high production costs, stimulating interest in extremophilic and halotolerant microorganisms that can support robust fermentation processes under selective cultivation conditions. In this context, hypersaline environments represent a largely underexplored reservoir of microbial biodiversity with potential for the discovery of novel PHA-producing strains.

In this study, a halotolerant strain, *Photobacterium halotolerans* 1B3.2(2), isolated from the Tarquinia saltworks (Italy), was investigated as a new microbial platform for intracellular PHA production. Genomic analysis revealed the presence of genes associated with PHA biosynthetic pathways, supporting the metabolic potential of the strain for biopolymer synthesis. Shake-flask screening revealed that PHA accumulation was strongly dependent on carbon source and salinity, with glucose and 5% NaCl providing the most favorable condition.

Scale-up to controlled batch bioreactor cultivation further improved process performance compared with shake-flask conditions, demonstrating the importance of optimized cultivation parameters for enhancing polymer accumulation. Finally, implementation of a fed-batch strategy based on controlled glucose feeding and automatic pH regulation substantially increased PHA production, reaching intracellular polymer contents of up to 75% of cell dry weight

P10

A hybrid whole-cell biosensor for high dynamic range pyruvate sensing

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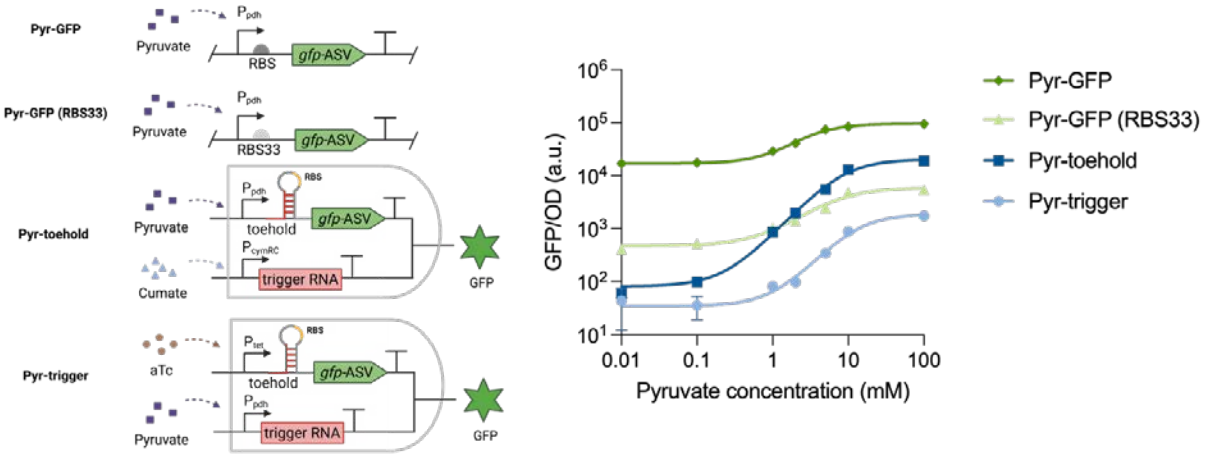
Abstract

The whole-cell biosensors based on transcription factors (TFs) provide a powerful approach for metabolite sensing, but their dynamic range can be constrained by the coupling of ligand recognition and reporter expression within a single transcriptional regulatory layer. Here, we developed a modular TF–toehold switch (TF–TS) biosensor architecture that couples TF-mediated metabolite recognition to downstream translational activation through an additional RNA regulatory layer. Using two rounds of Design–Build–Test–Learn cycles guided by design of experiments (DoE), we systematically optimized the toehold switch module by tuning plasmid copy number, ribosome binding site (RBS) strength, and inducer-controlled RNA expression. A medium-copy-number construct with a strong RBS achieved the highest ON/OFF ratio and exhibited efficient signal decay. This optimized module was coupled to the pyruvate-responsive transcription factor PdhR. The resulting Pyr-toehold biosensor showed a 44.7-fold higher dynamic range and a 210-fold lower basal expression compared with the conventional PdhR-based biosensor. Temporal induction experiments further demonstrated that the two regulatory layers could be activated in different temporal orders, enabling the timing and magnitude of reporter activation to be modulated by either input. Together, these results demonstrate that coupling TF-mediated metabolite recognition with programmable RNA-level translational control can improve both the dynamic range and temporal controllability of whole-cell biosensors. This modular architecture provides a potential framework for engineering biosensors with independently tunable signal output and regulatory dynamics.



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P11

Yue Guan
Wageningen University

Aflatoxin B_1 (AFB_1) contamination by *Aspergillus flavus* poses significant threats to food safety and public health. Herein, we developed a spore-forming *Bacillus*-based whole-cell biosensor array for early detection of *A. flavus* contamination and subsequent AFB_1 risk assessment in maize. Metabolomic analysis identified styrene and 2-hexyl-1-octanol as early volatile markers of mold contamination. Guided by transcriptomic analysis, 20 biosensors were constructed and 8 responsive strains were assembled into a biosensor array. Coupled with a Random Forest classifier, the array achieved reliable discrimination of contaminated maize (AUC = 0.957). Early biosensor responses also enabled prediction of AFB_1 threshold exceedance at 5 dpi (AUC = 0.963), allowing risk assessment up to 3 days in advance. In addition, the biosensors retained high sensitivity (<1 μg/kg) and analytical performance after one month of room-temperature storage as spores. Overall, this work provides a promising strategy for early mold detection and mycotoxin risk assessment in grain storage.

