South Coast Biosciences Doctoral Training Partnership
SoCoBio DTP

2026 Annual Conference at the University of Sussex
24-26 March 2026

BOOK OF ABSTRACTS

We are pleased to recognise the generous sponsors
of the 2026 SoCoBio DTP Annual Conference:

South Coast Biosciences Doctoral Training Partnership (SoCoBio DTP)
Website: www.southcoastbiosciencesdtp.ac.uk

Contents

Biotechnology and Biological Sciences Research Council

SoCoBio DTP

Conference Programme

SoCoBio DTP Annual Conference DAY 1, 24th March 2026 Zoom link for online attendees, password will be emailed to attendees					
Start	**Finish**	**Duration**	**Room**	**Sessions**	**Chair**
12.30pm	1:00pm	30 minutes	Fulton G15	Arrival, registration and refreshments	
1:00pm	1.15pm	15 minutes	Fulton Lecture Hall B	Welcome by the DTP Director Prof Matthew Terry	Anastasia Kolesnikova & Macy Martin
1:15pm	1:45pm	30 minutes	Fulton Lecture Hall B	Translating research into impact led by Prof Dave Goulson	Anastasia Kolesnikova & Macy Martin
1:45pm	2:00pm	15 minutes		Group Photograph *Location: outside the Fulton B lecture*	
2:00pm	2:45pm	45 minutes	Fulton 107	Yr 4: Thesis writing skills led by Prof Daniel Osorio	
2:00pm	2:45pm	45 minutes	Fulton 104	Yrs 2-3: PIPS unpacked: Insights from experience and Q&A led by Dr Binuraj Menon	Zoom link for this session only (password will be emailed to attendees)
2:45pm	3:00pm	15 minutes	Fulton G15	Refreshment Break	
3:00pm	4:00pm	60 minutes	Fulton Lecture Hall B	**Presentation Session 1** Fiona Lancelotte (USusx) Matthew Ellis (UPort) Annie Robertson (USusx) Joy Adzovie (NIAB) Natasha Ward (UKent) William Edwards (UKent)	Iolanta Spanner & Adam Green

4:00pm	5:00pm	60 minutes	Fulton Lecture Hall B	Keynote Speaker Dr Mahoud Maina	Lucy Unwin & Dylan Lamptey
7:15pm Evening Dinner Yrs 2 &3 7:30pm Year 4 Celebration Meal					

SoCoBio DTP Annual Conference DAY 2, 25th March 2026 Zoom link for online attendees, password will be emailed to attendees					
Start	**Finish**	**Duration**	**Room**	**Sessions**	**Chair**
8:30am	9:00am	30 minutes	Fulton G15	Registration	
9:00am	10:20am	80 minutes	Fulton Lecture Hall B	**Presentation Session 2** Joseph Davies (UKent) Prince Cobbinah (NIAB) Jacob Hudson (UKent) Mahzad Nasir Shalal (UKent) Olivia Keers (UKent) Jo Fish (USoton) Molly Slade (USoton) Tatum Sevenoaks (USusx) Ria Hunt (UPort)	Anastasia Kolesnikova & Jacob Willcox
10:20am	10:35am	15 minutes	Fulton G15	Refreshment Break	
10:35am	11:40am	65 minutes	Fulton Lecture Hall B	**Presentation Session 3 (CASE)** Samuel Liu (USoton) David Cotriscau (USoton) Shubhangi Mahajan (USoton) Grace Heath (UPort) Shahd Al Balushi (USusx) Toby Jones (USusx) Matthew Irwin (USoton) *not attending*	Fiona Lancelotte & Annie Robertson
11:40am	12:40pm	60 minutes	Fulton Lecture Hall B	Keynote Speaker: Dr Catherine Green OBE	Dylan Lamptey & Lucy Unwin
12:40pm	1:40pm	60 minutes	Bramber Gallery 1 & 2	Networking Lunch	

SoCoBio DTP Annual Conference DAY 2, 25th March 2026 Zoom link for online attendees, password will be emailed to attendees					
1:40pm	3:10pm	80 minutes	Fulton Lecture Hall B	**Presentation Session 4 (CASE)** James White (UKent) Simon Thundow (UKent) Caitlin Price (UKent) Dmytro Prasolov (UKent) Reece Lane-Cartwright (USoton) Theo Hornsey (USoton) Xavier Jeanne (USusx) Iolanta Spanner (USoton) Sandra Usidamen (UPort) Michelle Lin (USoton)	Liliana Jeziorska & Palita Udomjarumanee
3:10pm	3:25pm	15 minutes	Bramber Gallery 1 & 2	Refreshment Break	
3:25pm	4:55pm	90 minutes	Bramber Gallery 1 & 2	**Spotlight & Strategy: Industry Pitches and Leadership Roundtables** led by Prof Arthur Butt	Chair TBC
4:55pm	5:10pm	15 minutes	Bramber Gallery 1 & 2	Break	
5:10pm	6:10pm	60 minutes	Bramber Gallery 1 & 2	**Poster Session 1** *Poster location in bold* **Group A:** *presenting 5:10pm to 5:40pm* **2** Daniel Beach (USusx) **5** Rachel Buchanan (USoton) **8** Ana Ferreira (UPort) **11** Miya Giragosian (UKent) **14** Liliana Jeziorska (USoton) **17** Christian Hollingbery (UKent, not present) **18** Thomas Jamieson (UKent) **Group B**: *presenting 5:40pm to 6:10pm* **23** Macy Martin (USoton) **3** Joshua Byrne (USoton)	Adam Green & Jacob Wilcox

SoCoBio DTP Annual Conference DAY 2, 25th March 2026 Zoom link for online attendees, password will be emailed to attendees					
				9 Holly Champney (USoton) **12** Joshua Fennell (NIAB) **21** Ateeqa Naim (UKent, not present) **26** Muhammad Zalkifal (USoton)	
7:30 Conference Dinner					

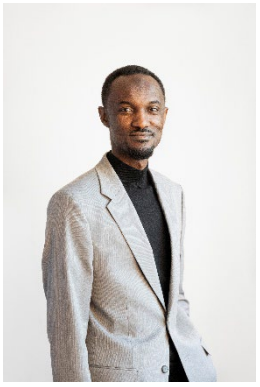
SoCoBio DTP Annual Conference DAY 3, 26th March 2026 Zoom link for online attendees, password will be emailed to attendees					
Start	**Finish**	**Duration**	**Room**	**Sessions**	**Chair**
8:30am	9:00am	30 minutes	Fulton G15	Registration	
9am	10:30am	90 minutes	Fulton Lecture Hall B	**Presentation Session 5** Juri Westendorf (USoton) Rio Coleman (USoton) Dyuti Basu Choudhury (USoton) Ewan Reed (USoton) Anastasia Kolesnikova (USoton) Felicitas Liessem (USusx) Oliver Clark-Hattingh (USusx) Nikolaos Sideris (USusx) Matthew Rice (UKent) Mackenzie Stevens (UKent) Oya Canik (UKent)	Sandra Usidamen & Xavier Jeanne
10:30am	10:45am	15 minutes	Bramber Gallery 1 & 2	Refreshment Break	

SoCoBio DTP Annual Conference DAY 3, 26th March 2026 Zoom link for online attendees, password will be emailed to attendees					
10:45am	11:45am	60 minutes	Bramber Gallery 1 & 2	**Poster Session 2** *Poster location in bold* **Group C:** *presenting 10:45am to 11:15pm* **1** Daniel Aspiazu (USoton) **7** Claudia Chitty (UKent) **13** Tia Fletcher (UPort) **16** Linda Guantai (USoton) **19** Emily Jones (USoton) **22** Courteney Pienaar (USusx) **24** Tom Roberts-Mcewen (UPort, not present) **Group D:** *presenting 11:15pm to 11:45pm* **4** Lydia Bennett (UKent) **6** Alex Cahill (UPort) **10** Emmanuel Denu (UKent) **15** Adam Green (USoton) **20** Emily Millerchip (USusx, not present) **25** Lucy Unwin (USusx)	Chair TBC
11:45am	12.45pm	60 minutes	Fulton Lecture Hall B	**Presentation Session 6** Afsheen Shahbaz (UKent) Matthew Shaw (UKent) Selale Cuce (UKent) Jack Bragg (UKent) Graham Lunn (UKent) Callum Ellis (USoton) Emily Woods (USusx)	Macy Martin
12:45pm	1:45pm	60 minutes	Bramber Gallery 1 & 2	Lunch and Laboratory Tours	

SoCoBio DTP Annual Conference DAY 3, 26th March 2026 Zoom link for online attendees, password will be emailed to attendees					
1:45pm	2:45pm	60 minutes	Fulton Lecture Hall B	**Presentation Session 7** Ian Hunter (UPort) Palita Udomjarumanee (USoton) Dylan Lamptey (USoton) Charles Ellis (USoton) Ryan Boughton (UKent)	Juri Westendorf
2:45pm	3:00pm	15 minutes	Fulton G15	Refreshment Break	
3:00pm	4:00pm	60 minutes	Fulton Lecture Hall B	**Presentation Session 8** Rhianne Broadway (USusx) *not attending* Jacob Willcox (USoton) Yomna Moqidem (USoton) Abigail Edwards (USusx) Emily Lucas (USoton) *not attending* Abhishek Johan Issac (USoton) *not attending* Alex Clarke (USoton) *not attending*	Macy Martin & Juri Westendorf
4:00pm	4:45pm	45 minutes	Bramber Gallery 1 & 2	Wellbeing Workshop with the DTP Wellbeing Dr Jenny Tullet	
4:45pm	5:00pm	15 minutes	Bramber Gallery 1 & 2	Concluding remarks & prizegiving by DTP Director Matthew Terry	

Keynote Speaker Bios and Abstracts

Dr Mahmoud Bukar Maina



Dr Mahmoud Bukar Maina is a Wellcome Trust Career Development Fellow based at the Biomedical Science Research and Training Centre (BioRTC), Yobe State University, with aspects of his work conducted at the Department of Neuroscience, University of Sussex, UK. His research focuses on the molecular mechanisms of tauopathies, including Alzheimer's disease, with a particular interest in the role of ancestry. His team develops and uses somatic cell and induced pluripotent stem cell (iPSC) models derived from indigenous African populations to investigate disease mechanisms.

With over a decade of experience strengthening African science ecosystems and leading dementia cohort development in rural communities, Dr Maina serves on several local and international committees and is Science Adviser to the Yobe State Government. His contributions have been recognised with multiple honours, including The Transmitter's Rising Stars in Neuroscience Award (2025), EMBO Global Investigator Network membership (2025), and the ALBA-FKNE Diversity Prize (2022).

Presentation Title: Developing Somatic Cells and iPSC Models from African Populations to Uncover the Role of Ancestry in Dementia

Abstract: Most cellular and genetic models of Alzheimer's disease and related dementias are derived from populations of European ancestry. This limits our understanding of how genetic background and life-course exposures shape disease mechanisms. African populations harbour the greatest human genetic diversity globally, yet remain largely absent from disease modelling.

In this lecture, I will describe the African iPSC Initiative, a programme established to generate somatic cells and induced pluripotent stem cell (iPSC) lines from deeply phenotyped African donors. Embedded within a growing ageing and dementia cohort in Northern Nigeria, this platform integrates cognitive assessment, blood and skin biopsy collection, genomics, and future neuroimaging with downstream cellular modelling. Over 1,000 skin biopsies and matched blood samples have been collected from older adults, creating an ancestry-informed cellular resource.

By linking population-level phenotyping with genome-wide genotyping and patient-derived neuronal models, this work aims to refine dementia biology using genetically diverse systems. Our approach provides an opportunity to identify ancestry-informed pathways of risk and resilience that may improve disease modelling and therapeutic development.

Prof Catherine Green OBE

Catherine Green is Professor of Clinical Biomanufacturing at the University of Oxford and a Fellow at Exeter College, Oxford. She formed part of the team who developed the Oxford-AstraZeneca Covid-19 vaccine and speaks widely about her experiences of hard work and cutting-edge science in a race against the virus. She is a cell biologist and geneticist who primarily researches medicines manufacturing and creates vaccines for clinical trials. Her team have produced several novel vaccines for human trials for malaria, Ebola, TB, influenza, Zika, MERS, amongst others.

Catherine's research career started in cancer genetics, with a PhD in Cancer Research UK's Clare Hall laboratories, she was then an EU Marie Curie Fellow at the Institut Curie, Paris, where she studied DNA damage in human cells. She worked at the University of Sussex exploring sunlight exposure damage to DNA, and then was a Cancer Research UK Research Fellow in the Department of Zoology, University of Cambridge, before moving to Oxford in 2012 to join the Wellcome Centre for Human Genetics.

Awarded an OBE for services to public health, Prof. Green is the author of the best selling book Vaxxers, and currently heads the Clinical BioManufacturing Facility at the University of Oxford.

Presentation Title: The challenges and rewards of GMP in academia

Abstract: Catherine Green is Professor of Clinical Biomanufacturing at the University of Oxford. She also heads the Nuffield Department of Medicine's Clinical Biomanufacturing Facility and is a Fellow at Exeter College, Oxford.

Professor Green's passion for science was solidified during her years spent studying biochemistry as an undergraduate at the University of Cambridge. She went on to receive an Imperial Cancer Research Fund (now Cancer Research UK) scholarship to complete her PhD research in the genetics of yeast DNA damage responses. Prior to joining the University of Oxford in 2012, Green held several prestigious fellowships, including a Marie Curie Fellowship at the Institut Curie in Paris, and a Cancer Research UK Research Fellowship in the Department of Zoology at the University of Cambridge, investigating the repair and replication of DNA damage in human cells.

Currently, Professor Green specialises in creating IMPs for clinical trials. She and her team at the Clinical Biomanufacturing Facility have developed several novel vaccines for first-in-human trials, targeting diseases such as Ebola virus, Zika virus, Middle East respiratory syndrome, plague, gonorrhea, and rabies, amongst others. The CBF aims to provide the link between academic research and clinical drug development, to allow all our collaborators to make rapid progress into clinical trials.

In 2021, Green was awarded an OBE for her services to science and public health following her significant contribution as manufacturing lead in the development of the OxfordAstraZeneca COVID-19 vaccine.

There are particular challenges to the cost-effective manufacturing of novel, one-off, small batches for clinical delivery in academic research programmes. Solving these requires operating to cGMP with phase appropriate validation, using a risk-based approach. I will give some examples of ways we have tackled these complexities, using recent projects as exemplars. Enabling more products to progress from the research group to the trial setting within universities, will hopefully result in more and better medicines moving towards clinical readiness, at lower overall cost.

Student Abstracts (in presentation order)

3MT – three-minute thesis style talk by Year 2 students
8MT – eight-minute talk by Year 4 students

Supervisory team format – SoCoBio DTP student, secondary supervisors, primary supervisor

Tuesday 24th March

Presentation Session 1 3:00pm to 4:00pm

8MT: Multivariate imaging of knowledge and memory in youth and ageing

Fiona Lancelotte (University of Sussex), Zara Bergström (University of Kent) and Alexa Morcom (University of Sussex).

As people age, memory for specific events (episodic memory) declines, due in part to less effective encoding into memory. Prior knowledge is critical for memory encoding and is preserved or increases in later life, but recent data suggest that the ability to access and use this information in a controlled manner becomes impaired. This reduced semantic control ability may partially explain episodic memory encoding difficulties. In an ongoing functional magnetic resonance imaging (fMRI) study, we test how the critical interplay between encoding and prior knowledge differs with age. Using multivariate methods, we will compare neural patterns to representational matrices capturing fine and coarse-grained semantic information, as well as low-level visual properties, and investigate how these are linked to successful or unsuccessful encoding. In line with previous work, we predict that coarse-grained semantic processing in the left inferior frontal gyrus (LIFG) will be associated with unsuccessful memory encoding and detailed semantic processing in the fusiform gyrus (FG) with successful encoding. We expect that older adults will represent fine-grained semantic information less strongly in the LIFG and FG – particularly in the semantic control task – and may be biased towards coarse-grained semantic information. This analysis, alongside planned univariate and task-based connectivity methods, will improve the fundamental understanding of memory difficulties in healthy older people.

3MT: Targeted surface modification with de novo designed enzymes

Matthew Ellis1, Prof Andrea E. Russell2, Prof Ross Anderson3, Prof Andy Pickford1, Dr Bruce R. Lichtenstein1
Affiliations: 1 University of Portsmouth, 2 University of Southampton, 3 University of Bristol

The biodegradation of synthetic pollutants is often dependent on natural enzymes that act on structurally-similar substrates. However, these proteins did not evolve specifically for such targets, typically requiring extensive mutagenesis to enhance their activities for

industrial applications. Although effective, this approach is time-consuming and limited by the native protein scaffold.

De novo protein design offers a powerful alternative, with the potential to develop rationally-tailored proteins for different industrial applications. However, current sequence design tools are not a one-shot solution, requiring extensive screening to identify optimal candidates. To address this limitation, we have developed an evolutionary design pipeline that expands the sequence search space, whilst simultaneously optimising any measurable property - applicable to a variety of industrially relevant targets.

We aim to demonstrate the flexibility of this approach by designing binders for copper atoms and a synthetic dye. Copper binding is intended to act as a stepping stone to a laccase-like de novo enzyme capable of assisting in the degradation of plastics, particularly those lacking natural analogs. The second design target aims to control the spectral properties of the dyes using the protein environment. A refined control over these properties will be useful in facilitating various photochemical reactions. Preliminary results already demonstrate strong fluorescence enhancement with a moderate sub-micromolar binding affinity. Additionally, early in silico results suggest that our pipeline will further enhance the binding strength and future integration of electric fields will help achieve a refined control over the spectral properties of the dye.

8MT: Risky decision-making: revealing the neural mechanisms of behaviour selection that maximise survival.

Robertson. A. 1, Ratnayaka. A. 2, Baden. T. 1, Kemenes. G. 1, Staras. K. 1
Affiliations: 1 University of Sussex, 2 University of Southampton

To maximise their chances of survival, animals must combine sensory inputs from their environment (e.g. the presence of a predator) with information about their internal motivational state (e.g. how hungry they are) to compute appropriate actions. The nature of these inputs can often lead to conflicts in decision-making. How does a hungry animal, under immediately threat of predation, decide whether it is more beneficial to feed or flee? The neural mechanisms involved in computing the most advantageous response to such scenarios is poorly understood. The pond snail, Lymnaea stagnalis, is a well-established model for detailed investigation of neural mechanisms underlying rhythmic behaviours such as feeding and locomotion which are crucially involved in survival motivated decision-making. This model lends itself to circuit interrogation due to its large and identifiable neurons, allowing for the use of intracellular electrophysiological recordings to investigate neural activity. However, this method is limited in its ability to monitor and characterise circuit operation at scale across the Lymnaea brain. To resolve this, we developed a voltage-sensitive dye imaging approach to assay neuronal activity across hundreds to thousands of neurons simultaneously. Using the commercially available photo-electron transfer (PeT)-based dye, FluoVolt™, we demonstrate faithful tracking of intracellular voltage changes across the central nervous system. By integrating this method with targeted intracellular

electrophysiology and stimulation approaches, we are able to simulate behavioural paradigms of threat conflict in our ex vivo model. This provides novel insights into how sensory threats are perceived and encoded across the central nervous system.

3MT: Optimizing Phosphorus Input in Strawberry Production

Joy Adzovie (University of Southampton), Dr Louisa Robinson-Boyer (NIAB), Dr Helen Cockerton (University of Kent), Prof. Mark Chapman (University of Southampton), Dr Eleftheria Stavridou (NIAB).

Phosphorus (P) is a crucial mineral resource for all life forms on Earth. All plant species, including strawberry, utilize P for their cellular metabolism, signalling, growth and development. However, indiscriminate P use has proven inimical to the environment as it poses toxicity risks for soil biodiversity, aquatic health and even human health through contamination of groundwater bodies.

P inputs for strawberry production are unsustainable, highlighting the need for alternative approaches, such as supplementation with microbial inputs like Arbuscular Mycorrhizal Fungi (AMF). AMF are beneficial microbes that form symbiotic associations with over 80% of land plants, with a key benefit being the enhancement of P uptake in exchange for photosynthetically derived carbon. This ancient relationship is conserved across many angiosperms and is triggered by P starvation. Notably, significant natural variation exists among strawberry cultivars in their ability to engage in AM symbiosis, suggesting genotype-specific regulation of symbiotic and potentially phosphate starvation response genes.

We have shown from preliminary studies that distinct AMF colonization patterns exist between two commercial strawberry varieties under contrasting P levels. In this study, I intend to dissect symbiotic and developmental signalling pathways to understand the molecular mechanisms underpinning P acquisition and AMF-induced root architectural remodelling in strawberries. This project will improve our understanding of P acquisition in modern strawberry production and guide strategies for sustainable P use in strawberries and other food systems.