P12

Abstract NBC 2026

The robustness of *Escherichia coli* redox homeostasis to perturbations in NAD(H) levels

Elisabeth van der Heijden[1], Johan van Heerden[1], Frank Bruggeman[1]

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Abstract

Redox metabolism lies at the heart of cellular energy conversion and strongly influences the metabolic capacity of living systems. Imbalances in cellular redox state are linked to major diseases such as Parkinson's disease, cancer, and mitochondrial disorders. Conversely, rational engineering of redox metabolism has proven highly effective for improving product yields in biotechnology. Yet despite the importance of redox cofactors such as NAD(H), many fundamental questions about redox metabolism and its regulation remain unresolved.

This project focuses on trying to understand how redox state shapes metabolic behaviour in *Escherichia coli*, a microbial workhorse in biotechnological and biomedical research. Through multi-omics screening of wild type strains in diverse conditions, as well as titratable mutant strains with perturbed NAD(H) pools, we characterize the cells robustness in changing redox states. We aim to gain fundamental insight in how microbes adapt to different redox states, offering new insights for both metabolic engineering and the understanding of redox-related pathologies.

P13

Loles Hoogerland

Poster withdrawn

P14

Upstream process development for cell-tolerant direct capture of monoclonal antibodies

Stefan Kint[1], Ivo Tjalma[2], Marcel Ottens[2], Marieke Klijn[2], Dirk Martens[1], Michel Eppink[1] and René Wijffels[1]
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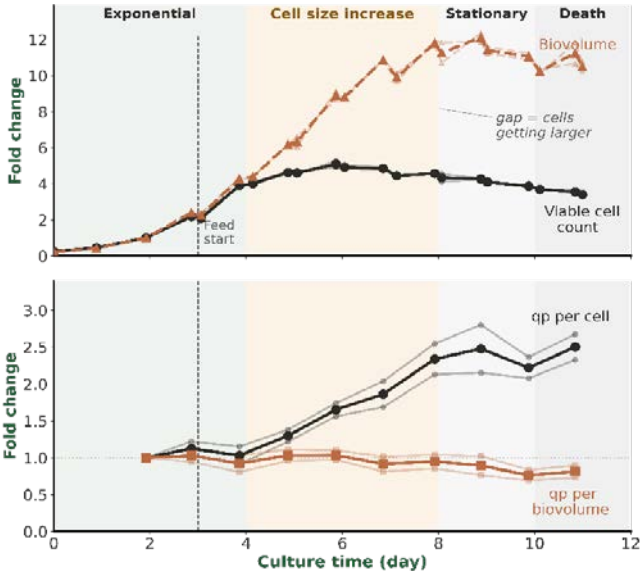
Abstract

Continuous antibody manufacturing may remove clarification unit operations by loading whole CHO culture broth directly onto a cell-tolerant Protein A capture column. In this direct-capture technique, cells pass through the column while antibody is captured and later eluted. This could simplify the process, but it also changes the role of upstream processing. The capture column is now exposed to the biological and physicochemical state of the culture rather than to clarified harvest.

This project asks whether upstream process development can define and control the harvest-state requirements for direct capture. The work focuses on three classes of column-relevant harvest variables: particle-related properties, including viable biomass, size distribution, aggregates and debris; dissolved components, including mAb product, host cell proteins, and metabolites; and physicochemical properties, including pH, osmolality, conductivity and viscosity. These variables will be linked to capture-relevant outcomes such as pressure development, breakthrough, dynamic binding capacity, recovery and fouling.

The first biological focus is cell size dynamics in CHO fed-batch culture. Preliminary fed-batch data show that viable cell density alone can become an incomplete process metric when cell size changes. It was found that cell count plateaus while viable biovolume continues to increase. Productivities expressed per cell and per biovolume can therefore lead to different interpretations of the same culture state. This matters for feeding strategy, productivity analysis and the biomass load presented to direct capture. Cell size may also co-vary with aggregation, viability decline and lysis-related impurity release.



The research strategy is to quantify the phenotype across CHO cell platforms, perturb candidate triggers such as amino acid balance, organic acids, osmolality and feed timing, test reversibility and cell-cycle involvement, and translate the resulting culture-state map into upstream control targets for column-compatible fed-batch and perfusion operations. The intended output is an upstream framework that connects CHO culture physiology to direct-capture process design.

P15

From Off-Gas to Insight: Real-Time Monitoring with Dual-Comb Spectroscopy

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[1] *Delft University of Technology, The Netherlands*

Abstract

Volatile organic compounds (VOCs) in bioreactor off-gas provide a non-invasive view of bioprocesses[1], yet their real-time monitoring remains a major bottleneck in industrial biotechnology. Current analytical approaches, such as gas chromatography, lack temporal resolution for dynamic process monitoring[2], limiting the use for applications such as advanced process control and early contamination detection.