8MT: Memory molecules and where to find them – does our brain store memories in binary format?

Natasha Ward (University of Kent), Prof Kevin Staras (University of Sussex), Dr Christopher Mulligan (University of Kent), Prof Dan Mulvihill (University of Kent), Dr Ben Goult (University of Liverpool).

Synaptic plasticity allows the brain to rewire itself in response to everything from learning a new skill to traumatic brain injuries. In the context of learning, removing unnecessary synaptic connections is as vital as creating new ones. However, when these processes go wrong they

can have disastrous consequences. Alzheimer's disease (AD), Schizophrenia and temporal lobe epilepsy have all been linked to altered synaptic plasticity. Understanding the mechanisms that allow the brain to choose which connection to enforce and which to prune may be the key to understanding how these diseases develop and ultimately how to treat them. Several hypotheses on how the brain rewires itself have been put forward, including the synaptic tagging and capture hypothesis, which suggests the existence of synaptic tags and plasticity-related proteins. While the identity of these tags has yet to be determined, the mechano-sensitive protein Talin has been suggested as a potential candidate. I will present data on my work on four rare Talin point mutations found in epilepsy patients, establishing the biochemical impact of the altered Talin proteins. I will also present data demonstrating that Talin can bind to the Amyloid Precursor Protein (APP), a protein involved in AD.

3MT: Investigating the role and effect of microbiome in regenerative farming practices

William Edwards (University of Kent), Dr Robert Barker (Co-PI, University of Kent), Dr Marc Dumont (Co-PI, University of Southampton), Dr Gary Robinson (chair, University of Kent) Anastasios Tsaousis (PI, University of Kent).

Presentation title: utilisation of next generation sequencing to monitor the effects of regenerative agricultural and ecological practices

A presentation showcasing various examples of how metagenomics and multi-omics approach can be used to support, validate and investigate novel agricultural practices as well as regenerative ecological practices (such as rewilding).

Biochar supplementation of cattle to alter cattle microbiomes. Metagenomic testing revealed broadly insignificant changes in gut microbiome diversity, with minor change being attributed to the supplementation of biochar (including significant increases in Anaerobutyricum and Corynebacterium). The study confirmed the importance of factoring in cattle diet, which had a greater effect than biochar supplementation.
Observational study on rewilded European bison. Bison released into Kent woodland to restore ecological diversity were monitored to track gut microbiome alterations upon release. Significant and consistent microbial trends were identified across all animals, including development of an 'adult' microbiome in the herd's calf. Parasite screening revealed that animals were infected by an increased diversity of parasites post-release.
Broiler poultry were supplemented with a diet of black soldier fly larvae, reared on lactose rich diets, to positively manipulate poultry microbiomes and overall health. Metagenomics identified increases of predicted probiotic taxa (Selenomondaceae), but not in lactic acid bacteria. Metabolomics confirmed the BSFL supplement significantly altered the metabolome of the poultry. Bone health analysis supported the supplementation confirming improved cortical area and rigidity.

All projects aim to validate (myth bust) up-and-coming or established regenerative practices and provide the scientific evidence needed to support their wider adoption or discourage ineffective methods.

Wednesday 25th March

Presentation Session 2 9:am to 10:20am

8MT: Live long and prosper: probing the mechanism of a transporter family linked to lifespan extension, protection from diabetes and obesity, and cancer.

Joseph Davies (University of Kent), Prof Da-Neng Wang (New York University), Prof Jonathon Essex (University of Southampton) and Dr Chris Mulligan (University of Kent).

DASS (Divalent Anionic Sodium Symporter) transporters are a group of membrane transporters found in both eukaryotes and prokaryotes that are defined by transporting anionic compounds with sodium ions across the cell membrane. One of the key DASS transporters is the human citrate transporter NaCT, encoded by the gene SLC13A5. Citrate is important for metabolism as it plays roles as an intermediate for the TCA cycle and as a regulator of fatty acid synthesis. NaCT is predominantly found in liver cells and is the primary way that citrate is transported making it an appealing target for inhibition for potential new drug treatments for both diabetes and obesity. Here, I discuss how the small molecule ETG5773 (A2) acts as an allosteric inhibitor for NaCT. Using an in vivo approach of expressing recombinant NaCT in HEK293 cells we were able to monitor citrate transport and elucidate the key inhibitor binding determinants by mutating key residues in the allosteric binding site. We were able to conclude that both the residues F323 and I151 are important for coordinating the binding of ETG5773 with the F323A mutation resulting in a 30-fold increase in IC50 when compared to WT.

3MT: Understanding the Interplay of Plant Genetics and Microbiome for Improved Disease Resistance

Cobbinah Prince1,2, Cernava Tomislav1, Chapman Mark1 and, Papp-Rupar Matevz 2
Affiliations: 1School of Biological Sciences, Faculty of Environmental and Life Sciences, University of Southampton, Southampton SO17 1BJ, United Kingdom, 2 NIAB, East Malling, Kent ME19 6BJ, United Kingdom

European canker, caused by Neonectria ditissima, reduces apple yield by over 30%. Canker management lacks effective chemical and biological controls. With canker resistance being polygenic, breeding resistant varieties remains unsolved challenge. Disease outcomes are influenced not only by host genetics but also plant defence pathways and microbiome interactions. This project investigates how variation in phenylalanine ammonia-lyase (PAL) gene activity influences apple microbiome and susceptibility to European canker.

PAL shows higher expression in canker-resistant apple genotypes. Preliminary genomic analyses of 11 apple cultivars identified five PAL genes. Phylogenetic reconstruction showed that the resistant 'Golden Delicious' and its susceptible descendant 'Gala' cluster closely at MdPAL1, MdPAL4, MdPAL5, and MdPAL3, reflecting shared ancestry, but diverge at MdPAL2, suggesting gene-specific differentiation and highlighting MdPAL2 as a potential candidate associated with canker susceptibility. Field and controlled inoculation assays are being conducted to determine whether PAL activity variation in apple genotypes corresponds with canker susceptibility. Bacterial and fungal communities will be characterised using amplicon sequencing to assess the relationship between PAL activity variation and microbiome composition. Finally, microbiome effects at infection time on canker outcomes are investigated, and culturable apple microbes are tested for inhibiting N. ditissima spore germination and sporulation, identifying protective taxa. PAL activity variability across apple genotypes may modulate canker susceptibility and microbiome structure, which will be investigated in the project.

Integrating host genetics, defence metabolism, and microbiome ecology, this research advances understanding of mechanistic links between PAL diversification, microbial community structure and canker resistance, supporting sustainable microbiome-informed strategies for improved apple health.

8MT : Pangenomics Predicts Antifungal Siderotype of Pseudomonas aeruginosa

Jacob Hudson, University of Kent; Marta Farré, University of Kent; Rebecca A Hall, University of Kent.

Bacteria produce a broad spectrum of metabolites with key clinical and industrial applications. One such metabolite produced by Pseudomonas aeruginosa is the iron chelating siderophore pyoverdine (PVD), of which three major (PVDI-III) and one minor (PVD-IV) type are known. We have previously demonstrated that PVDI, produced by P. aeruginosa PAO1, has antifungal efficacy against Mucorales fungi. These WHO priority pathogens are causative agents of mucormycosis, a disease with mortality rates reported as high as 96%. approaching

96% in disseminated infections. With only Amphotericin B and some Triazoles displaying limited efficacy further treatments are sorely needed. Identifying and characterising the lesser explored, and potentially unknown, PVD types would provide a range of new potential drug candidates. We identified the PVD biosynthesis region across all 464 complete P. aeruginosa genomes in the Pseudomonas Genome Database, and produced a pangenome graph of the region. This revealed three branches, differing in key PVD biosynthesis and import genes, likely corresponding to the three main PVD types. This allowed >98% of genomes to have a PVD type predicted. HMMs of type specific genes allowed concordant predictions of PVD type, which was validated with six strains producing a known PVD molecule. Finally, we showed that each PVD type has antifungal efficacy against Mucorales, demonstrating the power of pangenomics to predict new metabolites of medical relevance and increasing the pool of potential mucormycosis treatments.

3MT: Vesicle trafficking: a novel transformative technology for cellular engineering

Mahzad Nasir Shalal (University of Kent), Professor Dan Mulvihill (University of Kent), Professor Tim Fenton (University of Southampton), Professor Michelle Garrett (University of Kent).

Despite significant advances in cancer research and therapy, current treatments remain associated with severe side effects, cellular toxicity, high costs, and the development of resistance leading to recurrence. These limitations underscore the urgent need for innovative therapeutic strategies that improve specificity while minimizing systemic toxicity, particularly in advanced-stage disease.

This study investigates a novel targeted drug delivery technology based on synthetic vesicle nucleating peptide (VNp). VNp, derived from Escherichia coli (E. coli), promote the formation of membrane-bound vesicles capable of encapsulating active recombinant proteins. The aim is to genetically engineer vesicles to display a Programmed Death-1 (PD-1) tag on their surface, allowing specific binding to its ligand, Programmed Death-Ligand 1 (PD-L1), which is overexpressed on the cell surface of multiple cancer types. Five variants of untagged synthetic vesicles were generated and assessed using LB agar plating, microscopy, spectrophotometry, and SDS-PAGE analysis. Their cytotoxic effects were evaluated in two cancer cell lines and normal epithelial cells using the Sulforhodamine B (SRB) assay, while vesicle–cell interactions were assessed through live-cell imaging.

Preliminary findings demonstrate minimal cytotoxicity of vesicles in both cancer and normal cells. Live-cell imaging confirms vesicle binding to cancer cells, although intracellular

internalization remains limited. Ongoing cloning strategies aim to generate new plasmid constructs incorporating the PD-1 sequence to enhance targeting specificity and cellular uptake. Combining this fast and cost-effective technology with chemotherapy or immunotherapy may contribute to more effective antitumor responses while minimizing side effects.

8MT: Designing the next generation of small molecule cell surface targeting agents.

Olivia Keers (University of Kent), Prof Jonathan Essex (University of Southampton), Dr Hamish Ryder (CRUK Therapeutic Discovery Laboratories), Prof Michelle Garrett (University of Kent), and Prof Jennifer Hiscock (University of Kent).

Cancer remains a leading cause of mortality worldwide, yet effective targeting of cancer cells presents significant challenges due to cellular heterogeneity and adaptive resistance mechanisms. Supramolecular self-associating amphiphiles (SSAs) are an unconventional class of therapeutic agents, which demonstrate promising cytotoxic activity despite lacking a clearly defined, traditional molecular target. This work investigates the mode of action of SSAs through a combination of physicochemical and biological assays designed to probe membrane interactions and cellular responses.

Model membrane systems, including lipid vesicles, were employed to evaluate SSA-induced membrane fluctuations. Membrane integrity and lysis were quantified using calcein leakage assays and lactate dehydrogenase (LDH) release assays, while laurdan fluorescence studies provided insight into changes in membrane fluidity. Complementary three-dimensional spheroid models were utilised to better approximate tumour architecture and assess SSA activity in a physiologically relevant context.

Results indicate that SSAs interact with lipid bilayers, inducing membrane disruption rather than engaging specific protein targets. LDH assays on live cells revealed concentration-dependent membrane permeabilisation, and calcein leakage assays suggest that SSAs can induce complete membrane breakdown in vesicles. Laurdan studies demonstrated alterations in lipid packing caused by SSAs. Collectively, these data suggest that SSAs exert their anticancer effects via a membrane-targeting mechanism, distinct from conventional drug modalities. The development and integration of these assays provide a robust framework for elucidating the activity of non-traditional therapeutics. This work advances understanding of SSA function and highlights their potential as a novel strategy for overcoming limitations associated with target-specific cancer therapies.

8MT A chemical approach to biology.

J. A. Fish[a,b*], M. G. J. Baud[a], G. Giamas[c], and D. C. Harrowven[a].
Affiliations:
[a]School of Chemistry, University of Southampton, Southampton, SO17 1BJ
[b]School of Biological Sciences, University of Southampton, Southampton, SO17 1BJ
[c]School of Life Sciences, University of Sussex, Sussex, BN1 9RH

Significant advances in drug discovery and chemical synthesis are often inspired by nature: many successful pharmaceuticals are derived from natural product derivatives. Understanding how these compounds interact within cellular systems is key to further developing them to be selective, more potent, and to reduce side effects. Whilst this has the potential to vastly improve patient quality of life compared to traditional therapeutics, it creates significant synthetic challenges for chemists. The manufacturing of these medicines can be extremely difficult, including cost effectiveness of synthesis, mass making, formulation and storage of the medication, and the safety and environmental impact of production. This can lead to medicine shortages and high costs which create barriers to receiving care. Our research focusses on upscaling syntheses of a class of medicines, increasing the selectivity and potency of medicines by understanding more about the protein pocket, and developing new functionalities with our understanding of organic chemistry. This has led to a new hit compound for VHL-based PROTACs that could be used as a new exit vector to increase selectivity of these medicines whilst reducing their susceptibility to fast metabolism in the body. Further, our innovation with photochemistry has given us access to a range of drug fragments, which are synthetically very challenging and rarely accessible to chemists. These building blocks allow new motifs to be incorporated into drug discovery and have demonstrated the ability to synthesise these on scale. Our future aim is to engage chemical suppliers with our technology to supply these compounds cheaply.

3MT: SOD2 as a regulator of mitochondrial stress responses. Balancing mitochondrial quality control and disease

Molly Slade, University of Southampton; Dr Jana Ratnayaka, University of Southampton; David Tumbarello, University of Southampton.

Traumatic brain injury (TBI) is associated with an increased long-term risk of Parkinson's disease, yet the biological mechanisms linking acute injury to chronic neurodegeneration unclear. A common feature of both is oxidative and glutamatergic stress within neurons,

particularly the mitochondria; which are essential for cellular recovery and survival. Neurons rely on mitochondrial quality control systems to manage biochemical damage, yet how these systems fail after injury is not well understood.

This research investigates the role of the mitochondrial antioxidant superoxide dismutase 2 (SOD2) in regulating mitochondrial oxidative stress and resilience. Using live-cell imaging with the mitochondrial superoxide indictor MitoSOX, mitochondrial oxidative stress was measured under basal conditions, and following stimulation designed to model the biochemical environment of TBI. Cells lacking SOD2 showed significantly higher mitochondrial superoxide levels, even at baseline, with further exacerbation following injury-like stress.

These findings suggest that SOD2 act as a critical buffering system that defines a threshold between adaptive mitochondrial responses, and damaging pathways. When this defence is lost, mitochondria are pushed beyond a recoverable threshold, increasing neuronal vulnerability and potentially promoting long-term degeneration.

Understanding how SOD2 regulates mitochondrial stress responses, and whether it influences mitochondrial quality control systems, may help explain why some individuals develop Parkinson's disease years after brain injury. This work highlights mitochondrial antioxidant pathways as potential targets for protecting neurons after injury and reducing the progression towards neurodegeneration.

8MT: Understanding reward and withdrawal mechanisms underlying habitual caffeine use – The effect of caffeine consumption and acute withdrawal on resting-state fMRI brain connectivity, mood and cognition.

Tatum Sevenoaks, University of Sussex, Fiona Lancelotte, University of Sussex, Dr Nick Souter, University of Sussex, Dr Lorenzo Stafford, University of Portsmouth, Dr Charlotte Rae – University of Sussex, and Prof Martin Yeomans – University of Sussex.

Caffeine is the most widely consumed psychoactive substance, yet few studies have investigated how habitual and acute consumption and withdrawal impacts resting-state brain connectivity. Notably, prior research lacks adequate control for deprivation state, despite evidence that caffeine reinforcement occurs primarily by alleviating withdrawal. This study used a between-participants design to assess resting-state fMRI brain connectivity, mood, and cognition in three groups: (1) moderate consumers (200-500mg/day) tested after overnight abstinence (caffeine withdrawn, CW); (2) moderate consumers tested after

overnight abstinence followed by 100mg of caffeine (caffeine not-withdrawn, CNW); and (3) non-consumers of caffeine (<50mg/day, NC). Sixty healthy volunteers, aged 18-45 (n = 20/group) completed the Bond-Lader mood battery, a rapid visual information processing task and a resting-state fMRI scan. For resting-state brain connectivity, the CW group showed altered nucleus accumbens connectivity with primary visual cortex compared to CNW and NC groups. The CNW group showed stronger anterior insula connectivity with precuneus cortex compared to CW and NC groups. For network-level analyses, the CNW group exhibited reduced limbic within-network connectivity and altered connectivity between limbic and occipital cortex compared to CW and NC groups. The anterior salience network showed group differences in connectivity with the putamen, pallidum, and thalamus. The supplementary somatomotor network showed greater connectivity with the bilateral putamen in both caffeine groups, but reduced connectivity with the right middle temporal gyrus for the CW group. No significant main group effect emerged for mood and cognition. These findings demonstrate that caffeine consumption and withdrawal produce distinct alterations in resting-state brain connectivity.

3MT: Development of a 3D neural-glial cell culture model derived from human iPSCs and application to studying human neurodegenerative disease mechanisms

Ria Hunt (University of Portsmouth), Sandrine Willaime-Morawek (University of Southampton), Ryohei Sekido (University of Portsmouth), Sassan Hafizi (University of Portsmouth).

Chronic neuroinflammation plays a central role in the progression of neurodegenerative diseases CNS microglial dysfunction, involving TAM receptor signalling, is a major underlying factor to this process. Current in vitro models do not adequately encapsulate human neurological disease processes, limiting their translational relevance. This project aims to develop a novel human iPSC-derived microglial culture model with which to investigate TAM-mediated regulation of inflammatory signalling.

Initial experiments were conducted on the mouse microglial cell line BV-2, which were confirmed to express TAM receptor MERTK. Activation of TAM signalling by TAM ligand Gas6 or by vitamin K significantly reduced proinflammatory cytokine TNF-α expression and secretion in these cells. Also, ongoing experiments are measuring phagocytosis in the cells to further assess TAM-mediated cellular functionality.

Recently, human fibroblast-derived iPSCs have been propagated in culture. Using a standardised protocol, these will be differentiated into haemopoietic progenitor cells and

then subsequently into microglia. At all stages, the cells will be characterised phenotypically (marker expression, morphology). The ensuing microglia will first be verified functionally, then studied both alone as well as in co-culture with astrocytes as part of a physiologically relevant 3D neural-glial model. Parallel validatory experiments will be conducted on the BV-2 microglial cell line.

The establishment of the human microglial cultures and neuroglial co-cultures will enable an in-depth study of the role of TAM receptor signalling regulation of neuroinflammation. This model will provide a valuable new tool by which to further elucidate the pathological mechanisms of neurodegenerative disorders as well as identify novel therapeutic targets.

Presentation Session 3 10:35am to 11:40am

8MT: Immune signatures for Healthy Aging

Samuel Liu – University of Southampton, Fabio Strazzeri – TopMD Precision Medicine, James Schofield - TopMD Precision Medicine, Paul Skipp - TopMD Precision Medicine, Jay Amin – University of Southampton, Jessica Teeling – University of Southampton.

Introduction: Neuroinflammation is a central component of Alzheimer's Disease (AD), with inflammatory events, leading to earlier onset and faster progression. Artificial Intelligence (AI)-based methods can help identify novel pathways of inflammation in AD which could be overlooked by conventional analysis. Here we describe a novel contributor of inflammation, Enhancer of Zeste Homolog 2 (EZH2), in AD, from its identification using a custom topology-based AI system, to in-vitro confirmation of its potential importance, and an in-vivo pharmacological intervention study.

Materials and Methods: Using a custom AI algorithm, developed by TopMD, we generate topological maps using blood-based transcriptomic data from over 1000 participants. Topology of AD patients is compared against healthy, age-matched individuals, with changes in gene clusters being analysed for significant differences. Differentiated THP1 cells and mice were pre-treated with tazemetostat before a stimulation of LPS. Gene expression of cells and brain tissue was quantified by qPCR

Results: Differences in the topology between control and AD patients highlighted many potential pathways, including EZH2 pathways, which was chosen for subsequent exploration.

Results from both the cell and mouse models show that pre-treatment with tazemetostat significantly reduce the inflammatory response to LPS stimulation. Future experiments will advance the models used to be AD models that include amyloid pathology.

Significance: Our AI model highlights EZH2 as important driver of inflammation in AD. Inhibition of EZH2 successfully modifies the response to inflammation in. Upcoming experiments will combine AD pathology with inflammation and inhibition of EZH2, to provide greater understanding in a mechanism of disease acceleration in AD.

3MT: Novel microbes for novel solutions: Bioprospecting for properties with uses in many sectors

David Cotriscau (University of Southampton), Dr Renaud Toussaint (Lesaffre International), Prof Vladimir Jiranek (University of Southampton).

Brettanomyces bruxellensis is the most common spoilage yeast in winemaking, characterised by its ability to persist in wine and produce volatile phenols, with “barnyard”-like aromas. Its tolerance to ethanol, low pH and sulfur dioxide, along with its ability to enter a VBNC state and form biofilms make it difficult to control. The emergence of sulfur dioxide–tolerant strains (the main preservative used in wine), together with growing consumer demand for low-sulfite wines, underscores the need for sustainable biological alternatives. This PhD project aims to identify and characterise novel yeast-based control agents capable of reliably inhibiting B. bruxellensis.

We employed a high-throughput pipeline screening 1,000 yeast strains via agar diffusion. Preliminary results identified eleven candidates whose cell-free supernatants demonstrate antimicrobial activity in fermentation conditions. Inhibitory compounds will be characterised through protease sensitivity, ultrafiltration, and FPLC to determine their biochemical nature. Flow cytometry coupled with fluorescent viability staining will quantify survival of B. bruxellensis in the presence of the inhibitory compound.

The core of this project will evaluate a lead candidate’s feasibility as a winemaking starter culture. Direct yeast–yeast interactions will be assessed in fermentation simulations using RT-qPCR to track Brettanomyces populations. The candidate's impact on sensory integrity will be determined by analysing volatile phenols and fermentation metabolites via HPLC and GC-MS. This research directly addresses the wine industry’s need for reliable, natural spoilage control. Through the industrial collaboration with Lesaffre and Fermentis, the project aims to bridge mechanistic discovery with scalable, sustainable application.

8MT: Role of daily timekeeping in the Plutella xylostella–Brassica rapa pest–plant interaction

Shubhangi Mahajan[1], Lena Smith[1], Dr Connor Tyler[1], Dr Haruko Okamoto[2], Dr Stephanie Bird[3], Dr Hayley Jones[3], Dr Samuel Robson[4], Dr Herman Wijnen[1]
Affiliations: [1] School of Biological Sciences, University of Southampton, UK [2] School of Life Sciences, University of Sussex, UK [3] Plant Health Team, Royal Horticultural Society (RHS) Wisley, UK [4] Centre for Enzyme Innovation (CEI), University of Portsmouth, UK

The diamondback moth (Plutella xylostella, DBM) is a major specialist pest of Brassica crops, causing global agricultural losses estimated at approximately US$5 billion annually. Increasing resistance to insecticides and concerns surrounding their use highlight the need for alternative and sustainable pest management strategies. My PhD research investigates how temporal regulation influences interactions between DBM and its host plants, with a focus on the role of daily biological timekeeping.

Laboratory experiments examined how alignment between the circadian phases of host plants and DBM affects herbivory and gene expression. Feeding behaviour was significantly altered when caterpillars were exposed to plants with disrupted defence signalling or arrested circadian clocks, supporting the hypothesis that rhythmic plant defences shape patterns of herbivory. Time-course RNA sequencing of late-instar caterpillars revealed that transcript rhythms of core DBM circadian clock genes remained largely unaffected by host plant phase, whereas broader diel transcriptional programmes, including resistance-related genes, were influenced.

During a three-month internship at RHS, DBM caterpillar feeding preference trials were conducted comparing different Brassica varieties. DBM preferred the Chinese Leaf (Wong Bok variety) in these initial trials.

Together, these findings indicate that rhythmic plant defences shape patterns of DBM herbivory and influence transcriptional responses in the herbivore, highlighting the importance of temporal dynamics in pest–plant interactions

3MT: Development and evolution of diverse corona structures in Narcissus (Amaryllidaceae)

Grace Heath1, Steven Dodsworth2,3, Kalman Konyves4,5, John David5, Natalia Przelomska1,3

Affiliations:
1 University of Portsmouth
2 Birkbeck College, University of London
3 Royal Botanical Gardens, Kew
4 Royal Horticultural Society, Wisley
5 University of Reading

Flowers typically follow a set layout, having two outer layers of perianth organs, followed by the male reproductive organs (stamens), and the inner female reproductive parts (carpels). However, in the genus Narcissus there is an additional layer- the corona (trumpet) in between the perianth (tepals) and stamens. The developmental and evolutionary origin of this structure is debated. This project aims to identify the genes governing the development of the corona, as well investigating corona structures across the family (Amaryllidaceae) to infer the evolutionary patterns that led to the emergence of the Narcissus corona. Understanding how charismatic structures are formed can in the future allow us to breed new and exciting cultivars.

We used whole transcriptome sequencing and differential gene expression analyses to identify genes associated with corona tissue and which likely contribute to the development of the corona, discovering that the corona is more genetically similar to the tepals rather than the stamen. We have also used low-copy nuclear genes to infer a new nuclear phylogeny of Amaryllidaceae. We will then perform ancestral trait reconstructions using this tree to gain a better understanding of how corona traits evolved within the family.

In future work, we aim to identify the genetic differences between the Narcissus corona and the staminal cup (a trumpet-like structure formed within the staminal layer which appears several times within the family), and identify genes controlling extreme corona morphological variation. This may give insight into the evolutionary developmental processes that led to the Narcissus corona.

8MT: Accessing and recording task-related neuronal activity in the cerebral cortex: using targeted recording configurations.

Shahd Al Balushi, University of Sussex; Alejandra Carriero, University of Sussex; Moira Eley, University of Sussex; Andre Maia Chagas, University of Sussex; Miguel Maravall, University of Sussex.

Rodents have sophisticated capacities for context-dependent decision-making and navigation. We developed an experimental modular maze allowing mice to express these capacities. The maze includes automated stimulus presentation and reward delivery triggered by mouse tracking. This approach enables study of foraging behaviour without restricting mouse movement or access to nutrition, and provides robust experimental control while ensuring flexible design of tasks and open protocol sharing. To allow flexible reconfiguration of the maze and set up arbitrary associations between stimuli, locations and rewards, we replaced standard wall panels with devices for reward dispensing or stimulus delivery. Device motion was triggered in real time by animal entry into regions of interest (ROIs). An animal could encounter multiple stimuli as it moved from the maze's origin to any endpoint, and could shuttle freely between cage and maze. We found that mice habituated to the maze within minutes and were intrinsically motivated to explore it with no need for fluid or food restriction. Mice then learned to navigate to arbitrary locations for rewards. We provide examples of engaged, exploratory and settled/nest-building behavioural states. Trials ended when the mouse chose to leave the maze, and mice shifted between behavioural states during the course of a single trial, often triggered by collecting a food reward. Our results demonstrate the complexity of state modulation during naturalistic exploration and suggest the need for fuller characterization of the state-dependent modulation of sensory processing. We provide examples of testing approaches to detect neural activity in animals exploring the maze.

3MT: Project title: Characterising the antigenic cross-reactivity of arboviruses to aid vaccine assessment and development, and serosurveillance.

Toby Jones (University of Sussex), Dr Scott Jones (UKHSA), Dr Edward Wright (University of Sussex)

Arthropod-borne viruses (arboviruses) represent a major and expanding global health burden, causing substantial morbidity, mortality, and economic disruption. A central challenge in arbovirology is the extensive antigenic cross-reactivity among related viral species, which shapes vaccine design and complicates serological diagnosis. Despite the global need for effective vaccines and robust serosurveillance programmes, the mechanism by which prior exposure to one arbovirus influences antibody recognition of related viruses remains poorly understood.

This PhD project will improve our understanding of the antigenic landscape of high-consequence arboviruses by characterising the breadth, potency and specificity of cross-reactive antibody responses. A broad suite of immunoassays, including pseudotyped virus and

replicon systems, multiplex binding platforms, and functional receptor-blocking assays, will be used to define cross-reactivity within and between viral genera. The results will be used in bioinformatic analyses also incorporating viral sequence and structural information, which will identify conserved epitopes capable of eliciting broadly reactive antibody responses. In parallel, deep mutational scanning will assess how viral mutations modulate epitope recognition, providing predictive insight into antigenic drift and the emergence of immune-escape variants.

By elucidating the molecular determinants of cross-reactive immunity, this work will refine our approach to serosurveillance and inform the design of next-generation arboviral vaccine antigens with enhanced breadth and effectiveness.

8MT Microbial biotechnology approaches to optimize chemical oxygen demand and enhance nitrogen and phosphorus removal in wastewater treatment

Matthew Irwin – University of Southampton, Dr Yongqiang Liu – University of Southampton, Dr Franklin Nobrega – University of Southampton, Juhani Kostiainen – Plantworks System Limited, Prof John Williams – University of Portsmouth, Prof Jeremy Webb- University of Southampton

Abstract pending – not attending

Presentation Session 4 1:40pm to 3:10pm

3MT: Unlocking DNA Repair Pathways: Industrial Collaboration and Cutting-Edge Technology

James White (University of Kent), Prof Peter McHugh (University of Oxford), Dr Mina Brett Pitt (Lumicks), Prof Neil Kad (University of Kent)

Over time, DNA accumulates damage from many sources, such as DNA duplication errors, UV radiation and genotoxic chemicals. Consequently, cells can accumulate mutations, which can result in cell death or transformation. DNA repair pathways are therefore crucial to cellular function and understanding the fundamental molecular mechanisms underpinning these pathways is important.

Studies into DNA repair have been performed in whole organisms, cells, and at the molecular level, with numerous studies being done using single-molecule (SM) methods. To date, most

SM studies have used purified proteins to observe dynamics in isolation. In the cell, the crowded nuclear environment can affect their dynamics, meaning that conclusions drawn from purified samples are not necessarily applicable in a cell.

This project will get closer to observing in vivo mechanisms by using impure proteins, either from whole cell lysates, for prokaryotes, or a technique known as SMADNE (Single-Molecule Analysis of DNA-binding proteins from Nuclear Extracts), for eukaryotes. This both more closely resembles the conditions inside a cell and also allows the probing of complex molecular interactions.

We will measure these interactions using ssDNA-tightropes probed with fluorescently-labelled proteins. These will be visualised using SM resolution on the Lumicks C-Trap microscope, yielding unprecedented information about the kinetics, targeting and dynamics of DNA-repair proteins in their native context.

8MT: Safeguarding UK hop production from Verticillium nonalfalfae: Race-specific diagnostics and effectoromics

Simon Thundow (University of Kent) Dr Andrew Armitage (University of Greenwich), Klara Hajdu (Wye Hops), Prof Xiangming Xu (NIAB), Dr Helen Cockerton (University of Kent).

Hop (Humulus lupulus) production in the United Kingdom has declined by over 70% since 1981, in part due to the emergence of highly pathogenic strains of the fungal pathogen Verticillium nonalfalfae, which causes Verticillium wilt disease in hops. Hop cultivars which had previously been considered resistant to Verticillium wilt have since shown susceptibility to the disease, suggesting the emergence of resistance-breaking pathotypes. Highly virulent pathotypes of V. nonalfalfae are hypothesised to combat the resistance of hop cultivars via either the production of Secreted Effector Proteins (SEPs) which interact with plant immune responses, or the avoidance of host-induced RNA interference (RNAi) via the modification of targeted fungal genes or motifs. This study seeks to investigate how highly-virulent pathotypes of V. nonalfalfae have evolved and to identify candidate SEPs and RNAi targets involved in virulence on hops.

Through the generation of multiple genomic and transcriptomic assemblies of Verticillium nonalfalfae isolates, we will investigate the phylogenetic and evolutionary relationships between pathotypes. We aim to characterise candidate SEPs which may be involved in increased virulence on hop, and identify potential targets of interfering RNAs produced by hop cultivars in the genomes of V. nonalfalfae isolates. Ultimately, we wish to determine

whether variation between pathotypes of V. nonalfalfae can inform future disease control strategies such as via Host Induced Gene Silencing (HIGS) or in-field, pathotype-specific diagnostics. Overall, we aim to advance the understanding of how V. nonalfalfae causes wilt disease in hops and to inform future strategies to control the disease.

3MT: Spider Venomics – Understanding the Genomics of Venom in Spiders

Caitlin Price – University of Kent, Prof Adam Eyre-Walker – University of Sussex, Dr Mark Wass – University of Kent, Dr Marta Farré Belmonte – University of Kent, Dr Peter Ellis – University of Kent.

Spiders have thrived for over 450 million years; a clade comprising of more than 53,000 species and colonising almost all terrestrial habitats. Their success is often attributed to their unique use of venom and silk. Despite this, the genomic changes underpinning their evolution remain largely unexplored. In my thesis I use genome assembly, annotation and ancestral reconstruction to uncover and explore the genomic evolution behind spiders and how key traits such as venom have evolved.

This project involves generating reference-level genomes for key tarantula species using PacBio sequencing, with a specific focus on identifying venom genes. To better understand the genomic evolution of spiders, I am reconstructing the ancestral genomes of both tarantulas (Theraphosidae) and orb-weaving spiders (Araneoidea). Both gene-based (AGORA) and alignment-based (DESCHRAMBLER) reconstruction methods are used to compare and uncover how the two groups have evolved to diversify specific traits.

Preliminary results reveal a high level of complex intrachromosomal rearrangement, suggesting the ability to thrive under rapid chromosomal changes may be a key driver for their ecological success. This research will provide key insight into how genomic rearrangements influence adaptability, a key trait in the face of climate change. By understanding how venom has evolved we can begin to identify specific species and proteins which may have potential future medical or ecological applications.

8MT: Next generation mitochondrial inhibitors – a new approach to prevent fungal biofilm formation on medical implants

Dmytro Prasolov - University of Kent, Prof Anthony Moore – University of Sussex, Eric Pagan – Smiths Medical Inc, Dr Campbell Gourlay - University of Kent

Objectives:

Cryptococcus neoformans is an opportunistic fungal pathogen that predominantly affects immunocompromised individuals, causing as many as 200,000 cases annually, with a staggering mortality rate of 75.8%. Current therapy of antifungal drugs has been successful for many years, however several issues arose over the recent years. These include the development of antifungal drug resistance in as many as 30% of *C. neoformans* clinical isolates; current therapies having considerable side effects on patients such as nausea and nephrotoxicity; and finally, drug supply chain issues with some of the producers ceasing their operations. Targeting fungal mitochondria holds promise due to their pivotal role in C. *neoformans* physiology, including virulence, defence against immune cells, and energy production. Here we describe the results of tests to evaluate our newly developed fungal specific inhibitor of *C. neoformans* respiration, Inz-Bob.

Materials & Methods:

The effects of Inz-Bob were assessed by growth rate, minimum inhibitory concentration (MIC), and viability. Titan cells production in the presence of Inz-Bob was assessed by microscopy and image analysis and mitochondrial respiration was assessed using high resolution respirometry. The induction of an alternative oxidase to support respiration upon Inz-Bob treatment was conducted using an anti-Aox1 antibody developed in our lab. Macrophage *C. neoformans* engulfment assays utilised murine macrophage cell lines and effects on virulence were assessed in the *Galleria mellonella* infection model. Inz-Bob cytotoxicity was assessed in macrophage, red blood cell and *Galleria mellonella* systems.

Results:

We have designed a new drug, Inz-bob, that targets the bc1 subunit of complex III of C. neoformans. Here we show that Inz-bob successfully inhibits *C. neoformans* growth and respiration at low concentrations. Inz-bob treatment also reduces viability and prevents the key virulence trait of Titan cell formation. Notably, it does not decrease the respiration of murine macrophages, does not exhibit haemolytic activity and is non-toxic in a *Galleria mellonella* model organism, confirming its fungal specificity. Crucially Inz-bob does not lead to upregulation of the alternative oxidase, Aox1, which has previously been shown to be essential in *C. neoformans* response to the electron transport chain inhibition and to the development of resistance to bc1 class inhibitors.

Conclusions:

Overall, the mitochondria of *C. neoformans* shows great promise as a target for antifungal therapy. Our data suggests that Inz-bob is a highly effective and non-toxic drug *in-vitro*. Our data warrants further research into the development and delivery of fungal specific inhibitors of respiration in *C. neoformans*.

3MT: Antimicrobial resistance in captive animals: understanding the potential for environmental persistence, and transfer to other species

Reece Lane-Cartwright1, Dr Judith Lock1, Professor Philip Riordan2, Dr William King1, Dr Sandra Wilks1

Affiliation: 1 School of Biological Science, Faculty of Environmental and Life Sciences, University of Southampton, Southampton, UK. 2 Marwell Zoo, Winchester, UK

The gut microbiome holds a consortium of biotic and abiotic factors that interact as a large community, from eukaryotes to fungi and bacteria, and mobile genetic elements such as bacteriophages. The project focuses on the bacterial constituent of the gut microbiome, assessing compositional and metabolic profiles in captive endangered mammals of interest (Grévy's zebra and Scimitar-horned oryx). The current focus is to investigate dietary utilization and metabolite production, with the project already highlighting phylogeny, gastrointestinal morphology, and environmental location as drivers of compositional divergences. Metabolic assessment from dietary intake is integral to understanding metabolite profiles and how this production profile may affect other bodily systems such as the immune system, cardiovascular system, and the gut: brain axis, with this regulating overall health. Current metabolic profiling is now highlighting dietary sources that promote increased community growth, with future work aiming to highlight key genera enriched with these dietary sources. This work aims to give better insight into the gut microbiome in a captive setting, with the aim of comparative assessment in wild animals. The final aim, assessing how this may change in response to antibiotic perturbation due to veterinary intervention, aims to highlight key framework considerations of animal and diet management to guide better conservation outcomes.

8MT: Using Machine Learning to Predict Bone Stress Injury through Analysis of Sexual Dimorphism in Bone Structure and Biochemical Properties

Theo Hornsey – University of Southampton, Dr Jemma Kerns – Lancaster University,
Prof Julie Greeves – Army Health and Performance Research, Prof Claire Clarkin – University of Southampton.

Bone is sexually dimorphic and bone stress injuries (BSIs) in healthy individuals resulting from overuse e.g. during arduous military training, occur up to six times more in women compared with men. Although bone matrix composition and microstructure are key determinants of skeletal integrity, pre-clinical understanding of sex differences in these properties and their

relevance to BSI risks remains limited. Identification of these sex differences in the bone may be critical in producing tools capable of reducing BSI risk.

Herein, we present pre-clinical data using Raman spectroscopy and computed tomography (CT) to define regional and sex-specific variation in bone extracellular matrix composition (ECM) and microstructure. µCT analysis of adult murine bone identified significant differences in cortical porosity between sexes; Regionalised Raman spectroscopy of the murine cortex revealed spatial variation in ECM chemistry, with sex differences predominantly located in mechanical loading regions of the bone suggesting mechanical loading as a potential driver of these adaptations. Translation of these findings is underway through analysis of human tibial CT datasets, and the development and validation of approaches for in-vivo Raman assessment of human tibia through skin tissue. These data are being integrated into machine learning models aimed at predicting bone stress injury risk during military training, with promising initial performance.

Together, these findings demonstrate that sex-specific ECM and microstructural signatures may underlie differential injury susceptibility and support development of clinically translatable predictive tools.

3MT: Development of LA1011 for high affinity binding to Hsp90 for use towards healthy aging and preventing Alzheimer's disease development

Xavier Jeanne (University of Sussex), Jasmeen Oberoi (University of Sussex), Mark Roe (University of Sussex), Laszlo Vigh (LipidArt), Zsolt Torok (LipidArt), Mattias Baud (University of Southampton), Chris Prodromou (University of Sussex), John Spencer (University of Sussex).

Heat shock protein 90 (Hsp90) is a chaperone protein that, together with a network of co-chaperone proteins, regulates the folding of client proteins. However, this network undergoes changes in the brain during ageing. These alterations in the expression of chaperone and co-chaperone proteins negatively impact the progression of Alzheimer's disease, contributing to the accumulation of amyloid-β plaques and tau neurofibrillary tangles.

LA1011 presents a potential solution. Originally designed for hypertension, this dihydropyridine has been shown to induce Hsp90 ATPase activity and disrupt formation of the Hsp90–FKBP51 complex by interacting with the C-terminal domain (CTD) of Hsp90. In mice models of Alzheimer's disease, LA1011 administration reduced tau pathology and improved spatial memory. However, given its relatively low affinity for Hsp90 and the

uncertainty surrounding its precise binding site, there remains scope for development and mechanistic understanding.

We aim to develop a high-affinity ligand targeting the Hsp90 CTD and determine how modulation of this site affects alternative co-chaperone complexes and influences Alzheimer's disease progression. We are combining computational screening and structure-based design with biochemical and biophysical approaches to characterise protein–protein interactions and compound effects.