Dual-comb spectroscopy (DCS) is currently explored as a process analytical technology (PAT) to enable continuous, high-resolution monitoring of VOCs in off-gas[3,4]. By providing real-time access to the VOCs produced by the cells, DCS has the potential to complement existing liquid-phase PAT and expand process variables without invasive sampling.

DCS-based off-gas monitoring has broad biotechnological potential. In industrial biotechnological processes, continuous VOC measurement may enable improved process monitoring, support mass balancing, and facilitate control strategies based on metabolic activity[5]. In food-related bioprocesses, off-gas VOC profiles provides insights into the formation of volatile flavor compounds and byproducts[6], enabling quality monitoring during production. Additionally, deviations in VOC signatures offer a promising route for early detection of contamination or process disturbances[7].

Together, these capabilities position DCS as a versatile PAT tool for enhancing process understanding, enabling data-driven control strategies, and supporting robust scale-up of biotechnological processes.

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P16

Jeroen Koendjbiharie

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P17

Development of a large-scale process for mycelial whole-cut meat alternatives.

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Abstract
Mycelium-based whole-cut meat alternatives are a promising candidate for reducing the environmental footprint of food production, while moving away from the ethical concerns tied to conventional livestock farming. To achieve commercial viability at a scale and cost competitive with conventionally farmed meat, the scale-up of production processes for these alternatives is essential. However, transitioning to larger bioreactor scales introduces potential scale-up issues which may affect bioprocess performance, both in terms of product quantity and quality.

The MycoStruct project focuses on the development and scale-up of mycelium-based whole-cut meat alternatives. Within this project, we characterise the scale-up challenges inherent to mycelial cultivation for whole-cut meat production, and to develop an optimised large-scale bioreactor design. This will be achieved through a combination of fundamental bioprocess modelling, and detailed computational fluid dynamic (CFD) to obtain insights in the local cultivation environment in large-scale reactors. With this, we aim to evaluate the design parameters that have most impact on the product quality and quantity. This framework aims to inform the optimisation of bioreactor designs and operating conditions at target scales between 500 L and 100 m^3 for industrial mycelium production.

Acknowledgement: The MycoStruct project is supported by the Circular Bio-based Europe Joint Undertaking and its members and co-funded by the European Union under Grant Agreement No. 101292039. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or CBE JU. Neither the European Union nor the CBE JU can be held responsible for them.

P18

Cyanobacterial conversion of concentrated CO_2 streams into functional food, feed, and cosmetic ingredients

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Abstract

Replacing fossil carbon with renewable feedstocks to produce functional platform molecules is a key focus for both academia and industry. Cyanobacteria are promising candidates: powered by sunlight and CO_2, they convert waste carbon streams directly into high-value proteins, carbohydrates and pigments. This process offers higher selectivity, lower energy demand, and a smaller environmental footprint than fossil-based routes. Nonetheless, industrial uptake is still limited due to incomplete optimization of conversion pathways under real-world CO_2 load conditions.

The project addresses this bottleneck by producing functional ingredients from cyanobacteria cultivated directly on concentrated CO_2 streams such as industrial emissions. The work presented here covers the first stage: identifying strains that tolerate elevated CO_2 while maintaining high bioactive content. Subsequent stages of the project encompass cultivation optimization and the development of a solvent-minimized, multi-product downstream process designed for scale-up.

Screening has so far identified seven cyanobacterial strains capable of sustained growth at CO_2 concentrations up to 5% v/v. For some strains, increasing CO_2 from 2% to 5% v/v boosted biomass productivity by 30–40%, indicating that higher carbon concentrations act as a productivity enhancer rather than a stress factor in specific cases.

P19

Developing and testing novel approaches for sustainable hydrogen production via direct biophotolysis in Synechocystis PCC 6803

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[2] *Uppsala University, Sweden*

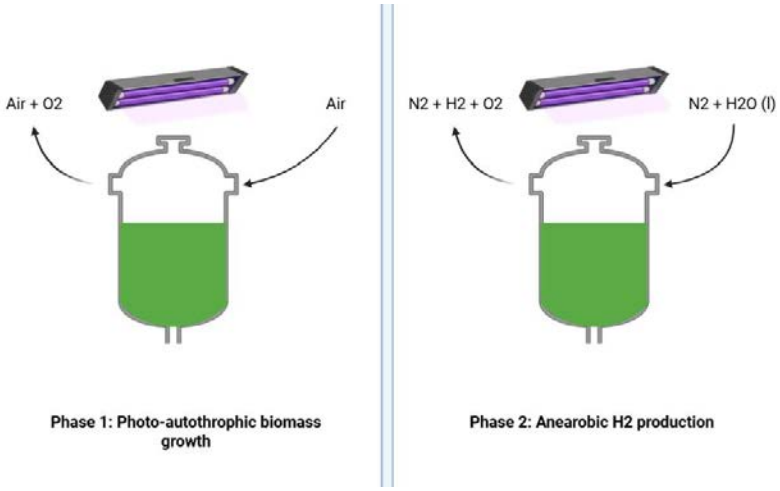
Abstract

In the current day and age, cleanly produced hydrogen gas (H_2) is still not abundantly available to fulfill its projected role in the energy transition alongside electricity. To truly make H_2 production competitive and large-scale, direct conversion of solar radiation to hydrogen gas is required. Within nature, inside all photosynthesizing organisms, this conversion already partly takes place during a process called biophotolysis. Here, water is split into protons, electrons and oxygen, forming all the constituents necessary for hydrogen gas generation.

Since the 1970s, numerous strategies have been developed to capitalize on this process. But so far, scientists have consistently encountered challenges related to the oxygen sensitivity of hydrogenase enzymes, competition with growth-related enzymes such as RuBisCO for reducing equivalents, and the formation of inhibitory by-products. However, with the rise of new genetic engineering techniques, a better understanding of the photosynthetic apparatus and the physiology of cyanobacteria in particular, a foundation for new approaches has been laid in the last two decades.

In this Master's thesis, the student proposed and tested three original ideas to enable efficient and sustainable hydrogen production in *Synechocystis*. First, production was suggested to be separated into a biomass yielding photo-autotrophic growth phase under ambient conditions and an anaerobic H_2 production phase in light. When sufficient biomass is reached, a switch in the gas composition of the headspace from air to 3rd grade N_2 is realized through a weak vacuum. Consequently, the two substrates of RuBisCO, CO_2 & O_2 are minimized, reducing the pull of the main electron sink. Second, several oxygen sensitive promoters were either screened or synthetically constructed and subsequently tested for their *in vivo* response. This with the aim to only allow for transcription of the hydrogenase enzyme under anaerobic conditions, aiding enzyme stability. Third, the phycobilisome interacting domain of FNR_l from *Synechocystis* was copied and put on the N-terminal side of the hydrogenase. With this, the hydrogenase is positioned physically close to the source of reducing equivalents at PSI, optimizing the direct conversion into H_2. Due to time constraints, the results are not available yet.

Illustration



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P20

Retroviral vector production scale-up – Developing a downscale model increases process development efficiency

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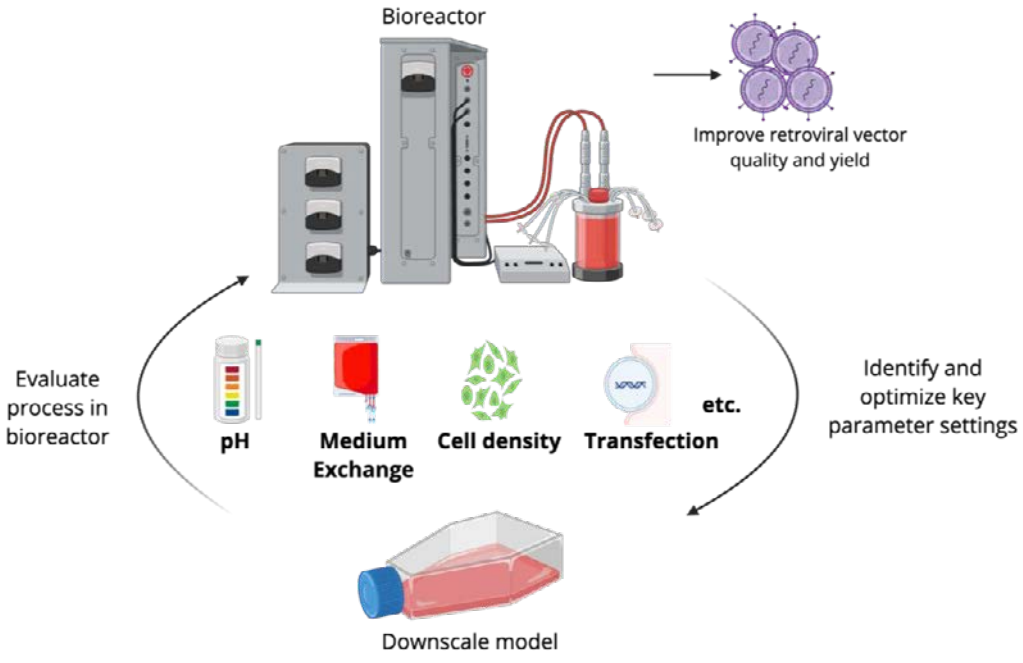
Abstract

Limited access to scalable and GMP-compliant viral-vector manufacturing constrains academic translation of gene-modified cell-based advanced therapy medicinal products (ATMPs). A survey of EU academic, nonprofit and commercial ATMP facilities identified scale-up complexity as the most frequently reported production challenge, with cost-effectiveness and regulatory compliance identified as key priorities.