To date, we have evaluated the effects of LA1011 on multiple Hsp90 co-chaperone complexes implicated in Alzheimer's disease. We have virtually screened 130,000 compounds and begun isothermal titration calorimetry validation of top candidates. We have also initiated the synthesis of a diazirine-based crosslinker derived from the LA1011 scaffold to identify its binding site. This work aims to further establish Hsp90 CTD targeting for Alzheimer's disease modulation.

8MT: Understanding the antimicrobial properties of natural plant extracts and herbal infusions

Iolanta Spanner – University of Southampton; Prof Bill Keevil- University of Southampton, Dr Vivien Rolfe – Curiosity Research Ltd, Dr Sandra A Wilks – University of Southampton.

Biofilms represent the cause of many persistent upper respiratory tract infections (URTIs), which can lead to burdensome healthcare complications and resistance to antimicrobials. This project aims to investigate the antibiofilm properties of various natural plant extracts from herbal teas, how we can enhance our current repertoire of prevention and treatment options with novel approaches. Planktonic and biofilm cultures of Streptococcus pyogenes were exposed to Matcha green or Raspberry tea and analysed using a variety of techniques including Scanning and Transmission Electron Microscopy, traditional culture viability testing and confocal laser scanning microscopy (CLSM) to understand changes to the three-dimensional biofilm architecture under different treatment conditions. After treatment with herbal tea, there were drastic changes to the bacterial cell membrane morphology, with the presence of membrane vesicle formation, cell aggregation, cell membrane integrity loss and a reduction in electron density, corresponding to various stages of cell death. Consistent antibiofilm activity was observed, with a significant reduction in the viable cell counts of mature biofilms after treatment with either Matcha or Raspberry, when compared to controls, and CLSM imaging confirmed a large presence of dead cells and significant changes to the biofilm matrix structure This demonstrates the ability of plant extracts to cause a

significant reduction even against highly established biofilms, which usually exhibit high tolerances for antimicrobials – and highlights the potential of these extracts to be used as additional treatments against clinical biofilms or as adjuvants in combination with antibiotics. Future work will involve transcriptomics to understand gene expression in response to treatment.

3MT: Investigation into Factors Affecting Biofilm Formation on Natural and Synthetic Dental Materials

S. Usidamen1, M. Mutahar1, R. Bonithon1, M. Roldo1,R. Howlin2, A. Hunt2, D. J. Bradshaw2.
Affiliation: 1 University of Portsmouth, Portsmouth, UNITED KINGDOM, 2 Oral Health R&D, Haleon Consumer Healthcare

Background/Introduction:
Effective long-term control of biofilm on dental materials remains a significant challenge, as current cleaning approaches primarily target removal rather than prevention. Most studies focus on PMMA and short-term, single-species models, which do not adequately reflect the complexity of oral biofilms. Addressing these limitations is essential to better understand how surface properties and pellicle interactions influence biofilm development and to guide the design of more effective preventive strategies.

Objectives:
This study aimed to characterise biofilm formation on four clinically relevant dental biomaterials and to evaluate how surface roughness, hydrophobicity, hardness, and porosity influence bacterial adhesion and biofilm development in the absence of a salivary pellicle.

Methods:
A mixed-species biofilm derived from saliva was cultivated on four materials (n = 9 per material)—titanium (Ti), stainless steel (SS), hydroxyapatite (HA), and poly (methyl methacrylate) (PMMA)—over a 7-day period using a CDC bioreactor. The biomaterials were characterised by profilometry to assess surface roughness, contact angle measurements to determine hydrophobicity, Vickers hardness testing for mechanical properties, and XCT imaging to evaluate the porosity of HA. Biofilm formation was quantified through crystal violet staining to measure total biomass and colony-forming unit (CFU) counts to determine viable bacterial load.

Results and Discussion:

Surface characteristics, including roughness (Ra), hardness (HV), and contact angle, exhibited varying degrees of correlation with biofilm formation. Overall, rougher surfaces (HA and PMMA) showed a positive correlation with biofilm accumulation, indicating that increased surface roughness promotes bacterial adhesion by providing more anchoring sites. Contact angle and hardness correlated negatively with both CFU and crystal violet results, suggesting that hydrophobic and hard surfaces tend to inhibit microbial adhesion, likely due to smaller real contact areas.

Conclusions:
This study demonstrates that, in the absence of a salivary pellicle, surface and material properties collectively influence biofilm development on biomaterials. Findings indicate that biofilm formation is promoted by rough, soft, and hydrophilic surfaces, while smoother, harder, and more hydrophobic biomaterials resist colonisation.

To strengthen the current argument, biofilm DNA from the different materials was also extracted to perform 16S genetic profiling to determine whether specific keystone taxa within the inoculum contributed to the higher bacterial biomass observed on PMMA and HA.

3MT: Expansion of the DISARM repertoire to target Pf filamentous phage

Michelle Z. Lin (1), Ryan T. Bell (2), Eugene V. Koonin (2), Franklin L. Nobrega (1), and Jeremy S. Webb (1)

Affiliation: 1. School of Biological Sciences, University of Southampton, SO17 1BJ Southampton, UK. 2. Division of Intramural Research, National Library of Medicine, National Institutes of Health, Bethesda, United States.

Filamentous, ssDNA phages form liquid crystals around bacterial cells and play a role in the formation and maintenance of biofilms. Whole genome sequencing estimates 50 – 60 % of P. aeruginosa are lysogenised by at least one filamentous Pf phage contributing to the bacteria's virulence and chronic infection. Bacteria have evolved an arsenal of anti-phage systems to protect against a diversity of phages. Notably, P. aeruginosa is a species abundant in anti-phage systems with an average of 13 systems per genome and possesses two core defence hotspots (CDHS1 and CDHS2) in which anti-phage systems have accumulated. DISARM (Defence Island System Associated with Restriction- Modification), is a ssDNA targeting anti-phage system located in CDH1 of around 3 % of the P. aeruginosa population, which is revisited for ssDNA filamentous phage targeting. Here, we reclassify the canonical DISARM Class I and Class II to Types 1 - 5, and identify Type 1 and Type 4 as prime candidates to target

Pf filamentous phages. This work motivates the development of DISARM vaccines, which through disruption to biofilm structural integrity enable amplified sensitivity for phage-antibiotic combination therapy.

Poster Session 1 5:10pm to 6:10pm

Group	Poster Location	Name
A	2	Daniel Beach (USusx)
A	5	Rachel Buchanan (USoton)
A	8	Ana Ferreira (UPort)
A	11	Miya Giragosian (UKent)
A	14	Liliana Jeziorska-Clifford (USoton)
A	17	Christian Hollingbery (UKent)
A	18	Thomas Jamieson (UKent)
B	23	Macy Martin (USoton)
B	3	Joshua Byrne (USoton),
B	9	Holly Champney (USoton)
B	12	Joshua Fennell (NIAB)
B	21	Ateeqa Naim (UKent)
B	26	Muhammad Zalkifal (USoton)

Poster presentation group A – 5:10pm to 5:40pm

Poster Location 2: Using AI and big data to identify a set of biologically validated drug targets for hard-to-treat cancers.

Daniel Beach – University of Sussex, Prof Michelle Garrett – University of Kent, Prof Stuart Farrow - Cancer Research Horizons (formerly CRUK Therapeutic Discovery Laboratory), Dr Frances Pearl - University of Sussex.

Abstract pending – not attending

Poster Location 5 - Phage mitigation of Escherichia coli: A new approach for treating UTIs

Rachel Buchanan (University of Southampton), Nela Nikolic (University of Southampton), Matthew Wand (UK Health Security Agency- CASE Partner), Franklin Nobrega (University of Southampton).

Antimicrobial resistance is a rising global threat, with novel treatments urgently needed to treat the rise of antimicrobial resistant bacterial infections which caused over one million deaths in 2019. Escherichia coli has emerged as a pathogen with increasing antibiotic resistance and is a causative of multiple conditions including bloodstream infections and urinary tract infections (UTIs). While non-recurrent urinary tract infections caused by E. coli occur around 75% of the time, almost a quarter of UTI patients will suffer with chronic infections, which are typically less responsive to treatment with antibiotics. Bacteriophages, viruses which can infect and lyse bacteria, show potential as an alternative treatment for urinary tract infections. To demonstrate this, the RAB phage collection was created, which is comprised of 138 bacteriophages isolated from water samples from Portswood (Hampshire, UK), the Isle of Wight (UK), and five wastewater treatment plants in Denmark. Phages were isolated utilising four strains of E. coli. Testing of the phage collection against diverse E. coli strains allowed the development of a five-phage cocktail capable of lysing 95% of 327 tested strains. Future work will address the therapeutic potential of this phage collection with regards to the human immune response and testing on uropathogenic E. coli to further the argument for using phages as an alternative therapeutic.

Poster Location 8 - Comparative effects of alcohol and GABA mimetics on the brain-gut-microbiota (BGM) function

Ana Carolina Gomes Nascimento Pita Ferreira - University of Portsmouth, Murphy Wan - University of Portsmouth, Delia Belelli - GABALabs, David Nutt - GABALabs, Jerome Swinny - University of Portsmouth.

SENTIA is a plant-based beverage that was developed as a non-alcoholic alternative. SENTIA is proposed to mimic the activity of GABA in the brain, producing feelings of relaxation, without alcohol's toxic effects. However, its influence on the enteric nervous system (ENS) remains largely unexplored, which is adversely affected by alcohol. The ENS contains many neurons that communicate through GABAA receptors (GABAAR), a well-established alcohol molecular target. Activation of GABAARs significantly influences GI motility and contractility. However, whether SENTIA alters intestinal contractility through similar mechanisms is currently unknown.

This study aimed to examine the effects of SENTIA on the mammalian intestine contractility, exploring the underlying molecular pathways involved. Experiments were conducted using adult (>2 months old) male and female C57BL/6J mice. Isometric tension recordings were obtained from isolated ileal segments using an organ bath. Measurements included changes

in basal tone, force, and frequency following exposure to varying SENTIA concentrations, both alone and in combination with selected neurotransmitter receptor ligands.
In a concentration-dependent, triphasic reduction in spontaneous intestinal contractility, SENTIA significantly decreased ileal basal tone ($F=31.20$; $P<0.0001$, repeated measures one-way ANOVA, RM-ANOVA; N=6), force ($F=4.974$, $P=0.04$, RM-ANOVA, N=6), and frequency ($F=17.54$, $P=0.0001$, RM-ANOVA, N=6). The reduction in force was partially prevented by Picrotoxin ($P=0.2792$, RM-ANOVA and Tukey's post hoc test, N = 8), indicating involvement of GABAARs.

This study proves that SENTIA directly induces intestinal relaxation, offering therapeutic benefit in conditions characterized by GI hyperactivity. Ongoing research is investigating GABAAR subtypes, neurotransmitter systems, and comparisons between SENTIA and alcohol in the gut.

Poster Location 11 - Understanding adult stem cell-niche interactions using the Drosophila intestine

Miya Giragosian – University of Kent, Dr Nahuel Villegas – Vivan Therapeutics, Dr Jerome Korzelius – University of Kent.

The human intestine is maintained by intestinal stem cells (ISCs) which differentiate into two main cell types: absorptive enterocytes (ECs) and secretory enteroendocrine cells (EEs). Ageing, diet, and various genetic factors can cause dysregulation of ISC proliferation leading to inflammation and tumorigenesis. However, identifying signals secreted from the surrounding epithelium that influence ISC behaviour remains an underexplored area of ISC biology that may provide novel therapeutic insights.

The intestine of Drosophila melanogaster is anatomically and genetically similar to humans, maintained by ISCs, and serves as a useful model to investigate ISC function. The Notch signalling pathway promotes ISC to EC differentiation. When Notch is inhibited, there is a rapid expansion of ISC/EE-like overgrowths in the midgut. Conversely, mutations in the EGFR/Ras/MAPK pathway cause overproliferation of ISCs and excess growth of EC cells.

By combining the Gal4-UAS and LexA-LexAOp binary expression systems, we are developing models that simultaneously induce ISC proliferation (via NotchRNAi and RasG12V) and knock down the expression of a pre-selected set of secreted molecules from surrounding ECs and EEs. Using these two inducible systems, we can track ISC turnover to identify candidate molecules that enhance or suppress ISC proliferation and differentiation and assess impact

on overall lifespan. We will also test conserved hits from our Drosophila screen in human intestinal organoid cultures to classify novel conserved factors governing ISC proliferation in a mammalian context. Ultimately, this work will enhance our understanding of gut tissue maintenance under age-related and oncogenic stress conditions.

Poster Location 14 - Nanobody technology: feeding target authentication and mitigation strategies in crop protection.

Liliana Jeziorska-Clifford – University of Southampton Dr James Dillon – University of Southampton, Marcus Guest – Syngenta, Prof Vincent O'Connor – University of Southampton

Conventionally used compounds targeting parasitic nematodes lack target selectivity, in turn leading to off-target effects, negatively impacting the environment (1). Thus, we should explore options improving target selectivity, such as nanobodies. Emerging capability of engineered nanobodies against membrane proteins, such as V-ATPases (2), raises the possibility of utilising nanobodies in mitigation strategies.

To develop this approach, we use Caenorhabditis elegans and the recombinant expression of the native proteins with the ALFA-tag, renowned for its highly selective interaction with anti-ALFA nanobodies. Moreover, targeting recombined epitopes addresses the pharmacokinetic limitations regarding the accessibility to interfering nanobodies. We rationalised readily accessible tissues, e.g. the intestine and sensory neurons, as delivery routes.

Since nanobody feeding to the intestine promises binding to the luminally exposed epitopes, we designed a bioinformatics pipeline to mine for accessible proteins on the apical membrane. Starting with the 2,484 intestinal genes, we narrowed the candidate pool to the 18 physiologically important candidates. Using AlphaFold and DeepTMHMM, we predicted their membrane topology, focusing on exposed loops. This determined the positions for the ALFA-tag recombination using the CRISPR/Cas9.

We confirmed in-frame insertion of the tag in the two engineered candidates: vha-6 (intestine-specific a3 subunit of the V-ATPase) and sid-2 (RNAi transporter). Interestingly, the ALFA-tag insertion into one of the VHA-6 luminal loops phenocopied previously observed genetic deletion mutant, with 10% of worms arrested at the early-larval stage and lack of the homozygous adults (3). On the other hand, we observed a viable homozygous strain with the ALFA-recombined SID-2 transporter.

Therefore, this converges on approaches which flag membrane proteins as the prime candidates, and indicates specific protein loops worth considering when engineering selective nanobodies to achieve a disturbing interaction. Whereas the SID-2::ALFA argues that this system provides tools for feasible pharmacokinetic testing of the interaction between the nanobody-ALFA-tag in vivo.

1. Chen J, Li QX, Song B. Chemical Nematicides: Recent Research Progress and Outlook. Journal of Agricultural and Food Chemistry. 2020; 68(44). doi: 10.1021/acs.jafc.0c02871
2. Knight K, Park JB, Oot RA, Khan M, Roh SH, Wilkens S. Monoclonal nanobodies alter the activity and assembly of the yeast vacuolar H+-ATPase. bioRxiv. 2025. doi: https://doi.org/10.1101/2025.01.10.632502
3. Allman E, Johnson D, Nehrke K. Loss of the apical V-ATPase a-subunit VHA-6 prevents acidification of the intestinal lumen during a rhythmic behavior in C. elegans. American Journal of Physiology Cell Physiology. 2009;297(5):C1071–81. doi: 10.1152/ajpcell.00284.2009

Poster Location 17 – Using a holistic and multidisciplinary approach to investigate the effects of regenerative agriculture on the soil microbiome, animal health and CO2 emissions

Christian Hollingbery (University of Kent), Robert Barker (University of Kent), Marc Dumont (University of Southampton), Supervisory Chair, Gary Robinson (University of Kent), Anastasios Tsaousis (University of Kent).

Regenerative agriculture is widely promoted as a means of improving soil health, particularly through enhancing soil microbiological activity. However, clear field-based evidence explaining how regenerative practices influence soil microbial communities remains limited. This PhD adopts a holistic and multidisciplinary approach, combining field trials, soil chemistry, microbial community analysis, and improved experimental design to better understand these relationships.

A replicated field plot study showed that soil microbial communities were strongly influenced by interactions between soil pH and cations concentration, especially magnesium (Mg). Rather than acting independently, Mg affected microbial diversity and community composition differently depending on soil acidity. This finding highlights the importance of chemical context and suggests that regenerative practices may influence the microbiome indirectly through shifts in soil chemistry and nutrient balance.

Ongoing work builds on these findings through controlled laboratory experiments to further test how Mg and pH interact to shape microbial communities. Additional field studies are examining how wheat genotype (heritage versus modern varieties) and different composting approaches influence soil chemistry and microbiome responses under regenerative management. Together, this research advances both mechanistic understanding and practical methodology for evaluating regenerative agriculture and its impacts on soil microbial systems.

Poster Location 18 - Manipulation and Engineering of the Lipid Metabolic Pathway in CHO Cells to Improve the Downstream Processing of Cell Culture Supernatants.

Thomas Jamieson, University of Kent; Maria Stanley, University of Kent; James White, UCB; Mark Ellis, UCB; Matthew Hinchliffe, UCB; David Humphreys, UCB; Mark Smales, University of Kent.

Chinese hamster ovary (CHO) cells are the current industrial system of choice for the expression of complex, post-translationally modified recombinant biopharmaceutical proteins. For many monoclonal antibodies (mAbs) production yields of 5g/L and higher are routinely achieved, however many new format and antibody inspired modalities (such as Bispecific antibodies) can be difficult to express and/or cellular components can present problematic downstream processing issues. Recent research has shown that upregulation of key genes responsible for lipid metabolism in CHO cells can result in an expansion of the ER, leading to increased secretory biotherapeutic recombinant protein production. This project will investigate (1) bioprocesses that modulate lipid metabolism in a cell line specific manner, which ultimately impact downstream processing, and (2) manipulation of key genes and pathways in lipid metabolism in a range of CHO host cell lines, determining the subsequent impact on culture viability, cell growth, yield and quality of secreted biotherapeutic protein, vesicle (specifically exosome) production and on primary downstream processing events

Poster presentation group B – 5:40pm to 6:10pm

Poster Location 23 - Smart Architecture: use of antimicrobial copper alloys in public infection prevention strategies

Macy M. Martin (University of Southampton), C. William Keevil (University of Southampton), Mike McGrath (Necon Technologies Ltd.), Sandra A. Wilks (University of Southampton).

Healthcare-associated infections (HAIs) are a global burden with high mortality rates. HAIs often arise from patient contact with contaminated hospital surfaces, on which bacteria persist despite rigorous cleaning procedures – possibly due to the presence of dry surface biofilms (DSBs). DSBs survive long-term in the absence of moisture and resist chemical and mechanical removal. Details of DSB development remain elusive, whilst worsening antimicrobial resistance calls for strengthened infection prevention strategies. Copper is a highly effective antimicrobial due to its direct contact mechanism of action, although its ability to prevent DSB formation remains undetermined.

This research aims to model DSB formation on high-touch surfaces to elicit understanding of structural and molecular properties. We developed a novel laboratory model for DSB growth using an artificial human sweat medium (AHS). We contrasted DSBs of four ESKAPE pathogens with hydrated biofilms using culturable colony counts, epifluorescence microscopy and confocal microscopy.

For the first time, we report the effect of AHS on bacterial biofilm development, including survival past 28 days on steel surfaces and successful establishment of mature DSBs. 6-day DSBs exhibited 0-6.36 log10 culturable CFU/coupon across four species, overlapping with 5.37–7.27 log10 CFU/coupon of 7-day hydrated biofilms. Viability staining revealed the suspected presence of viable but nonculturable cells in both biofilm conditions, whilst matrix glycoprotein material appeared more concentrated in DSBs. We also report the inability of ESKAPE DSBs to form on pure copper surfaces. These findings offer three-dimensional insight into DSB composition and development in the healthcare environment, informing effective infection prevention strategies and supporting the architectural role of copper.

Poster Location 3 - Designing exosomes for nervous system repair

Joshua Byrne - University of Southampton, Dr James Dillon - University of Southampton, Prof Arthur Butt - University of Portsmouth, Dr Melissa Andrews - University of Southampton.

Prospects for recovery after spinal cord (SC) injury are low due to the reduced regenerative capacity of SC neurones. Interventions that promote regrowth of damaged axons are required to restore function. Integrins are a transmembrane protein that mediate communication between the cell and the extracellular matrix (ECM). Specifically, α9 integrin overexpression in dorsal root ganglia (DRG) neurones can promote axon growth after injury by binding to tenascin-C (TNC), an upregulated ECM protein.

However, when neurones reach maturity, α9 integrin is not expressed and is excluded from axons following overexpression. Therefore, effective delivery of α9 integrin is needed. Exosomes, a subtype of secreted small extracellular vesicle (sEV), can carry functional integrins between cells. Previous work has shown that exosomes purified from HEK-293T cells, that artificially overexpress α9, promotes outgrowth in adult DRGs grown on TNC in vitro. However, exosomes from other cell types may have greater capacity to increase outgrowth. Therefore, could sEVs from a different source further enhance the α9-mediated growth?

This project investigates if secretions from embryonic fibroblasts (EF) can enhance α9-mediated growth. Thus far, we have established α9 over-expression and secretion by embryonic fibroblasts from rodents. Our data demonstrates that conditioned media from α9-expressing rat EFs can increase neurite outgrowth of PC12 cells grown on TNC in vitro. The next steps will include exosome isolation from α9-expressing EFs to evaluate if increases in neurite outgrowth on TNC are retained.

Poster Location 9 - Molecular and genetic mechanisms underlying the selective assembly of the plant microbiome

Holly Champney – University of Southampton, Dr Franklin Nobrega – University of Southampton Dr Xiangming Xu – NIAB, Dr Tomislav Cernava – University of Southampton.

Crop production depends heavily on synthetic pesticides and fertilisers, but these practices are often ineffective and come with harmful side effects. In response, biological solutions, such as microbial inoculants, have gained popularity as more suitable alternatives. However, the rapid adaptation of pathogens makes long-term use of specific microbial strains for biocontrol unsustainable.

To address this challenge, a promising solution is to focus on altering the plant microbiome as a whole. By shifting the microbiome to a disease-resistant state, we can reduce the likelihood of pathogens overcoming this multifaceted form of resistance. In practice, this approach can be implemented by selectively breeding or genetically engineering crops based on specific genes, known as Microbiome/M genes, that shape the entire microbiome.

This project builds on knowledge that certain M genes affect plant exudation patterns, which, in turn, shape the microbial community. By studying microbial responses to these exudation patterns, we can observe how different microbes - both beneficial and pathogenic – respond to specific exudates.

To advance the understanding of the interplay between plants and microbes, the growth responses of multiple Pseudomonas strains to an aromatic compound, whose exudation is known to be modulated by M genes, were analysed. The genomes and transcriptomes of distinct responders were profiled and compared to identify the underlying molecular mechanisms.

Future work will involve large-scale analysis of pathogenic Pseudomonas genomes alongside publicly available Metagenome Assembled Genomes (MAGs) to assess whether modifying the plant microbiome could be a sustainable alternative to current biocontrol methods, or whether this system has already been hijacked by plant pathogens.

Poster Location 12 - Adaptation of cutting-edge photonic tools to understand food spoilage biology.

Joshua Fennell - University of Kent/ NIAB, Prof Adrian Podoleanu - University of Kent, Prof Xiangming Xu – NIAB, Dr Michael Hughes - University of Kent, Dr Manuel Marquez - University of Kent and Matevz Papp-Rupar – NIAB.

In the study presented, cherries and plums have been scanned using dynamic OCT (Dy-OCT) to observe the development of brown rot below the surface of the fruit. Thanks to the non-destructive nature of the method, individual samples could be measured over multiple time points to detect and track infection progression in the same fruit.

The study highlighted here is novel in several ways. Firstly, Dy-OCT is a relatively new and exciting approach using OCT. This study is the first to look at fungal infections in fruit and serves as a showcase that it is possible to see the effects and growth of the fungi itself. Secondly, I propose two novel methods in the processing of the images that require only 8-16 scans per lateral position to produce dynamic images. This is significantly less than most studies. One method utilises FFT and normalization, while the other uses PCA. This reduction is significant as it opens the possibility of future studies that could produce dynamic images in real-time of fruit in the orchard or at the sorting-line. This is because the amount of data and processing time is significantly reduced. The results presented show that both approaches can meaningfully differentiate between deep fruit tissue and living fungi that is visually easy to see.

Poster Location 21 – An industrial collaboration to develop new microscopy tools to image ATP usage in muscle

Ateeqa Naim - University of Kent, Prof Mike Geeves – University of Kent, Prof Neil Kad - University of Kent.

Cardiac muscle contraction results from interactions between the force-generating motor protein myosin, and the actin-containing thin filament within the sarcomere, the fundamental contractile unit. Myosin generate force through ATP hydrolysis, therefore, given the vast number of myosins in the heart, if all were producing force simultaneously this would lead to hypercontractility, delayed relaxation and a detrimentally rapid depletion of ATP. To prevent this, a slow ATPase state, termed the 'super relaxed' (SRX) state exists in which a population of myosins reside until they are recruited, typically during increased stress (e.g., during exercise). However, in diseases such as hypertrophic cardiomyopathy (HCM), the most common genetic heart disease, affecting 1 in 500 people, it is suggested that the population of myosin in this cardioprotective SRX state is significantly reduced. Our research aims to utilise single-molecule imaging to determine the spatial distribution of this SRX myosin population across the sarcomere and understand how this distribution is dysregulated by disease-associated mutations, force and pharmacological interventions. Ultimately, we aim to scrutinise the cardiac contractile system at a single molecule level to develop a comprehensive understanding of cardiac myosin regulation.

Poster Location 26 - Yeast Filamentation and Biofilms: Triggers and Applications.

Muhammad Zalkifal – University of Southampton, Prof Campbell Gourlay – University of Kent, Prof Vladimir Jiranek – University of Southampton.

Yeast are single-celled and non-motile. On solid (agar) media a single cell yields a population that piles-up to form a tightly packed, hemispherical colony visible to the naked eye. In some cases, cells instead spread widely in a mat-like biofilm comprising cells attaching to the surface and each other in a self-produce viscous matrix. Alternatively, colonies can broadcast hyphal-like structures comprised of chains of elongated cells, which not only spread across an agar medium but also invade it. Biofilms are more resistant to antimicrobial therapies and chemical stress aiding population survival, as too are filamentous and invasive growth, which are also vital to the virulence of many pathogenic yeast. A deeper understanding of the mechanisms behind the architecture of biofilms, and filamentous and invasive growth, as well as the triggers for initiation and development of these has huge potential to impact on the detrimental and beneficial aspects of yeast in many contexts.

This project will utilise Saccharomyces cerevisiae, the workhorse of the baking, brewing/wine and biofuel industries, to study why, how and when these yeast switch to a biofilm, filamentous or invasive mode of growth, and how these structures develop. This knowledge will be harnessed to improve antifungal strategies for pathogenic yeast as well as to enhance targeted processes within diverse industrial fields that are key to achieving a net zero economy, such as biofuel, recombinant protein and mycoprotein production and crop yield enhancement.

The project will utilise advanced microbiological, genetic engineering and high-resolution microscopy and image analysis techniques to understand the impact of nutrient availability, signalling compounds, and growth medium on the development of yeast multi-cellular structures in S. cerevisiae as well as other relevant yeast species.

Thursday 26th March

Presentation Session 5 9:00am to 10:30am

3MT: Data-driven identification of translational control

Juri Westendorf – University of Southampton, Prof Mark Smales – University of Kent, Dr Owen Rackham – University of Southampton.

DNA transcribes into RNA, which translates into protein. Traditionally, gene expression has largely been synonymous with the first of these two processes: transcription. With the advent of ribosome profiling and advanced AI-powered computational tools, translation has come into the spotlight as an independent regulatory layer. Here, we employ deep learning to identify the sequence determinants of translation. We extract embeddings per gene using open-source state-of-the-art sequence models — including Translatomer, RiNALMo, Evo2, Helix-mRNA, GEMORNA, and Orthrus — and train an XGBoost classifier to predict translation efficiency from sequence across diverse human tissues. Analysis of matched RNA sequencing and ribosome profiling data reveals tissue-specific translational variation, with UTR length, GC content, and RNA-binding protein motifs within UTRs emerging as key distinguishing features. We systematically evaluate performance via ablation studies, by testing different embedding combinations and excluding non-translation-relevant embedding dimensions. The classifier achieves AUROC ~0.73–0.78 and accuracy ~72–76% (5-fold CV), with multi-embedding combinations outperforming single models. Once optimisation is complete, generative models will be trained to design mRNAs with enhanced translation efficiency for

therapeutic applications, with model predictions experimentally validated in the Smales Lab at the University of Kent.

3MT: Individual Differences in Human Colour Processing

Rio Coleman – University of Southampton, Dr Jenny Bosten - University of Sussex, Dr Nick Kelley – University of Southampton, Dr Christoph Witzel – University of Southampton.

Colour vision results from a pathway of different processing stages, extending from the eye to the visual centres of the brain. Each stage depends on the output of the previous stages, including their limits and individual variations, thus it is of interest to examine each independently. This project develops computer-based tasks that measure each stage of colour vision individually, using the phenomenon of complementary colours that arise from different sources across the visual pathway. These complementary colours arise from negative afterimages, perceptual mixture, spatial contrast induction, and subjective contrast. Building on results establishing afterimages as a measure of first-stage colour processing, we have investigated a heterochromatic flicker task to measure perceptual mixture, using comprehensive measurements across a hue circle that were replicated five times per observer. We established the results of this task as distinct from afterimages and following key predictions of second-stage colour processing. Tasks have been developed to measure spatial contrast induction and subjective contrast, with preliminary results suggesting that their results are distinct from one another, including some indication that their results align with other stages of colour vision. Upcoming work will expand on this preliminary data to more robustly support these initial findings, building a large body of data that samples across the hue circle and extensively replicates findings for each observer. This work could result in a new set of measurements to probe colour vision and understand its individual differences with impressive detail, which can be performed with just a colour calibrated monitor.

8MT: Unveiling the role of APOE in microglial development

Dyuti Basu Choudhury - University of Southampton, Sarah L King - University of Sussex, Diego Gomez- Nicola - University of Southampton.

Microglia are the brain's innate immune cells and play protective roles during early brain development. In Alzheimer's disease (AD), microglia respond to the buildup of protein aggregates by upregulating apolipoprotein E (APOE), a major cholesterol transporter in the brain. However, microglia can act as double-edged swords, particularly when expressing the APOE4 allele, a major genetic risk factor for AD. APOE4 disrupts lipid homeostasis in microglia,

leading to inflammation, impaired phagocytosis, and reduced debris clearance, which contribute to dysfunctional microglial responses.

Previous studies in our lab showed selective upregulation of APOE in microglia during healthy development, particularly around early postnatal days (P4-7). Here, we investigated whether different human APOE alleles (APOE3 vs APOE4) differentially affect microglia during early development potentially influencing AD onset. We studied mouse models carrying human APOE3 or APOE4 alleles using immunostaining and morphological analysis of microglia. We observed increased microglial density in the corpus callosum at P7 in APOE4 mice compared to APOE3 mice. Adult APOE4 microglia also displayed reduced branching, suggesting impaired maturation. We further examined Dectin-1, a marker seen in microglia at early development, associated with myelination, and found that APOE4 P7 brains lacked Dectin-1^{+} microglia present in APOE3 brains. Similar morphological alterations were observed in healthy human samples, with APOE4 microglia displaying reactive morphology compared to APOE3 homozygous individuals. Additionally, APOE4 samples showed increased accumulation of degraded myelin basic protein (dMBP), indicating myelin loss. Future work will examine changes in gene expression in APOE3 and APOE4 microglia in young and adult mice.

3MT: Investigating a novel relationship between proteins regulating cell division and DNA repair

Ewan Reed – University of Southampton, Dr Jerome Korzelius – University of Kent, Dr Salah Elias – University of Southampton, Dr Marcin Przewloka – University of Southampton.

The nuclear mitotic apparatus protein (NuMA) is a large and complex scaffold protein with essential roles in both the interphase nucleus and during mitosis. During mitosis, NuMA interacts with multiple binding partners in a spatiotemporally regulated manner to organise mitotic spindle fibres and ensure accurate chromosome segregation. Disruption of NuMA expression, through either depletion or overexpression, leads to mitotic defects and ultimately cell death. This makes studying non-mitotic functions challenging. These nuclear functions are proposed to include roles in DNA repair and the regulation of nuclear morphology, processes that are critical for cellular homeostasis and the prevention of tumorigenesis.

This project aims to elucidate the poorly understood roles of NuMA during interphase by introducing a GFP tag into the endogenous NuMA locus via CRISPR–Cas9-mediated knock-in. This will enable proteomic analysis of interphase cells via GFP-trap approaches, alongside live-cell imaging, without perturbing native expression levels. Currently the GFP tag has been successfully knocked-in and I am selecting GFP-expressing cells.

Once novel NuMA interaction parters have been identified, expansion microscopy will be employed to investigate precise localisation. This is because this technique overcomes the usual diffraction limit for light microscopes (~200 nm) by physically expanding samples within a swellable gel matrix, thereby increasing fluorophore separation and enabling super-resolution imaging. I have now optimised this method for several proteins such as NuMA and tubulin in both mitotic and interphase cells. Together, these approaches provide a robust platform to uncover previously uncharacterised functions of NuMA.

8MT: **Phenotypic constraints on crop improvement and the domestication of novel crops - Close together, far apart: does the localization of QTL impact plant domesticability?**

Anastasia Kolesnikova, University of Southampton, UK; Prof Abdullah Kahraman, Harran University, Turkey; Dr. Adrian Brennan, University of Durham, UK; Yann Bourgeois, Research Institute for Development (Institut de Recherche pour le Développement, formally at the University of Portmsouth), France; Mark Chapman, University of Southampton, UK.

Before the advent of agriculture, humans collected and cultivated a large variety of plants. Out of the thousands of managed species, only 250 are considered domesticated, with the rest having been abandoned. The reason why certain wild plants were successfully domesticated, and not others, remains unknown.

We use the term domesticability to describe an organism's ability to be domesticated. Genetic architecture, or the localization of QTL associated with traits of interest may play a role in domesticability, as recombination may separate or bring together QTL associated with traits selected for during domestication. In addition, QTL effect size may play a role in domesticability, as a large-effect QTL may be easier to select compared to several small-effect QTL.

Co-localization between QTL for traits of agricultural interest may increase domesticability, as beneficial trait pairings will be consistently inherited by offspring. Conversely, large distances between QTL of interest may decrease domesticability, as recombination could separate beneficial trait combinations. We test the hypothesis that QTL of agricultural relevance in progenitor species are more frequently co-located compared to QTLs in never-domesticated wild (NDW) species.

We grew and phenotyped two F7 populations of progenitor (C. reticulatum) x domesticated (C. arietinum) and NDW (C. echinospermum) x domesticated chickpea crosses. Using ddRAD-seq, 96 individuals from each population were genotyped and QTL maps for agriculturally important phenotypes were generated with rqtl2. We test for differences in the localisation of QTL and discuss whether genomic architecture could have contributed to the domesticability of progenitor species.

3MT: Applying new technologies to dissect RNA dynamics in response to cellular stress

Felicitas Liessem (University of Sussex), Mark Smales (University of Kent), Ben Towler (University of Sussex).

Extracellular vesicle (EV) communication between different brain cell types, including neurons and astrocytes has long been shown to co-ordinate responses to changing cellular environments. The molecular mechanisms underpinning how EVs affect the recipient cell under stress remains unclear. RNA is a major cargo type shuttled by EVs but how efficiently RNA is trafficked into recipient cells and how they aid cell survival or induce apoptosis is unknown. EVs from a genetic MND astrocyte model alone have been shown to induce cell damage in otherwise healthy neuronal cells.

Therefore, the study of EV RNA dynamics is an important step towards understanding how neurons and astrocytes communicate in health and associated diseases such as Motor Neuron Disease (MND). MND is a fatal neurodegenerative disease with a life expectancy of ~24 months after diagnosis and virtually no treatments. In MND, a toxic neuronal microenvironment induces cell death at the neuromuscular junction, where nerve and muscle connect, causing gradual muscle wasting and eventually death.

The cause of ~90% of MND cases remains unknown, making it difficult to model, therefore we will use a genetic (TDP-43) MND model to elucidate how EV RNA dynamics between astrocytes and neurons in control cells and how both stress and TDP-43 mutation impact these mechanisms. Initially, we will use neuronal SHSY5Y and astrocytic U373 Uppsala cells and our newly developed method to assess transfer of RNA via EVs in healthy cells and from TDP-43 mutated lines. Prospectively we will advance this model into MND patient IPSCs.

3MT: The Sounds of Soil – understanding the relationships between soil structure, biodiversity and ecoacoustics

Oliver Clark-Hattingh – University of Sussex, Dr. Katherine Williams – University of Portsmouth, Dr. Alice Eldridge – University of Sussex, Dr Christopher Sandom – University of Sussex.

Soil is composed of a network of interconnected microhabitats enabling it to host an unparalleled level of biodiversity. This biodiversity plays a crucial role in the healthy functioning and productivity of agricultural ecosystems, by regulating key processes such as nutrient cycling. However, soil's opaque nature, limits opportunities for direct observation, resulting in destructive and invasive sampling methods. These approaches are time-consuming, resource-intensive, and prevent repeated measurements. Consequently, restricting our understanding of species presence, community composition, and temporal and spatial dynamics of soil biodiversity.

Advances in acoustic sensors, offer a promising, non-destructive alternative. By enabling repeatable and cost-effective sampling across broader temporal and spatial scales, soil acoustics has the potential to reveal previously hidden ecological processes. However, developing this understanding depends on having accurate and reliable acoustic sensors, and a deeper understanding of the sounds we detect.

This research will test the accuracy of current sensors by investigating how they interact with changes in soil structure and compaction using X-ray CT; develop our understanding of soil sounds by building a soil sound library to link specific species to their unique sounds, enabling species-level identification and aiding the validation of current and future field recordings.

Initial field experiments indicate that present sensors can effectively detect differences in soil invertebrate activity, including the sounds of individual species. Ongoing collection of soil acoustic data, and addressing remaining uncertainties will help advance this technology, establishing it as a practical tool for farmers and landowners to monitor soil biodiversity.

8MT: Identifying microRNA-mRNA networks involved in carboplatin resistance in lung and ovarian cancer

Nikolaos Sideris 1, Benjamin Towler1, Martin Michaelis2, Mark Wass2, Leandro Castellano1
Affiliation: 1 University of Sussex, 2 University of Kent

Carboplatin is a platinum-based DNA-damaging chemotherapeutic widely used to treat lung and ovarian cancers. Despite improved survival rates, most patients eventually relapse due to resistance, though the underlying mechanisms remain unclear. MicroRNAs (miRNAs), small

non-coding transcripts that repress gene expression on the post-transcriptional level, have emerged as key regulators of cancer progression and drug resistance. Evidence suggests that miRNAs control genes crucial to therapeutic response, yet their role in carboplatin resistance has not been fully investigated.

We hypothesise that miRNA–mRNA interaction networks contribute to carboplatin resistance. To investigate this, we performed small RNA sequencing to identify dysregulated miRNAs between carboplatin-sensitive and -resistant cell lines and are defining their mRNA targets to uncover pathways involved in resistance. Functional validation is being conducted using oligonucleotide inhibitors and miRNA mimics to assess how candidate miRNAs influence drug sensitivity. We have selected one lead miRNA for deeper analysis and performed transcriptome sequencing following both inhibition and overexpression to characterise downstream regulatory effects. Ongoing analyses aim to identify its direct targets and the networks through which it modulates resistance. In parallel, we are investigating the contribution of non-canonical miRNAs, as well as differential polyadenylation and alternative splicing profiles between resistant and sensitive conditions.

By integrating small RNA, transcriptomic, and post-transcriptional regulatory analyses, this work will define molecular mechanisms driving carboplatin resistance and may reveal novel biomarkers and therapeutic targets to improve patient outcomes.

8MT: Developing novel techniques to elucidate the uptake and permeability of compounds across biological membranes

Matthew Rice - University of Kent, Professor Jennifer Hiscock – University of Kent, Dr Neil Wells - University of Southampton, Dr Charlotte Hind - UK Health and Security Agency, Dr Jose Ortega-Roldan- University of Kent

The accelerating crisis of antimicrobial resistance (AMR), driven by ESKAPE pathogens, alongside the sustained global burden of cancer, underscores the urgent need for new therapeutics. While many small molecules show potent antimicrobial or anticancer activity in vitro, their clinical success is often limited by an inability to efficiently cross biological membranes and achieve sufficient intracellular accumulation. Moreover, adaptive changes in membrane lipid composition can further reduce drug uptake and contribute to resistance. Addressing membrane transport is therefore central to overcoming therapeutic failure.

This work presents an integrated methodological framework to define the principles governing small-molecule permeation and cellular uptake across clinically relevant

membranes. We first developed novel Nuclear Magnetic Resonance based approaches to directly monitor membrane adhesion and passive permeation. Distinct spectral signatures enable discrimination between membrane association, translocation, and impermeability in systems derived from priority pathogens and cancer cell lines. Complementing this, we established a high-throughput platform to quantify active uptake of compounds into cells and tissues, allowing differentiation between passive diffusion and transporter-mediated processes. These methods enable scalable assessment of intracellular accumulation.