In response, a γ-retroviral vector manufacturing platform was developed for an engineered T-cell therapy targeting haematological malignancies. The process was transferred from T175 flasks to a scale-X hydro fixed-bed bioreactor, providing a closed system with controlled culture conditions and continuous monitoring. This reduced dependence on labour-intensive flasks for viral production. The fixed-bed bioreactor supports higher production capacity and process consistency while reducing contamination risk. Following the scale-up study, a flask-based downscale model is being developed and assessed for its reproducibility and comparability with the fixed-bed bioreactor. Preliminary studies with this model allowed identification of several process parameters that can affect vector functionality and yield. The settings of these parameters can be further optimized before being tested at bioreactor scale. The downscale model has shown the potential to increase the efficiency of process characterization and development by reducing the need for resource-intensive large-scale runs, while the fixed-bed bioreactor provides a platform for development of a robust, GMP-oriented production process.



P21

Sedimentation accelerates mixed-substrate conversion in sequential batch yeast co-culture systems

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Abstract

Fermentation of substrate mixtures from lignocellulosic biomass can reduce substrate costs, but is often hindered by inefficient, sequential consumption of sugars by a 'sugar-generalist' *Saccharomyces cerevisiae* strain. While co-cultures of 'sugar-specialist' *S. cerevisiae* strains can enable parallel consumption, their overall conversion time is dictated by the slowest fermenter, which limits volumetric productivity. This study presents a strategy to overcome this limitation by knocking out ACE2 in a slow-fermenting arabinose-specialist *S. cerevisiae* strain, resulting in a multicellular phenotype for fast sedimentation. Furthermore, by implementing a short settling phase between batch cycles in sequential-batch bioreactors, the specialist's biomass is selectively concentrated, thereby improving consumption kinetics in subsequent cycles. This approach reduced the overall fermentation time by 30% in monoculture and enabled near-simultaneous depletion of arabinose and glucose in co-culture of a fast-growing glucose-specialist strain with the sedimenting arabinose-specialist. These results show that selective sedimentation of co-culture partners can improve fermentation kinetics in sequential-batch cultures. If compatible with industrial process conditions, this strategy has the potential to improve economics of co-culture-based fermentation processes.

P22

Built to Last: Self-repair in Living Mycelium Materials

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Abstract

Mycelium-based materials are emerging as a promising sustainable alternative to conventional synthetic materials. In addition, Engineered Living Materials (ELMs) offer new possibilities for material functionalities, such as adaptive growth or self-repair. In this research, we investigate the production, mechanical properties, and self-repair capacity of a mycelium-based living material.

A mycelium-based material can be either a pure mycelium material or a mycelium-bound composite, where the fungal hyphae infiltrate and bind a lignocellulosic substrate. In our ELM, the hyphae function as the structural component of the material, whereas co-cultivated bacteria are engineered to carry out programmable functions. The fungus, *Schizophyllum commune,* can grow over non-nutritive environments (such as plastic or air) which is an important feature for self-repair. When growing blocks of *S. commune* composite, two blocks can adhere to each other through fungal growth, creating a biological bond or glue between the blocks. Additionally, *E. coli* can co-migrate with the fungal hyphae over a non-nutritive environment to cover a distance of at least 3 mm, demonstrating the potential transport and redistribution of the engineered functionality in an ELM.

Next, pure mycelium sheets were produced in monoculture or in co-culture with bacteria *E. coli* or *Pseudomonas putida*. Mechanical testing showed that monoculture sheets are stronger than co-cultures, while the elasticity remained unchanged. To assess self-repair, a cut was made in the mycelium sheet. Both mono- and co-culture sheets demonstrate self-repair when wet, and both fungal and bacterial cells are present in the repaired region. The repaired material retained mechanical properties comparable to undamaged material. And, although dried sheets normally do not self-repair, the addition of moisture enabled repair regardless of whether the damage occurred before or after drying. Together, these results show that mycelium-based living materials have the potential to self-repair after damage and can retain their strength and functionality.

Acknowledgements
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P23

Carl Schuurmans

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P24

Hap as a Key Extracellular Protease Driving Aeromonas salmonicida-Mediated Meat Spoilage

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Abstract

Dominant spoilage bacteria are the major microbial factors driving the spoilage process of chilled meat. Previous studies have found that *Aeromonas* is an important spoilage bacterium in chilled chicken, showing both numerical dominance and strong spoilage potential. However, the key spoilage effector proteins in its extracellular secretions and their mechanisms of action remain unclear. In this study, hemagglutinin protease Hap was identified from the extracellular secretions of *Aeromonas salmonicida* through extracellular protein separation, purification, and functional characterization. Hap belongs to the M4 family of metalloproteases and contains two domains, Peptidase_M4 and Peptidase_M4_C. It possesses the conserved catalytic motif HEVSH and shows sequence conservation among various dominant bacteria associated with meat spoilage. Subsequently, the role of Hap in meat spoilage was validated by constructing a *hap* gene deletion mutant, *⊿hap*, and a complemented strain, *⊿hap*-C. The results showed that *hap* deletion did not significantly affect bacterial growth, motility, or autoaggregation, but weakened its ability to degrade meat proteins, indicating that Hap is an important factor involved in *A. salmonicida*-mediated meat protein degradation and quality deterioration. Recombinant Hap protein (rHap) was further obtained through heterologous expression and purification, and its molecular mechanism of action was analyzed. rHap extensively hydrolyzed major myofibrillar skeleton proteins, including myosin, actin, tropomyosin, and troponin, leading to weakened protein bands, collapse of fibrous microstructures, and the release of abundant small peptides. Cleavage-site analysis showed that rHap preferentially recognized hydrophobic amino acid residues at the P1′ position, especially leucine, suggesting that it may mediate continuous hydrolysis of myofibrillar proteins by recognizing exposed hydrophobic sites. Overall, this study reveals the mechanism by which Hap drives meat protein degradation and quality deterioration from three levels: extracellular effector protein discovery and identification, *hap* gene knockout validation, and mechanistic analysis based on heterologously expressed rHap. These findings provide a theoretical basis for developing precise preservation strategies targeting key extracellular proteases.