Together, these approaches generate a unified dataset linking membrane interaction, passive permeability, and active uptake across diverse lipid environments. This information can be leveraged to guide intelligent drug design strategies that enhance cellular accumulation and improve the likelihood of therapeutic success against resistant infections and cancer.

3MT: A Novel Approach to the Development of next-generation Antimicrobials

Mackenzie Stevens1, George T. Williams2 and Jennifer R. Hiscock1*
Affiliation: 1. University of Kent, School of Natural Sciences, Canterbury, Kent, CT2 7NZ.
2. University of Southampton, School of Chemistry, Highfield Campus, Southampton, SO17 1BJ
Keywords: Co-formulation, supramolecular self-associating amphiphiles, efficacy enhancement

Antimicrobial resistance (AMR) represents a critical and escalating threat to global health, with projections estimating up to 10 million annual deaths by 2050. Increasing reports of reduced susceptibility and emerging resistance to marketed antiseptics such as chlorhexidine and octenidine further underscore the requirement for innovative strategies to enhance their clinical efficacy. Herein, we present a set of novel di-anionic carboxylate supramolecular self-associating amphiphiles (SSAs) as potential co-formulants to enhance the antimicrobial efficacy of chlorhexidine and octenidine, while also serving as prospective scaffolds to enable the formation of pseudorotaxane-based assemblies. SSAs are a class of amphiphilic salt that are naturally ‘frustrated’, enabling the access of multiple hydrogen bonding modes simultaneously. We report the characterisation of novel carboxylate SSAs, and their self-associated co-formulations following established methods described by Hiscock and colleagues, to elucidate both their solid- and solution-state properties. These studies establish a comparative framework for evaluating their suitability as efficacy enhancers in antiseptic formulations, while offering insight into how cation identity and self-associative behaviour influence aggregate formation and stability.

Quantitative 1H NMR spectroscopy, critical aggregation concentration (CAC) and dynamic light scattering (DLS) studies revealed that all synthesised SSAs and their co-formulations maintained the ability to form higher-order aggregates in a concentration-dependent manner. Furthermore, the data obtained to date reveals the presence of a dynamic equilibrium between monomeric and aggregated species in solution, modulated by the incorporated cation. Collectively, these findings lay the groundwork for the future evaluation of di-anionic carboxylate SSAs as supramolecular components within next-generation antimicrobial formulations.

8MT: Enhancing rAAV Gene Therapy Manufacturing: Improving Productivity and Genome Packaging through Plasmid and Cell Engineering

Oya Isilay Canik, University of Kent, Tim Fenton, University of Southampton, , Martin Stoffel, Danu Insights, C. Mark Smales, University of Kent.

When using viral vectors for gene therapies, producing high-titre yields at scale is challenging and contributes to cost. Recombinant Adeno-Associated Virus (rAAV) is a viral vector used in the clinic, however low yields of fully genome-packaged rAAV, and challenges in both scalability and characterisation, mean yields of rAAV are often unsatisfactory for clinical need. This study aims to enhance correctly genome packaged rAAV titre by generating high-yielding rAAV constructs. Initially, pAd-Helper, a low-copy plasmid, was engineered to produce a high-copy version. After verifying the functionality of the pAd-Helper High Copy Plasmid, the plasmid was used in triple transfection experiments in HEK293 cells where the AAV RepCap genes are in one plasmid, alongside transfection of a helper and genome (flanked by ITR sequences) containing plasmid. Individual Rep2 and Cap2 genes were engineered and cloned to allow investigation of different amounts of the genes (Rep78/68/52/40 and Cap2 genes VP1/2/3) on protein expression, rAAV packaging and the cytotoxic nature of individual Rep gene expression on HEK293 cells. Recombinant Rep and Cap protein expression was confirmed by western blotting. ELISA assay using individual Rep and Cap constructs showed the AAV2 capsid is not formed in the absence of Assembly-Activating Protein (AAP) and the amount of AAP impacts the yield of genome containing capsids. After establishing the amount of each individual gene that replicated subsequent protein expression from wildtype RepCap plasmid transfection, a design of experiment approach was used to investigate how individual Rep expression impacts rAAV production and genome packaging. This work is on-going.

Poster Session 2 10:45am to 11:45am
Group C presenting posters 10:45am to 11:15am
Group D presenting posters 11:15am to 11:45am

Group	Poster Location	Name
C	1	Daniel Aspiazu (USoton)
C	7	Claudia Chitty (UKent)
C	13	Tia Fletcher (UPort)
C	16	Linda Guantai (USoton)
C	19	Emily Jones (USoton)
C	22	Courteney Kayleen Pienaar (USusx)
C	24	Tom Roberts-Mcewen (Uport
D	4	Lydia Bennett (UKent)
D	6	Alex Cahill (UPort)
D	10	Emmanuel Denu (UKent)
D	15	Adam Green (USoton)
D	20	Emily Millerchip (USusx)
D	25	Lucy Unwin (USusx)

Poster presentation group C – 10:45am to 11:15pm

Poster Location 1 - Chemical Tools to Interrogate Protein-Misfolding Diseases

Daniel Aspiazu - University of Southampton, Dr Wei-Feng Xue - University of Kent, Dr Sam Thompson - University of Southampton

Amyloid formation is the process where normally soluble proteins misfold into toxic aggregates. It is associated with numerous widespread and incurable diseases, including Parkinson's and Alzheimer's. Cross-beta structures, where beta-sheets are layered alternately in a perpendicular arrangement, are characteristic of Amyloids. These structures exhibit polymorphism: the conditions present during their formation give rise to different types of amyloid structure. Synthetic mimics of beta strands – one of the peptide strands in a beta sheet – have the potential to selectively bind to endogenous beta-strand segments during amyloidosis, thus interfering with the beta-sheet assembly process and potentially inhibiting aggregation and/or driving formation of one polymorph over others.

This work presents a new class of beta-strand mimic, consisting of alternating 5-membered cyclic ureas and 5-membered heterocycles containing sulfur and nitrogen. Natural amino acids are derivatized to cyclic urea fragments, which are assembled rapidly via an iterative, modular synthesis - consisting of alternating transition metal cross-coupling and nosyl deprotection steps. Conformational control in the mimic backbone is achieved via non-

covalent sulfur-oxygen interactions and dipolar repulsion between the thiazole nitrogen and the carbonyl lone pair of the adjacent urea. These beta strand mimics recapitulate the angular and spatial representation of all residues on one face of a canonical beta-strand, as evidenced by x-ray diffraction and NOE NMR.

Poster Location 7 - Atomic Force Microscopy Image Analysis of Amyloid Filaments

Claudia Chitty, University of Kent; Prof Louise Serpell, University of Sussex; Dr Tobias von Der Haar, University of Kent; Dr Wei-Feng Xue, University of Kent.

Amyloid fibrils are protein fibres best known for their role in neurodegenerative disease, but they can also act as functional scaffolds and are being explored as building blocks for new biomaterials. These fibrils can adopt many different structures, or polymorphs, that are difficult to study with a single technique. My project focuses on using atomic force microscopy (AFM) to analyse individual amyloid filaments and link their structures to high-resolution cryo-electron microscopy (cryo-EM) structures. In the poster, I present a simulation AFM (S-AFM) framework built into the open-source Trace-y software, which converts cryo-EM Coulomb potential maps of helical filaments into realistic AFM-like height images using a virtual probe. The workflow also applies controlled augmentations, such as different twists, viewing angles, tip shapes, and noise levels, to generate large, diverse libraries of synthetic AFM images with known structural labels.

These simulated datasets will be combined with experimental AFM images of amyloid fibrils to quantify filament dimensions and shapes, classify polymorphs, and train machine learning models for automated fibril structure analysis. Ultimately, this integrative approach aims to map the full range of amyloid filament structures at both near-atomic and single-filament levels, improving our ability to detect rare, disease-relevant forms and supporting future diagnostic or therapeutic strategies, as well as informing future applications of amyloid-based biomaterials.

Poster Location 13 - Exploiting natural variants in potassium channel genes to understand their roles in neural function, behaviour and development

Tia Fletcher, Prof Diana Baralle (University of Southampton), Prof Mariana Vargas-Caballero (University of Southampton), Prof Matthew Guille (University of Portsmouth), Dr Annie Godwin (University of Portsmouth).

Poster Title: From Farms to Frogs: Identifying Novel Human Disease Genes

There are >10,000 human disorders caused by changes in a single gene. Diagnosis of these rare diseases is challenging with ~50% of patients remaining undiagnosed. Diagnosis relies on having sufficient data which links the genetic change and disease. Rare disorders have limited patient populations, therefore data from patients alone cannot support diagnosis. Animal models provide key insights into gene function and offer opportunities to study these disorders, while ascertaining data to support diagnoses.

In 2021, a calf with a severe neuromuscular disorder was sent to University of Bologna for examination. Genetic analysis identified a mutation in the KCNG1 gene. To date no cases of KCNG1 related human disorders have been reported, but genetic changes in the closely related genes KCNA1 and KCNQ2 are known to cause neurological disorders like epilepsy. We hypothesise that changes in KCNG1 are responsible for a human neuromuscular disease. Here we have altered kcng1 in Xenopus, a frog, to explore the link between genetic changes in this gene, neuromuscular alterations in the calf and neurological symptoms in humans.

Could a calf and a frog hold the key to uncovering a new rare disease in humans?

Poster Location 16 - Drug-host-microbiome interactions in Parkinson's disease

Linda M. Guantai1,3, Clementine E. Bavinton2, Jerome Swinny4, Nela Nikolic1,3, Franklin L. Nobrega1,3, Sam Thompson2,3, Fatima C. Pereira1,3

Affiliation: 1University of Southampton, 2University of Southampton, 3Institute for Life Sciences, University of Southampton, 4University of Portsmouth.

Drugs targeting human cells frequently interact with gut microbes, shaping microbial community function and host outcomes. Beyond enzymatic modification, microbes can influence drug efficacy, bioavailability, and toxicity through bioaccumulation, potentially altering microbial community dynamics. The molecular determinants of drug bioaccumulation by microbes remain poorly understood. This work aims to elucidate the genetic determinants governing intracellular drug uptake and retention in bacteria at the single-cell level. We focus on entacapone, a Parkinson's disease medication that we have previously shown to accumulate to high levels in bacteria. To investigate this process, we have developed chemical tools to characterize drug bioaccumulation using a clickable alkynated analogue of entacapone. By coupling this entacapone analogue with fluorescence-based click chemistry, we can quantitatively visualize intracellular compound accumulation at the single-cell level in bacterial populations. Using entacapone as a testbed, together with these tools,

we seek to identify the molecular determinants that drive its bioaccumulation. Our approach combines the clickable alkynated drug analogue with genome-wide mutant screening in Escherichia coli, leveraging the Keio single-gene knockout collection to systematically uncover genetic contributors to intracellular drug accumulation. Proof-of-concept experiments using a siderophore transporter mutant demonstrated reduced intracellular drug accumulation relative to wild-type cells, validating the sensitivity of the single-cell fluorescence workflow. The optimised chemical-genetic platform will be applied to systematic screening of the entire E. coli Keio mutant library to identify genes influencing pharmaceutical drug bioaccumulation and retention. This work will advance understanding of genetic determinants of entacapone bioaccumulation and enable prediction of microbial effects on drug efficacy.

Poster Location 19 - Synthetic biology approaches to construct metal analogues of vitamin B12 to act as anti-microbial and imaging agents for health applications

Emily Jones – University of Southampton, Martin Warren – University of Kent, Andrew Lawrence – University of Southampton.

Introduction:
Vitamin B12 is an essential vitamin for life, with a complex structure consisting of a corrin ring, an upper ligand, and a lower tethered base, both of which coordinate to a central cobalt ion. The ability to switch out the cobalt metal centre for another metal enables the production of antivitamins, or antimetabolites. Previously synthesized B12 antivitamins include various zinc, copper, rhodium, and nickel analogues.

A strain of E. coli (ED663) is used to produce Hby, which is the starting metal- free metabolite in many metal insertions. This lacks a lower loop, of which is important in recognition processes. This work entails the engineering of this strain to eventually make a full metal free B12 scaffold with a lower loop which could be used for making antivitamins.

Methodology
Plasmids containing genes from Rhodobacter capsulatus and Allochromatium vinosum have been assembled using both link and lock, and SLIC cloning.

Co-expression of these plasmids with the ED663 genome has been carried out, followed by purification of product material.

Hbi-Phosphate has been used in an enzymatic reaction with Allochromatium vinosum Cob U.

CuHby, NiHby, and ZnHby can be made via chemical reaction of Hby with a metal salt.

Results
The production and purification of Hbi-Phosphate have been carried out from a co-expressed plasmid with the ED663 genome.

Hbi-Phosphate can be converted to Hbi-GDP via Cob U.

Significance:
The easy production of these metabolic intermediates means that there is easier access to make and purify these metal analogues for investigating potential therapeutic use.

Poster Location 22 - Manipulating the molecular features of long non-coding RNAs to regulate gene expression in an industrial context

Courteney Pienaar - University of Sussex, Prof Tobias von der Haar – University of Kent, Oliver Rogoyski - University of Sussex, Sarah Newbury - University of Sussex, Benjamin Towler - University of Sussex.

Background:
Post-transcriptional regulation of gene expression via RNA stability is critical for cellular homeostasis and there is extensive evidence to show that dysregulation of RNA stability underlies numerous pathologies. As intracellular RNA levels depend on the balance between transcription and degradation, elucidating the molecular control of RNA decay is crucial for understanding disease aetiology. Previous studies on RNA decay have primarily concentrated on messenger RNA (mRNA) stability, but accumulating evidence suggests that long noncoding RNAs (lncRNAs) also have a range of biologically significant functions and their dysregulation is frequently associated with disease pathogenesis. Consequently, elucidating the molecular mechanisms governing lncRNA stability has emerged as a crucial area of investigation. An important aspect of lncRNA stability is lncRNA decay. Exoribonucleases are key enzymes in controlling RNA stability as they control RNA transcript levels by degrading transcripts. Previous work has shown that specific exoribonucleases target particular transcripts, but it is still not fully understood how specificity is determined. Here we investigate the mechanisms underlying lncRNA decay, focusing on cytoplasmic exoribonucleases Pacman or Dis3L2 in Drosophila melanogaster. Previous work suggests that the RNA decay enzymes target specific transcripts.

Aims:

We aim to elucidate the mechanisms governing lncRNA stability and test the hypothesis that increased translational efficiency of lncRNAs specifically sensitises them to Pacman-mediated decay, proposing a novel regulatory pathway for lncRNA regulatory control.

Methods:
We carried out poly-ribo-seq experiments on larval tissue from Drosophila that carry null mutations in pacman or dis3L2 together with isogenic controls. This allowed us to identify lncRNAs with ribosome occupancy and/or which vary in levels between mutant and wild-type. We then validated the translation of a subset of lncRNAs experimentally by C-terminal fluorescence tagging of the open reading frames (ORFs) and visualising expression in Drosophila S2 cells. We next established an ex vivo system using dissected Drosophila anterior tissue to examine lncRNA stability. Using actinomycin D, we blocked transcription and cycloheximide inhibited translation. Quantitative PCR (RT-qPCR) was used to measure transcript levels in wild-type and exoribonuclease-depleted tissues (Pacman or Dis3L2). Cycloheximide treatment was added to wild-type tissue to examine the impact of translation on the regulation of lncRNA stability.

Results:
Our analysis has identified and validated novel translation events in lncRNAs. Strikingly, lncRNAs with higher ribosome occupancy appear to be specifically sensitive to Pacman degradation. Our actinomycin D experiments confirmed the translational status of the ORFs as detected in poly-ribo-seq. The system confirms the effectiveness of actinomycin D in blocking transcription and the ability of cycloheximide to inhibit translation in dissected Drosophila tissue. We observed specific lncRNA decay patterns in tissues depleted of different exoribonucleases, suggesting different target preferences.

Conclusion:
This study explores the mechanisms of lncRNA decay, focusing on a potential novel pathway involving translation-couple decay by Pacman. By elucidating lncRNA stability regulation, our findings may improve insights into diseases associated with lncRNA dysregulation.

Poster Location 24 - Using group living spiders for biological pest control

Tom Roberts-McEwen, University of Portsmouth; Prof. William Hughes, University of Sussex; Dr. Yann Bourgeois, Institut de recherche pour le développement; Prof. Matthew Guille, and Dr. Lena Grinsted, University of Portsmouth

Collaborators: Jordi Moya Laraño, Estacion Experimental de Zonas Áridas (EEZA); Estefanía Rodríguez Navarro, Insituto de Investigación y Formación Agraria y Pesqueria (IFAPA); Jairo Fernández Quindos, HaciendasBio; Susan Kennedy, University of Trier.

Anthropogenic introduction of invasive agricultural pests, influenced by the effects of climate change, have contributed to increased levels of crop destruction, food insecurity, and economic detriment on a global scale. Additionally, increased pesticide use in response to more frequent infestations has resulted in pesticide resistance in many agriculturally significant pests. Therefore, assessing the biological control efficacy of natural predators as an alternative to chemical pesticides is becoming increasingly important. This study uses the biodynamic, greenhouse-based agroecosystem at HaciendasBio in Almería, Spain, to make this assessment.

Spiders are among the most diverse and abundant natural enemies in agroecosystems. This work will focus primarily on the pest control potential of the group-living tent-web spider Cyrtophora citricola. High levels of conspecific tolerance in the spider allow for the creation of large, predator-dense capture webs that cannot be obtained in highly territorial species.
To understand the biological control potential of these spiders, along with other common species within the greenhouses, DNA metabarcoding was used. For this, DNA was extracted from spider gut and faecal samples. Then, a 2-step PCR process was used to firstly amplify the DNA using newly developed primers, and secondly to introduce unique identifier tags that allow for the preservation of data from each individually tagged sample. After sequencing, the reads will be demultiplexed, and a detailed picture of the contribution of spiders to pest control in the agroecosystem will be produced. This research will deepen current understanding of the ecological niche that spiders fill within these understudied greenhouse ecosystems.

Poster presentation group D – 11:15pm to 11:45pm

Poster Location 4 - How does the brain stop us overeating? Neuro-genetic control of eating, and how it changes with age

Lydia Bennett (University of Kent), Dr Tim Fenton (University of Southampton), Prof. Michelle Garrett (University of Kent), Jennifer Tullet (University of Kent).

Obesity is a growing global health crisis driven in part by dysregulated appetite and energy balance. Humans and C. elegans share conserved appetite control mechanisms, enabling worms to be used as a simple model to study appetite regulation. SKN-1B is expressed in two

chemosensory ASI neurons and is orthologous to mammalian Nrf transcription factors. skn-1b mutants show phenotypes indicative of dysregulated appetite control, including altered foraging and satiety behaviours, fragmented mitochondrial networks in body wall muscle, increased body size, and reduced lipid levels compared to wild-type animals.

As SKN-1B is restricted to two neurons yet drives body-wide phenotypes, we hypothesised that neurotransmitters are required to mediate communication with muscle (movement and mitochondria) and intestine (lipid deposition). To test this, we analysed exploration and lipid deposition in skn-1b mutants combined with mutant strains unable to synthesise tyramine (tdc-1), octopamine (tbh-1), dopamine (cat-2), or serotonin (tph-1).

Both skn-1b and tdc-1 mutants exhibited reduced exploration, with no additive effect in double mutants, suggesting tyramine is required for SKN-1B-mediated exploration. However, dietary tyramine supplementation failed to rescue this phenotype, indicating a more complex interaction. Lipid analysis revealed that similar to skn-1b mutants, octopamine-deficient tbh-1 mutants showed reduced lipid levels. However, surprisingly, loss of skn-1b together with tbh-1 increased fat. Similar results were observed with tdc-1 and tph-1 mutants. This highlights complex genetic interactions between skn-1b and biogenic amines for both foraging and lipid phenotypes. Ongoing work investigates these pathways via octopamine supplementation and analysis of additional SKN-1B-dependent phenotypes (mitochondrial organisation and body size).

Poster location 6 - From Scratch Design of B12-Binding Proteins

Alex Cahill ,University of Portsmouth, Ross Anderson, University of Bristol, Martin J. Warren, University of Kent, Bruce R Lichtenstein, University of Portsmouth.