P25

Towards improving the adhesion of *Aureobasidium pullulans* as living and bio-based coating on wooden façade elements

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Traditional wood coatings rely on fossil-based components and synthetic polymers, creating environmental challenges that highlight the need for sustainable, circular alternatives. *Aureobasidium pullulans*-based coatings provide a promising alternative, supporting the transition towards a circular economy through the use of renewable biological materials. Such living coating would also have self-healing properties. The fungus can form a living biofilm on linseed oil-impregnated wood that protects the wood surface against damage and decay. However, a key challenge for the broader application of these coatings is achieving durable and reliable adhesion without compromising their circular properties. The fungus makes various cell types including blastoconidia, swollen cells, chlamydospores, and hyphae. In the present study these cell types were analysed for their adhesion behaviour using an oCelloScope imager. Results indicate differences in cell adhesion to cell culture polystyrene plates. A large proportion of the blastoconida (53 %) were removed by washing with 0.7 % NaCl. Hyphae adhered much stronger with only 20 % being removed by washing. These findings show that cell type composition within the coating influences the adhesion properties of *A. pullulans.* This provides a basis for controlling biofilm formation and the development of functional living coatings.

P26

Computational Design and In Silico Evolution of High-Affinity Trifluoroacetic Acid Binding Proteins for Water Filtration

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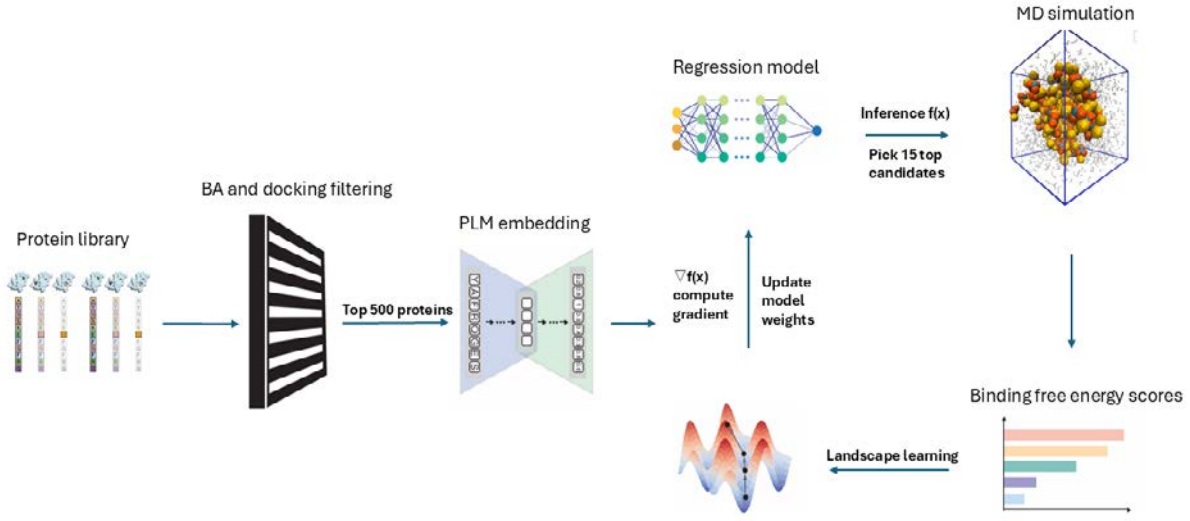
Abstract

Background The accumulation of ultra-short-chain fluorinated pollutants, specifically trifluoroacetic acid, poses a severe and growing threat to global water ecosystems. Due to its exceptionally small size and highly hydrophilic nature, this synthetic chemical easily evades conventional industrial filtration technologies, which either fail to trap it or merely concentrate it into toxic waste. While naturally occurring proteins exist that exhibit weak electrostatic interactions with this pollutant, there is currently no high-affinity biological protein capable of specifically capturing it. Developing a specialized engineered protein is therefore critical for integrating targeted extraction mechanisms into next-generation environmental water filtration systems.

Methods This project aims to computationally design and optimize novel proteins that bind trifluoroacetic acid with significantly higher affinity than any existing biological baseline. Furthermore, the research seeks to establish an automated computational evolution pipeline to iteratively maximize these binding interactions.