Vitamin B12 (cobalamin) and its derivatives are of high interest due to their involvement in many key biological and chemical processes, such as DNA methylation, transcriptional regulation, light-dependent gene regulation, and is able to catalyse chemical transformations that have proven challenging in chemistry and industry, such as dehalogenation and selective isomerisation. The role vitamin B12 and its derivatives play in these processes is well established, however it is still not well understood how proteins control its chemistry. De novo designed cobalamin binding proteins will allow close study of the fundamental engineering principles underlying the complex enzymes using cobalamin that are found in nature. This research aims to leverage structural information and recently developed deep-learning tools to design simple B12 binding proteins. This will simplify the study of the fundamentals of B12 chemistry without the complexities found within natural biological

systems. Small scale expression trials of the designs were conducted prior to large scale production, after which the fold of the expressed designs was evaluated using circular dichroism (CD). The CD spectra indicated the proteins were not fully folded, leading to a revaluation of the design pipeline. A second round of designs have been generated and expression trials conducted.

Poster Location 10 - Project: Avoiding the immune system: Using Candida albicans as a tool to understand microbial innate immune evasion strategies

Emmanuel Denu (University of Kent), Prof Paul Skipp (University of Southampton) Dr Rebecca Hall (University of Kent).

Candida albicans is an opportunistic fungal pathogen that lives as a commensal in the natural microbiota of humans. However, under certain conditions, the pathogen can disseminate through the blood to cause systemic infections that can be lethal in immuno-compromised individuals. Recent report reveals a worldwide incidence of 1.5 million annually, with an estimated 63% mortality. The higher mortality has been attributed to difficulty in treatment, with few antifungals present and an increasing antifungal resistance. Furthermore, difficulty in diagnosis as most cases are identified after autopsy. The kidney, which has the highest osmolarity amongst the organs of the human body is the most susceptible to systemic Candida albicans infection. This raise concerns on the adaptability of Candida albicans to the osmotic stress environment of the kidney to evade innate immunity. Combining immunological experiments, CRISPR/Cas9 gene editing and Protein analysis, we aim to unravel the molecular mechanism behind this innate immune evasion strategy. Our current findings show that C. albicans evade phagocytosis by macrophages under osmotic stress conditions. In cap1Δ/Δ strain, innate immune evasion is impaired, suggesting a key role of the Cap1 transcription factor in the immune evasion process. Furthermore, in response to osmotic stress, C. albicans undergo rapid thickening of the cell wall which mask important immune recognition receptors which lead to an attenuated immune response.

Poster Location 15 - How to build a chloroplast: Unravelling chloroplast communication with the nucleus.

Adam Green, University of Southampton, Professor Martin Warren, University of Kent, Professor Matthew Terry, University of Southampton.

The chloroplast is the site of photosynthesis, which provides the plant with the biochemical energy used for growth and development. Chloroplasts therefore need to develop efficiently

to ensure optimal photosynthetic performance. The chloroplast is an endosymbiotic organelle and thus, retains its own genetic material. However, the majority of the proteins in the chloroplast are now nuclear-encoded and post-translationally imported into the developing chloroplast. To ensure the chloroplast has everything it needs to become photosynthetically capable, it must communicate its developmental status to the nucleus in a process termed biogenic retrograde signalling. The current hypothesis is that the tetrapyrrole heme, which is synthesized in the chloroplast, is required for this signal and may itself be the signal. To test this hypothesis, Arabidopsis thaliana lines expressing the heme-degrading enzyme heme oxygenase 1 (HO1) in different cellular compartments are being used to determine if retrograde signalling is altered. Current findings show that key nuclear encoded genes (LHCB2.1, GUN4, HEMA1, CA1) have reduced expression when HO1 is overexpressed in the cytosol. The HO1 overexpression lines have also been crossed into the gun1 mutant, which has an enhanced heme-related retrograde signal. This will allow us to test whether degrading different heme pools reduces signalling under conditions in which the signal has been amplified. So far one cytosolic and one plastid double homozygous mutant have been isolated and are now being analysed.

Poster Location 20 - Perennial crops for sustainable cities

Emily Millerchip (University of Sussex), supervised by Dr Daniel Ingram (University of Kent), Prof David Goulson (University of Sussex) and Dr Elizabeth Nicholls (University of Sussex).

Given increasing evidence of the unsustainable nature of conventional intensive agriculture, alternative methods of food production must be considered. Urban agriculture (UA) is one proposed mechanism for increasing food system sustainability, given the potential to provide social and ecological benefits while increasing access to nutritious food. In conventional farming, the incorporation of more perennial crops has been proposed to increase sustainability through reduced soil disturbance, increased water retention and supporting higher biodiversity than annual cropping. However, little research has explored the possible benefits associated with perennial cropping in UA, or whether perennial crops incur any novel costs in urban settings. To answer these questions, we interviewed eleven managers of UA growing sites in England. Thematic analysis identified four key themes in respondents' answers 1) issues faced by growers due to their urban locations, 2) negatives and 3) positives associated with perennial growing and 4) the alternative growing practices utilised. The soil, water and biodiversity benefits associated with perennial crops in conventional agriculture are also perceived to be present in perennial UA. The previously reported health and social benefits for people of UA persist in perennial UA, and the permanent structures perennial crops create can enhance the benefits of these sites as community spaces. However, growers

identified novel social and ecological costs associated with growing perennials including their wide-spreading and long-lasting nature. Growers' experiences of the social and ecological benefits and costs of perennial UA highlight the need for management of urban growing spaces to consider multiple perspectives.

Poster Location 25 - Understanding the Genomics and Ecology of Floral Nectar to Enhance Crop-Pollinator Interactions

Chapter Title: Floral Trait Thermal Plasticity in a Common Crop

Lucy Unwin1, Emily Millerchip1, Alba Edwards1, Mark Chapman2, Maria Clara Castellanos1
Affiliation: 1 University of Sussex, United Kingdom, 2 University of Southampton, United Kingdom

Plasticity in floral traits, particularly those related to pollinator reward and attraction, can influence both the types of pollinators that visit a flower and the nature of those interactions. As flowers commonly exhibit suites of traits that align with pollinator preferences, environmentally driven (=plastic) changes in floral traits can alter plant-pollinator interactions in both crop and wild plants. The true extent of plasticity in floral nectar traits is poorly understood, but central to predicting the resilience of plant–pollinator interactions in the face of environmental change. We used an experimental setup to measure plasticity in response to temperature in floral nectar volume, flower size, and nectar sugar characteristics in the common bean Phaseolus vulgaris L., a globally important crop in the Fabaceae family. P. vulgaris individuals were grown in controlled greenhouse conditions, then allowed to flower at temperatures of 16, 23, and 30°C for 3-day periods. Individual plants experienced multiple temperature treatments to assess plasticity in floral traits. Nectar volume and flower size show significant plasticity in response to temperature. For both traits, the response to temperature was quadratic, consistent with the presence of a thermal optimum. Interestingly, plants varied in their baseline nectar production, but the shape of the plastic response was highly consistent across plants, suggesting plant-level physiological control of this trait. For flower size, plastic responses were less consistent. Understanding the plasticity of floral traits in crops provides key information on the potential to breed cultivars with stable reward production that can benefit both yields and pollinators.

Presentation Session 6 11:45am to 12:45pm

3MT: Effects of Secondary Structure on the Expression and Stability of RNA Therapeutics

Afsheen Shahbaz (University of Kent), Mark C Smales (University of Kent and National Institute for Bioprocessing Research and Training), Wei-Feng Xue (University of Kent), Ben Towler (University of Sussex), Tobias von der Haar (University of Kent).

Following recent success of the COVID-19 vaccine, mRNA technology has gained global attention with potential applications ranging from cancer treatments, protein replacement therapy for genetic disorders and control of infectious diseases. While effective mRNA therapeutics can be designed; their structural conformation cannot yet be fully controlled. Long in vitro transcribed (IVT) mRNAs tend to fold into heterogeneous ensembles of secondary structures giving rise to stems, bulges and loops which then undergo further interactions to form higher-order tertiary structures. Furthermore, due to codon degeneracy, numerous synonymous mRNAs encode the same protein with each sequence adopting different structural conformation. Structural features of mRNA directly dictate the lifetime of the transcript and expression levels of the designed therapeutics. However, lack of control over secondary structure content limits the production of highly effective mRNA-based drugs. Here, we aim to develop a portfolio of methods to characterise the diverse secondary structure landscape of synthetic mRNAs. We employ atomic force microscopy (AFM) to investigate the single-molecule structures of two nano-Luciferase mRNAs from our in-house collection, nLuc-LD and nLuc-OPT. Our preliminary data suggest that both RNAs differ significantly in their structural conformation, with nLuc-OPT likely exhibiting higher structural variance within the population as compared to nLuc-LD. We also observe that chemical modification with uridine analogues like N1-methyl-pseudouridine structurally stabilizes IVT RNAs. Better understanding of the intricate relationship between codon optimization, thermodynamic stability and structural polymorphism of synthetic mRNAs would allow us to design effective mRNA-based drugs with increased stability and enhanced translational efficiency.

8MT: CRISPR-Cas9 reveals adaptive roles of repeat-associated genome instability in Candida albicans

Matthew Shaw[1]*, Alessia Buscaino[2], Tobias Von der Haar[1]

[1] School of Natural Sciences, University of Kent, Canterbury, CT2 7NZ, United Kingdom
[2] Quadram Institute Bioscience, Norwich Research Park, Norwich, NR4 7UQ, United Kingdom

Candida albicans is a common member of the healthy human microbiome and an opportunistic pathogen capable of causing infections ranging from superficial mucosal disease to life-threatening systemic infections. Its ability to rapidly adapt to diverse host environments and acquire antifungal resistance is closely linked to genome instability. This instability generates genetic diversity, enabling the selection of fitter genotypes. Accordingly, clinical isolates of C. albicans are highly karyotypically diverse and frequently harbour chromosomal rearrangements associated with repetitive elements such as the Major Repeat Sequence (MRS).

We hypothesise that repetitive elements act as instability hotspots that facilitate chromosomal rearrangements and rapid genome evolution. To test this, we used CRISPR–Cas9 to target repetitive loci and experimentally induce chromosomal rearrangements. Rearranged strains were phenotyped and subjected to experimental evolution under clinically relevant stresses, including antifungal drugs.

Long-read, short-read and RNA sequencing were used to characterise the resulting genomes and transcriptomes. These analyses show that CRISPR–Cas9 can generate multiple classes of chromosomal rearrangement in C. albicans. While balanced rearrangements have relatively limited transcriptomic and phenotypic consequences, rearrangements that alter DNA copy number produce substantial changes in gene expression, morphology, and fitness, as well as reduced pathogenicity in in vivo infection models. This indicates that repeat-associated genome instability is sufficient to generate phenotypic diversity. Furthermore, exposure of rearranged strains to antifungal drugs promotes the rapid acquisition of resistance, accompanied by additional karyotypic changes. Together, these results provide evidence that genome instability can facilitate antifungal resistance in C. albicans.

3MT: Novel approaches in drug targeting and delivery to combat Gram-negative bacterial pathogens

Selale Cuce – University of Kent, Dr Nicholas Evans – University of Southampton, Dr Mark Shepherd – University of Kent.

The continued emergence of antimicrobial resistance is a burgeoning global health issue, demanding urgent attention and the need to drive for novel antimicrobial development. We propose a development route through the utilisation of current FDA-approved drug libraries to re-purpose, re-develop, and refine drugs to current antimicrobial targets of interest. We focus on one such promising drug target named cytochrome bd oxidases; they are respiratory terminal oxidases solely found within prokaryotes which aid in the generation of the proton motive force. Preliminary work at the Shepherd lab has identified that Quinestrol inhibits cytochrome bd in both Escherichia coli and Staphylococcus aureus. We aim to further determine the capacity of Quinestrol to inhibit cytochrome bd complexes of other gram-negative bacteria, namely Klebsiella pneumoniae. To assess the efficacy of Quinestrol in the inhibition of cytochrome bd function we employed a UV spectrophotometer assay to measure the conversion between duroquinol (as an alternative substrate) and duroquinone; and compare this conversion in the presence and absence of Quinestrol. In generating a dose response, we observed complete inhibition of purified cytochrome bd II of K. pneumoniae in the presence of Quinestrol at an IC50 of 1.308 µg/mL +/- 0.4719 µg/mL, with the highest concentration tested being 50 µg/mL. Our findings allude to Quinestrol being a viable candidate for further derivatisation as well as a good inhibitor of purified cytochrome bd complexes and as such we aim to further asses its efficacy on the cytochrome bd complexes present within Klebsiella pneumoniae, which is a gram-negative bacteria.

3MT: Investigating and harnessing the power of yeast biofilms

Jack Bragg – University of Kent, Prof Vladimir Jiranek – University of Southampton, Professor Campbell Gourlay – University of Kent.

Biofilms are communities of microorganisms that live in a collective entity and attach to living or inert surfaces. These microbial ecosystems can pose major problems in relation to human health. Ventilator associated pneumoniae is an infection associated with tracheostomy and endotracheal tube microbial growth and prevalence varies between 9-65% with mortality rates range between 15-76%. N-acetylcysteine is mucolytic and antioxidant agent which harbours antimicrobial activity, in particular it has been shown to prevent biofilm formation in numerous species such as C. albicans and a range of gram positive and negative bacteria. However no work has been carried out on polymicrobial biofilms. Although numerous papers have demonstrated its antimicrobial properties its mechanisms of action are still widely unknown. The work has thus far shown that NAC is effective against a range of single bacterial and fungal species as well as polymicrobial biofilms. It has also been demonstrated that NAC has a respiratory effect on a range of bacterial species. Differences in effectiveness between the pH 7 and non pH drug solution have also been shown. Finally, interactions between NAC and mucin proteins have been found to produce hydrogen peroxide, a molecule known to disrupt cell signalling and therefore biofilm formation. These findings can be used to promote the use of NAC in the clinic and also opens up the possibility for finding new ways to repurpose the drug.

3MT: Drug Discovery to Target Key Bacterial Respiratory Complexes: Towards Lipophilicity Efficient Inhibitors of Cytochrome bd

Graham Lunn, University of Kent; Dr Dave Beal, University of Kent; Prof Simon Waddell, University of Sussex; Dr Mark Shepherd, University of Kent.

The with the rise of multi-drug resistance, the world is in desperate need of novel antibiotics. Cytochrome bd in various pathogenic bacteria has been suggested as being a potential new antimicrobial target. Recent cryo-EM structure elucidation of cytochrome bd has enabled structure-based modelling of drug binding. The few inhibitors published to date from the screening of compound libraries have only moderate potency and have very poor lipophilic efficiency: namely for the potency they achieve, they are too lipophilic. In a drug discovery programme, this would mean poor pharmacokinetics and unacceptable toxicity risk from broad off-target pharmacology. Additionally, very lipophilic compounds have poor water solubility and the tendency to precipitate and adhere to equipment plastic, which significantly hampers key in vitro experiments to validate and understand the drug target. The project aim is to design and make potent, lipophilicity efficient inhibitors of cytochrome bd of key pathogens. Newly designed molecules will be iteratively docked in software which predicts binding orientation and strength, to develop an understanding of binding at the atom level. Using the corresponding docking-predicted dissociation constant (Kd) of each drug idea together with calculations of the octanol/water partition coefficient (clogP), the

relationship between structure and lipophilicity efficiency will be explored. This will help prioritise compounds chosen for chemical synthesis and in vitro testing against Cytochrome bd.

8MT: Good Vibrations: Using Molecular Dynamics and Raman Spectroscopy to Shed Light on the Aggregation Mechanism of Tau in Alzheimer's Disease

Callum Ellis, University of Southampton; Prof. Sumeet Mahajan, University of Southampton; Prof Jonathan Essex, University of Southampton

Alzheimer's disease (AD) is a neurodegenerative disorder that affects 36 million people worldwide, and by 2050 more 115 million are predicted to have AD.

The pathology of AD results from the accumulation of disease-specific protein aggregates (called amyloid plaques and neurofibrillary tangles) in the brain and no disease modifying therapies exist. Tangles are made up of Tau protein monomers that misfold, self-assemble and accumulate, disrupting cellular function, and the pathology-associated conformational changes which lead to this accumulation are disease-specific, and so understanding relevance of these conformational changes is vital for future treatment.

In this project, we combine in silico techniques (Molecular Dynamics) and novel spectroscopic (Raman spectroscopy) to explore the structure-disease relationships in Tau. We have shown that we can acquire the vibrational Raman spectra of molecular probes involved in Tau aggregation from solution, and have demonstrated that we can calculate the electric fields of molecular probes in silico, establishing their linear relationship.

Here we will combine these experimental and in silico data in order to calibrate and validate Molecular Dynamics outputs and allow us study tau aggregation in AD on an atomic level. This methodology has been tested on carbonyl motifs present in two relevant hexapeptides within Tau, which are essential for fibril formation in Tau and spontaneously aggregate.

Following refinement of computational models using calibration data, we should be able to predict the vibrational frequency of the probe as the peptide aggregates, and validate this experimentally using Raman, allowing development of in silico models of drug interactions with tau aggregates, giving insights into potential therapeutic interventions.

8MT: Unravelling the brain mechanisms behind how cognitive and physical stimulation dampens food cravings and food consumption in mice

Emily C. Woods 1, Kate Z. Peters 1, Zuzana Pedan 1, Scott B. Kinghorn 1, Olga Tsaponina 1, Jerome Swinny 2, Eisuke Koya 1
Affiliation: 1 Sussex Neuroscience, School of Psychology, University of Sussex, Falmer, BN1 9QG, United Kingdom. 2 School of Medicine, Pharmacy and Biomedical Sciences, University of Portsmouth, Portsmouth, PO1 2UP, United Kingdom.

Title: Sex differences in the behavioural roles of cue-reactive orbitofrontal cortex ensembles

Cues associated with food, such as fast-food advertisements can provoke food cravings, which lead to unhealthy overeating. In laboratory animals, such cues elicit food seeking and recruitment of neuronal ensembles in the orbitofrontal cortex (OFC), a brain structure that modulates motivated behaviors guided by appetitive 'cue-food' associations. Although much research has revealed sex differences in food motivation and regional brain activity, much remains to be established regarding sex differences in neuronal ensemble function. Here, we investigated sex differences in OFC ensemble functioning related to cue-evoked food seeking. To this end, we tested the effects of chemogenetic silencing of cue-reactive OFC ensembles on sucrose seeking in sucrose conditioned FosTRAP2 mice. OFC ensemble silencing decreased and surprisingly enhanced cue-evoked sucrose seeking in males and female mice, respectively. Furthermore, this silencing had no effect on sucrose consumption in both sexes, indicating that silencing effects were cue-driven and not due to differences in sucrose reward value. Since sucrose seeking was enhanced in female mice, our silencing may have acted on inhibitory interneurons and thus produced this behavioral effect through disinhibition of OFC output neurons. Thus, studies to reveal sex differences in the composition of inhibitory interneurons are now underway. Our findings reveal that OFC ensembles modulate food seeking in a sex-dependent manner and provide new mechanistic insights into why sex differences exist regarding food cue reactivity and cravings.

Presentation Session 7 1:45pm to 2:45pm

8MT: Role of Kir7.1 in maintaining neuron-glial function across the lifespan

*Ian T. Hunter1, Emma L. Veale2, Anthony Lewis1, and Arthur M. Butt1
Affiliation: 1School of Medicine, Pharmacy, and Biomedical Science, University of Portsmouth, UK. 2Anson, Medway School of Pharmacy, University of Kent, UK

Neurons and glial cells of the CNS express an array of inward rectifying potassium channels (Kir) with distinct biophysical properties and cellular functions. We have examined Kir7.1 expression and function in neurons and glia in 3- and 12-month old mouse brains. Immunohistochemical analyses demonstrate that Kir7.1 is widely expressed by neurons, astrocytes and oligodendrocytes, with regional variation and effects of age: in the cerebral cortex, the number of Kir7.1+ cells declines significantly with age, but in the corpus callosum the number Kir7.1+ cells increases with age. Specific block of Kir7.1 with ML418 resulted in the loss of oligodendrocytes and neurones in brain slices; neuronal cell death was differentially affected by age, with no significant effect of Kir7.1 blockade in the adult cortex and hippocampus, compared to a 30% loss of neurons in aged brain. In ex vivo brain slices, cerebral neurons and oligodendrocytes were susceptible to glutamate-mediated excitotoxicity, a model of cerebral ischemia, and this was exacerbated by Kir7.1 block in adults, although there was evidence it may be neuroprotective in aging. Imaging of

intracellular calcium and cell membrane potential (Em) in cultured cells showed Kir7.1 block disrupted calcium homeostasis and destabilised the Em. To advance this, we are examining the molecular mechanisms by which Kir7.1 maintain neuron-glial function. Our results provide evidence that Kir7.1 dysregulation results in degenerative changes. What is needed to protect against neurodegeneration, therefore, is positive modulators of Kir7.1 and we are addressing this using in silico modelling and validation in vitro in human cell cultures.
*IH is supported by the BBSRC SoCoBioDTP

3MT: The Role of Nuclear Phosphoinositides in the Regulation of Gene Transcription

Palita Udomjarumanee - University of Southampton, Anastasia Callaghan – University of Portsmouth, Nullin Divecha - University of Southampton.