Aim The workflow begins with the construction of a massive computational library comprising over two hundred thousand potential protein structures, derived from generative machine learning models, biological baselines, and rationally designed variants. To efficiently screen this pool, high-throughput molecular docking and binding affinity predictions will serve as a primary filter to isolate the top candidate structures. These promising proteins will then enter an active-learning evolution pipeline. Within this pipeline, protein language models and regression algorithms—trained on rigorous molecular dynamics simulations—will iteratively map the functional landscape to pinpoint and evolve the strongest binders. Finally, the optimized candidate proteins will be computationally fused to an anchoring domain to evaluate the structural and thermodynamic resilience of the engineered binding pockets under the physical constraints required for real-world deployment.



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P27

BioXtract: A modular, targeted approach for electronic waste recycling

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Abstract

Electronic waste (e-waste) has emerged as one of the fastest-growing waste streams. Driven by rapid technological advancement and increasing global reliance on electronic devices, the total volume of e-waste is projected to reach 80 million tons by 2030. Concurrently, demand for critical elements is expected to surpass primary mining capacity by 2030. Although the recovery of these materials from e-waste represents a significant opportunity, current contributions remain minimal: merely approximately 1% of rare earth element demand is met through recycling, and only 22% of e-waste is properly collected and processed.

A major constraint on wider adoption lies in the limitations of existing recycling technologies. Hydrometallurgical methods, which are commonly employed for the recovery of valuable elements from e-waste, typically require harsh chemical reagents and elevated temperatures, thereby reducing their economic and environmental attractiveness for large-scale industrial implementation.

The BioXtract project develops a targeted and sustainable approach for critical metal recovery by leveraging microbial redox processes, biosorption, biomineralisation, and biogeochemical principles for metal separation. This strategy provides a more sustainable and efficient alternative to conventional e-waste treatment methods.

The BioXtract system is a modular, nature-inspired biotechnological platform for the selective recovery of critical elements from e-waste and other waste streams such as mining waste or incineration ashes. It integrates biological and abiotic processes that mimic natural element cycling and comprises four key modules: (i) Waste characterization and pre-treatment to enhance element accessibility (ii) microbially driven bioleaching to reduce energy and harsh chemical inputs, (iii) selective (bio)sorption and biomineralisation for metal concentration and stabilisation, and (iv) controlled desorption and fractionation using geochemical triggers to achieve selective recovery. Its modular design enables both standalone operation and integration into existing recycling infrastructures.

Acknowledgement

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P28

Paraformaldehyde as Feedstock: A sustainable alternative for renewable methanol fermentations

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Abstract

Green methanol is emerging as a promising renewable alternative to fossil- and sugar-based feedstocks for sustainable bioproduction. However, methanol-based fermentation requires high oxygen input, which can increase energy demand and production costs at industrial scale. This project explores a more economical and sustainable approach for producing biochemicals, including Single Cell Protein (SCP).

FeedStocksUnited has proposed using paraformaldehyde, derived from renewable methanol, as an alternative carbon feedstock. Paraformaldehyde releases formaldehyde, which can be metabolized by suitable microorganisms as a source of carbon and energy while requiring substantially less oxygen than methanol-based processes.

In collaboration with HAN BioCentre, this concept was investigated through laboratory-scale experiments to establish its feasibility and generate proof-of-concept data. The research focused on the ability of selected microorganisms to utilize formaldehyde and on identifying process conditions that could support efficient production of SCP. The tunable chemical conversion of paraformaldehyde to formaldehyde also offers opportunities for improved process control, potentially reducing energy and feedstock consumption.

This poster presents findings from this innovative concept. It demonstrates the feasibility of using renewable methanol-derived paraformaldehyde as an alternative feedstock for SCP production. The findings from this collaboration between FeedStocksUnited and HAN BioCentre have laid the foundation for further optimization and future research to improve process efficiency and advance the concept toward industrial application.

P29

Evaluating Spectrum-Shaping Quantum Dots as a Light Management Strategy for N. oceanica.

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Wageningen University, Bioprocess engineering chair group
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Rising CO_2 levels combined with limited electrification options in aviation and shipping drive the need for sustainable fuels in these sectors. Microalgae such as *Nannochloropsis oceanica* are promising solar fuel producers due to their relatively high photosynthetic efficiency, rapid growth, and ability to accumulate lipids for biofuel while producing valuable co-products like EPA.

However, light management remains a critical challenge in microalgal production systems. While microalgae efficiently utilize blue and red wavelengths for photosynthesis, other portions of the solar spectrum are less effectively absorbed. At the same time, excess exposure to high-energy light can trigger photoinhibition, limiting photosynthetic performance and biomass accumulation. Modifying the spectrum of incident light may therefore improve overall light-use efficiency. In collaboration with the University of Amsterdam, this research project aims to improve light use efficiency by implementing polymeric foils containing quantum dots to shift the spectrum for optimal microalgae light use.

To evaluate foil performance in a high-throughput fashion, we screened twelve foil recipes using a biological oxygen monitoring device (Figure 1A). The first screening results show that foil 7.2 and 7.3 had increased oxygen production compared to the reference (Figure 1B). Currently, we are upscaling these foils and applying them to flat-panel photobioreactors, which will produce more industrially relevant data.

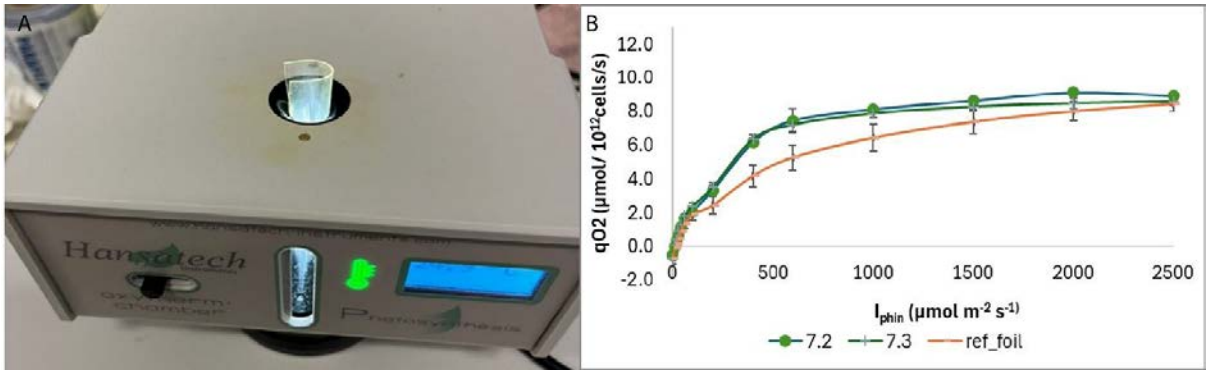

Figure 1: (A) The biological oxygen monitoring device (BOM) used to measure oxygen production of microalgae. (B) The oxygen production of microalgae cultures for foils enhancing the 600-700 nm range (7.2 and 7.3) compared to the reference.

P30

Elucidation and reconstitution of andrographolide biosynthetic pathway

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[1] *Agricultural Genomics Institute at Shenzhen, China;* [2] *Wageningen University & Research, Netherlands*

Abstract

Andrographis paniculata is an annual medicinal plant traditionally used for cold, fever, coughing, etc. The major bioactive component is a diterpene lactone named andrographolide. The production of andrographolide currently relies on extraction from the medicinal plant and is therefore restricted by the supply of plant materials. In this work, we applied transcriptomic and metabolomic methods to identify and validate key genes of andrographolide biosynthetic pathway, then introduce the whole pathway into *Saccharomyces cerevisiae* to obtain a yeast strain producing andrographolide. Optimization strategies will be applied to increase yield of engineered stains.

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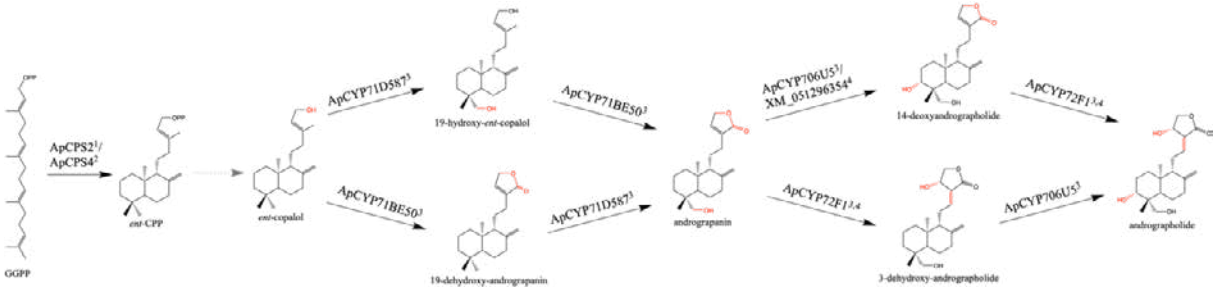
Illustration



Andrographolide biosynthetic pathway.

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Acknowledgement

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P31

Adaptive evolution in a novel culturing system is enabled by a metabolically driven convective flow

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Adaptive laboratory evolution (ALE) is a broadly used method to select mutant microorganisms with desirable phenotypes. Common methods include serial propagation and bioreactor cultivation, which are typically run for weeks to months. While these methods often provide the desired outcome, they are labour- and resource intensive and the phenotypic space that can be explored is still limited.

Here we present a novel method to culture microorganisms for several months without the need for intervention, creating a promising new tool for ALE. The method relies on near-horizontal, longitudinal growth through stationary liquid medium in tubing with inner diameters between 2-8 mm. We have successfully evolved various non-motile microorganisms such as *Lactococcus cremoris*, *Escherichia coli* and the obligate aerobe *Pseudomonas Putida*. These experiments, in some cases, involved uninterrupted growth over the course of 100+ days. The expansion speeds through the tubing vary with tube dimensions and material as well as media composition and the growth rate of the strain. While we can exclude cell motility and diffusion as a mode of expansion through the system, time-series imaging and numerical modelling showed that expansion occurs through a convective flow, generated by local density differences that originate from metabolic conversion of glucose to lactic acid. Mutant strains isolated at the end of the tubing exhibited different biomass yields and growth rates and the characterization of underlying point mutations is ongoing.

These results describe an unexplored mechanism to evolve novel phenotypes. We anticipate that, upon further characterization of the system, this approach will offer many possibilities for future strain development.