Nuclear polyphosphoinositides (PPIns) are key regulators of nuclear functions, known to interact with various nuclear proteins, including those involved in gene transcription regulation. Changes to the PPIns level can alter the localisation and functions of their interactors. Previous studies suggested a possible link between nuclear PPIns and Lamina-associated domains (LADs), which are transcriptionally repressed chromatin regions. This observed pattern strongly implies that PPIns interaction with LAD-associated proteins may influence their control of gene transcription.

Here, we investigate whether nuclear PPIns regulate gene transcription by modulating the function of LAD-associated proteins. Using a proximity labelling assay, potential nuclear PPIns interactors associated with LADs were identified. The interaction between PPIns and the candidate protein will be validated using lipid binding assays. In addition, the effect of PPIns interaction on transcriptional regulation through LADs will be examined. Preliminary analyses suggest that several LAD-associated proteins may interact with nuclear PPIns, supporting a potential role for phosphoinositide signalling in chromatin organisation and transcriptional control.

This project aims to provide further understanding of the mechanisms through which phospholipid signalling integrates with nuclear spatial organisation to regulate gene expression. These findings may reveal a previously underexplored regulatory layer linking lipid signalling to chromatin architecture and transcriptional repression.

3MT: Neurochemical Insights into Ageing via 3D Neural Culture

Dylan Lamptey – University of Southampton, Dr. Dipanjan Bhattacharya - University of Southampton, Dr Andrew Penn – University of Sussex, Professor Amritpal Mudher - University of Southampton, Professor Sumeet Mahajan - University of Southampton, Associate Professor Sandrine Willaime-Morawek - University of Southampton

As the global population ages, neurodegenerative diseases present a steeply rising health burden. While ageing is the primary risk factor for many neurodegenerative diseases, an

understanding of the precise contribution of cellular ageing processes to increased neural vulnerability remains elusive. To address this knowledge gap, more physiologically representative and accessible models of human ageing are paramount.

This project aims to aid this pursuit through the development of a 3D neural stem cell culture model of ageing. The highly complex mechanisms of ageing also necessitate an analytical toolkit to provide a holistic signature of ageing; consequently, we aim to optimise an analytical toolkit to assess these mechanisms comprehensively, comprising traditional fluorescent markers with advanced label-free techniques such as Raman spectroscopy and Coherent Anti-Stokes Raman Scattering (CARS) microscopy. Initially, these methods will be validated using drosophila melanogaster neural tissue as a complementary, rapidly ageing, in vivo model system.

This research holds the potential to provide a robust, human-relevant 3D model system alongside a validated experimental toolkit which could accelerate research into neural ageing mechanisms. Ultimately, this platform could enable deeper mechanistic interrogation of neural decline with age, and high-throughput screening for targeted anti-ageing therapies, helping to elucidate why the brain becomes vulnerable in advanced age.

8MT: The lysosomal phenotype of aged retinal pigment epithelium cells and their response to physiological cargo

Charles Ellis (University of Southampton), David S. Chatelet (Biomedical Imaging Unit, University of Southampton), David A. Johnston (Biomedical Imaging Unit, University of Southampton), Louise C. Serpell (University of Sussex), David A. Tumbarello (University of Southampton), J. Arjuna Ratnayaka (University of Southampton)*

Background:
Lysosomes are degradative vesicles integral to multiple cellular processing pathways. The retinal pigment epithelium (RPE) employs these pathways and extensive lysosomal networks to process cargo from overlying photoreceptor cells in the human retina. Here, we characterised the physical/spatial characteristics of mature lysosomal networks in aged RPE fed physiological cargos including photoreceptor outer segments (POS), oxidatively-modified POS (OxPOS), amyloid beta (Aβ) and dual cargos (POS/Aβ).

Methodology:
Human ARPE-19 cells were aged to 10 months. Porcine POS was isolated from enucleated eyes, then OxPOS produced by 3-hour ultra-violet exposure. Recombinant oligomeric Aβ1-42 was reconstituted. Transwells were probed for lysosomal-associated-membrane-protein 2 (LAMP2) with Z-stacks acquired by confocal imaging (Leica-SP8, 63x). Lysosomes were segmented using Otsu thresholding and size-based filters (1µm, 3µm and non-filtered). Co-localisation analysis used object-based and Costes methodologies. Lysosomal

volume/spatial analysis was performed on field-of-view (FOV) or machine-learning delineated single cells. All reported data arise from 3 independent experiments.

Results:
In aged RPE cells, all POS/OxPOS cargos demonstrated similar co-localisation to mature lysosomes; Costes (~60%) and OBCA (~40%). Without size filtering, a significant decrease in total lysosomal volume was seen following Aβ1-42 treatment versus untreated cells ($p=0.0427$, Dunnett's T3). Lysosomal volume across all size-based filters was not directly affected by cargo (~40,000-65,000 identifiable lysosomes per FOV). 3D sub-cellular spatial analysis is ongoing.

Implications:
In this work, we developed high-throughput workflows that "fingerprinted" the lysosomal network of aged RPE in response to physiological cargo. Understanding these molecular events provides valuable insights into healthy RPE ageing and the prevention of blinding/neurodegenerative diseases.

8MT: Drug discovery and repurposing to target key bacterial respiratory complexes

Ryan Boughton1, Prof Mark Wass1, Prof Simon Waddell2, Dr Mark Shepherd1
Affiliation: 1School of Biosciences, University of Kent, 2 University of Sussex

Tuberculosis is one of the most widespread and deadliest diseases currently, with a quarter of the global population estimated to be infected with Mycobacterium tuberculosis (MTb). Cytochrome bd is a terminal respiratory oxidase present in many bacterial pathogens allowing for the generation of the proton motif force. Herein, we investigate the efficacy of a known steroid drug inhibitor of cytochrome bd upon Mycobacterium smegmatis and employ a combination of in silico and laboratory techniques to identify potential anti-mycobacterial compounds.

A respiratory mutant strain of M. smegmatis was used to generate membranes that contain cytochrome bd as the sole respiratory oxidase, and complex assembly was confirmed using difference spectroscopy. Furthermore, we developed a novel method of measuring cytochrome bd activity through monitoring the spectroscopic changes during quinol oxidation. Dose response assays were performed using this new assay that which revealed an IC50 in the low µg/mL for the steroid drug quinestrol.

Subsequent work demonstrated for the first time the successful purification of M. smegmatis cytochrome bd that had been recombinantly expressed in E. coli. Dose-response inhibition experiments with the purified M. smegmatis cytochrome bd and quinestrol yielded an even lower IC50. Growth and viability experiments with wild type M. smegmatis cells revealed inhibitory effects on whole cells, with potential efficacy enhancement through combination therapeutics using current anti-mycobacterial compounds.

Presentation Session 8 – 3:00pm to 4:00pm

8MT: Viral variants: assessing the impact of natural strain variation on the structure and function of virus replication and transcription factors

Rhianne Broadway – University of Sussex, Prof Mark Wass – University of Kent, Prof Michelle West – University of Sussex.

Abstract pending – not attending conference

3MT: Identifying how glycan signalling regulates brain development and physiology

Jacob Willcox – University of Southampton, Prof Andy Pickford- University of Portsmouth, Prof Max Crispin – University of Southampton, Dr Richard Meek – University of Southampton.

Primary brain calcification (PBC) is a rare untreatable neurodegenerative disorder characterised by calcium-phosphate deposition around cerebral microvessels in the basal ganglia and other brain regions. Despite identifying seven causal genes converging on astrocyte-mediated phosphate dysregulation, upstream regulatory networks remain unknown. MYORG, an ER-resident GH31 α-galactosidase selectively expressed in astrocytes, is the most common cause of recessive PBC (~50% of cases). Its specificity for Gal-α1,4-Glc epitopes conspicuously absent from glycoprotein databases raises fundamental questions; its physiological substrates, interaction partners, and astrocytic role remain undefined. We hypothesise MYORG functions as a hierarchical ER regulator processing cryptic glycan modifications essential for folding and cell-surface delivery of multiple causal PBC proteins. Its loss would constitute a pleiotropic upstream lesion across distinct neurovascular pathways, explaining MYORG's clinical penetrance and severity relative to other PBC genes. To interrogate this, we developed a pipeline for profiling >25 patient-derived pathogenic variants spanning all structural domains. Preliminary data show an initial subset predominantly localise to the ER yet are absent from the secreted fraction, implicating structural destabilisation as a primary loss-of-function mechanism and identifying candidates for pharmacological chaperone rescue. Identifying stably localised catalytic variants, whose structural integrity implicates specific interface perturbations rather than global misfolding, would provide precise molecular tools to dissect MYORG's interactome and expose interfaces otherwise inaccessible to loss-of-function approaches. These variants will enter functional and structural pipelines characterising their catalytic efficiency, thermodynamic stability, and disrupted interaction interfaces. Together, these studies will define MYORG's function in astrocyte biology and reveal how its dysfunction drives PBC pathogenesis.

8MT: Loss of epithelial FIH drives pro-fibrotic signaling in Idiopathic Pulmonary Fibrosis.

Yomna Moqidem1,2, Xi Li1, Siyuan Wang1, Kun Zheng1, Nullin Divecha1, Chen Yin1, Andrea Bucchi3, Donna Davies4, Mark G Jones4, Yihua Wang1
Affiliation:
1 School of Biological Sciences, Faculty of Environmental and Life Sciences, University of Southampton, UK.
2 Institute for Life Sciences, University of Southampton, UK.
3 School of Electrical and Mechanical Engineering, Faculty of Technology, University of Portsmouth, UK.
4 Clinical and Experimental Sciences, Faculty of Medicine, University of Southampton, UK.

Idiopathic pulmonary fibrosis (IPF) is a progressive and fatal interstitial lung disease marked by irreversible fibrosis and impaired gas exchange. Persistent alveolar epithelial injury and dysregulated epithelial–mesenchymal communication are key drivers of disease progression. Although hypoxia and hypoxia-inducible factor (HIF) signaling are implicated in IPF pathogenesis, the role of Factor Inhibiting HIF (FIH), a critical negative regulator of HIF activity, remains poorly understood. Previous work from our group demonstrated that mesenchymal FIH depletion promotes profibrotic responses in IPF; however, the role of FIH in alveolar epithelial cells remains unknown.

To address this, we generated CRISPR/Cas9-mediated FIH knockout in human alveolar epithelial cells and performed transcriptomic profiling with pathway enrichment analysis. Loss of FIH induced a pronounced pseudo-hypoxic transcriptional program under normoxic conditions, recapitulating a hallmark molecular feature of IPF. Functionally, FIH deficiency significantly potentiated TGF-β–driven epithelial–mesenchymal transition (EMT), accompanied by increased expression of canonical EMT markers and enhanced mesenchymal phenotypes. Importantly, conditioned media from FIH-deficient epithelial cells promoted fibroblast differentiation into myofibroblasts, demonstrating a potent paracrine profibrotic effect. Mechanistically, CXCL1 emerged as a key mediator of this epithelial–mesenchymal crosstalk.

Collectively, our findings identify epithelial FIH dysfunction as a previously unrecognized driver of profibrotic signaling in IPF and reveal a novel mechanism linking oxygen-sensing dysregulation to epithelial-mesenchymal communication. These results position FIH as a potential regulator of epithelial plasticity and a candidate therapeutic target in fibrotic lung disease.

3MT: A Systems-Biology Approach Investigating the Impact of NFκB-Signalling and Crosstalk on Cytokine Secretion in the Lymph Node Microenvironment.

Abigail Edwards, University of Sussex; Dr Sean Lim, University of Southampton; Dr Fabio Simoes, Brighton & Sussex Medical School; Prof Simon Mitchell, Brighton & Sussex Medical School.

Diffuse Large B-cell Lymphoma (DLBCL) is an aggressive haematological malignancy, with approximately 6000 cases per year in the UK. DLBCL is a strikingly heterogeneous disease; despite this, most patients receive a one-size-fits-all immunochemotherapy regimen, conferring a relapse/refractory (R/R) rate of 30-40%. Chimeric Antigen Receptor T-cell (CAR-T) therapies have improved outcomes for R/R-DLBCL; however, despite their improved specificity, they only extend progression-free survival (PFS) by approximately 1 year. The tumour microenvironment (TME) represents a key point of CAR-T failure.

This project focuses on the heterogeneity in a molecular network that is central to DLBCL's response to therapies: the nuclear factor kappa-B (NF-κB) pathway, and how this network influences the TME. The project addresses this challenge by combining computational and experimental approaches. An established computational model that simulates NFκB signalling and induction of NFκB target genes is used to investigate how heterogeneity in two NFκB pathways (canonical/non-canonical) promotes the development of heterogeneous TMEs. Many TME-modulating cytokines are NFκB target genes, and pathway-specific control of cytokines can be investigated through activation of the NFκB pathways in-vitro and in-silico.

This systems-biology approach is informed by novel experimental and published data to inform parameters, and has revealed a potentially transformative new link between the non-canonical NFκB subunit RelB and the T-cell co-stimulatory molecule CD70. This interaction may be central to the failure of CAR-T approaches in DLBCL, therefore highlighting non-canonical NFκB as a potential therapeutic target in synergy with CAR-T approaches.

8MT: Investigating the role of molecular motors in neuronal connectivity: Implications for autism spectrum disorders and schizophrenia

Emily Lucas – University of Southampton, Prof Majid Hafezparast – University of Sussex, Dr Mariana Vargas-Caballero – University of Southampton

Abstract pending – not attending conference

8MT: Deciphering the bacterial signalling: Aptablotting of the HptRS two-component system in Staphylococcus aureus

Abhishek Johan Issac – University of Southampton, Dr Christopher Mulligan – University of Kent, Dr Seung Lee – University of Southampton.

Abstract pending – not attending conference

8MT: Killing Intracellular Pathogens with Antibiotic Nanocapsules

Alex Clarke, University of Southampton; Adam Whelan, DSTL Porton Down; Seung Lee, University of Southampton; Tracey Newman, University of Southampton; Mark Shepherd, University of Kent; Liku Tezera, University of Southampton; Nicholas Evans, University of Southampton.

Introduction

Antimicrobial resistance (AMR) is an increasing problem worldwide, with a predicted 10 million deaths a year from antibiotic-resistant infections by 2050, and no new antibiotics have been approved for over 20 years. An alternative method for overcoming AMR is the repackaging of existing therapies to improve their efficacy and reduce toxicity. Nanocapsules made of polymer (polymersomes) loaded with antibiotics can be used to effectively eliminate intracellular bacterial infection, without affecting uninfected cells. This project assesses whether anti-tuberculosis drugs can be encapsulated in polymersomes and whether encapsulated drugs can cause clearance of Mycobacterium tuberculosis.

Methodology

Polymersomes made of PEO-b-PCL loaded with doxycycline and rifampicin were made by nanoprecipitation and characterised. Drug-loaded polymersomes were added to free-living and intracellular Mycobacterium tuberculosis cultures and bacterial growth measured. Using a 3D human-cell granuloma model, the effect of polymersomes on granulomatous M. tuberculosis infection was measured.

Results

Doxycycline polymersomes were 99.32 nm ± 6.49 in diameter, had a mean polydispersity index (PI) of 0.09 ± 0.018, and contained a mean drug concentration of 32.64 µg/ml ± 33.67. Rifampicin polymersomes were 92.26 nm ± 6.83, had a mean PI of 0.09 ± 0.024, and contained a mean drug concentration of 28.39 µg/ml ± 18.50.

The minimum inhibitory concentrations of doxycycline and rifampicin against M. tuberculosis were 4 µg/ml and <0.03125 µg/ml, respectively. Polymersomes loaded with either doxycycline or rifampicin exhibited some inhibitory effect against free-living planktonic M. tuberculosis. Polymersomes loaded with antibiotics exhibited full bacterial inhibition against intracellular and granulomatous M. tuberculosis.

Sponsor Stall Schedule

Sponsor	Days Attending
Azenta/GenWiz	Wednesday 25 March 2026
Clinisciences	Wednesday 25 March 2026
Haier Biomedical	Wednesday 25 March 2026
MedChemExpress	Wednesday 25 March 2026 & Thursday 26 March 2026
Novogene	Wednesday 25 March 2026 & Thursday 26 March 2026
PCR Biosystems	Wednesday 25 March 2026 & Thursday 26 March 2026
Promega	Wednesday 25 March 2026 & Thursday 26 March 2026

Clini Sciences

At Clinisciences we commercialise the supply of reagents and tools for structural biology, biochemistry, immunology, cell biology and molecular biology offering high quality reagents for experiments including biochemicals, molecular tools, protein tools, specialist cell culture reagents and novel biological solutions to research, diagnostic and biotech labs.

As a very dynamic company, we do our best to be close to our customers' needs in terms of high quality reagents and the service we provide in getting the appropriate product to you with the relevant technical detail and lead time.

Our principal assets for better serving you: adaptability, flexibility, responsiveness and naturally the competence of the technical PhD qualified specialists at your service.

GENEWIZ®
From Azenta Life Sciences

GENEWIZ, from Azenta Life Sciences, empowers research by providing high-quality, reliable, precision-based solutions from research use only to pre-clinical/ clinical, enabling scientists to make

breakthroughs faster and more efficiently. Key services include Sanger sequencing, next-generation sequencing (NGS), gene synthesis, gene-to-discovery solutions including antibody production, viral packaging, and mRNA synthesis. For more information visit https://www.genewiz.com

GENEWIZ Europe | Leipzig and Oxford Labs

GENEWIZ provides superior data and high-quality sequencing and synthesis services from our Leipzig, Germany and Oxford, United Kingdom Labs

---

Haier Biomedical

Intelligent Protection of Life Science

Haier Biomedical supports academic and bioscience research through intelligent laboratory equipment and connected cold storage technologies. Our solutions are trusted by universities and research centres around the world to protect critical samples, optimise workflows, and enable scientific discovery. Our portfolio includes ultra-low temperature freezers, CO_2 incubators, spectrophotometers, centrifuges, and biological safety cabinets—backed by wireless monitoring and global R&D expertise.

Come and explore how our evolving product range can support your research journey. We're here to listen, collaborate, and help you solve lab challenges with sustainable, compliant, and future-ready technologies.

MCE® MedChemExpress

MedChemExpress (MCE) is a leading global supplier of research chemicals and bioactive compounds. Our extensive portfolio, featuring over 100,000 inhibitors & agonists, 60,000 oligonucleotides, and 20,000 life science products, supports drug discovery for research institutes, biotech, and pharmaceutical companies worldwide. We provide one-stop screening library services, backed by expert support.

MedChemExpress are sponsoring the Year 4 Student best presentation - £50

Biotechnology and Biological Sciences Research Council

SoCoBio DTP

Novogene

Novogene is a global leader in multiomics services, offering comprehensive solutions in genomics, transcriptomics, epigenomics, proteomics, metabolomics, and bioinformatics. With one of the world's largest sequencing capacities and labs across continents, Novogene enables coordinated multiomics workflows through a single provider. Backed by 70+ patents and 30,000+ publications in leading journals, and using platforms like Illumina, PacBio, Oxford Nanopore, 10X Genomics, and Olink®, Novogene supports research across academic, clinical, and pharmaceutical fields worldwide.

PCRBIOSYSTEMS
simplifying research

PCR Biosystems is a leading developer of PCR reagents for molecular biology research, diagnostics and NGS. We offer a wide range of solutions including high-performance polymerases, thermostable reverse transcriptases, and proprietary hot start technologies to maximise yield and sensitivity from the simplest to most challenging of reactions.
Founded by two PCR experts in 2012, the company believe researchers deserve better performance and value from their reagents. Alongside a broad range of standard and custom solutions, PCR Biosystems offer free samples, and tailored technical support to help customers achieve the most from their market-leading reagents.

Promega Corporation is a leader in providing innovative solutions and technical support to the lifesciences industry. The company's portfolio of over 4,000 products support a range of life science work across areas such as cell biology; DNA, RNA and protein analysis; drug development; humanidentification and molecular diagnostics. For over 40 years these tools and technologies have grown in their application and are used today by scientists and technicians in labs for academic and government research, forensics, pharmaceuticals, and clinical diagnostics. Promega is headquartered in Madison, WI, USA with branches in 16 countries and over 50 global distributors

---

BIOCHEMICAL SOCIETY

BioChemical Society are sponsoring the Networking Lunch on Day 3 and these prizes
3rd year poster prize - £50
2nd-year student best presentation - £50