Biotechnology and Biological Sciences Research Council

eastBIO

EASTBIO SYMPOSIUM 2026

Research in an Evolving World

24th-25th June 2026

John McIntyre Conference Centre (JMCC)

University of Edinburgh

18 Holyrood Park Road

Edinburgh

EH16 5AY

DAY 1 - 24TH JUNE

Time	Session	Location
10:30 – 10:55	**Registration and Refreshments**	Centro
11:00 – 11:10	**Welcome**	Pentland
11:10 – 12:00	**Keynote: Ageing in free living animals - and why it matters for the greatest challenge of the 21st century** *Professor Tom Little*	Pentland
12:00 – 12:45	**Workshop: Pitching Your Research** *Dr Sarah Jane Judge & Dr Edward Martin*	Pentland
12:45 – 13:45	**Lunch**	Centro
During Lunch	**Poster Presentation & Multimedia Sessions 1 & 2**	Prestonfield Duddingston
13:45 – 14:30	**Speed-Dating Your Research**	Pentland
14:30 – 15:15	**Year 2 Student Talks (Parallel Sessions)**	Prestonfield Duddingston Holyrood Salisbury
15:15 – 15:45	**Break (with poster presentation Session 3)**	Prestonfield
15:45 – 16:30	**Year 2 Student Talks (Parallel Sessions)**	Prestonfield Duddingston Holyrood Salisbury
16:30 – 17:30	**Pub Quiz**	Bar @ JMCC
18:15 – 20:30	**Dinner**	South Hall, Pollock Halls
20:30 – 23:30	**Ceilidh**	South Hall, Pollock Halls

DAY 2 - 25TH JUNE

Time	Session	Location
09:30 – 10:30	**EDI Panel Discussion:** *Dr Gwenetta Curry, Dr Eleanor Gaunt, Professor Srinjoy Mitra, Hope Obasi, Ali Somerville*	Pentland
10:30 – 11:00	**Break**	Centro
11:00 – 11:50	**Industry Placements: Lessons from the Front Line** *Dr Andrew Desbois, Christoph Wagner, Jed Hawes, Hope Obasi, Eleanor Swift, Dr Cesar Mendoza Martinez*	Pentland
11:50 – 12:45	**Industry Workshop & Debate: Hot Skills for Graduates Moving to Industry** *Dr Mary Doherty, Dr Raquel Arribas, Dr Ian Archer, Dr Jennifer Harbottle, Dr Edward Martin, Dr Samuel Gibbon*	Pentland
12:45 – 14:00	**Lunch**	Centro
13:30 – 14:00	**Wellbeing Walk** (Optional)	Meet in Foyer
14:00 – 14:10	**Next-Gen AMR Presentation** *Ava Drake & Larissa Chicoski*	Pentland
14:10 – 17:00	**SPRE-led Thematic Session** *Dave Blackbell*	Pentland
14:00 – 16:00	**EastBio Management Group Meeting**	Boardroom 1

Contents

WELCOME

DR ATTILA MOLNAR, UNIVERSITY OF EDINBURGH & DR SAM MILLER, UNIVERSITY OF ABERDEEN

To our conference attendees and participants,

Welcome to Edinburgh for the annual 2026 EastBio Symposium! This year's symposium is based around the central theme of Research in an Evolving World, beginning with our keynote lecture delivered by Professor Tom Little (University of Edinburgh)

The EastBio Partnership funds research of strategic priority for UKRI BBSRC across the broad areas of healthy people, animals, and plants; sustainable agriculture, and food systems, and a resilient bioeconomy. Nearly a quarter of our research is in collaboration with non-academic organisations, from SME to large biotech firms and our students also pursue separate projects as part of their professional placements (PIPS) in organisations and companies in the UK and abroad. The 2026 Annual Symposium is an opportunity to demonstrate funded research that crosses disciplinary boundaries and seeks to address the shifting priorities and challenges of our world, and to celebrate with our stakeholders such innovative and forward-looking work done within the EastBio programme.

We hope you enjoy the various lectures, workshops and panels that our organising committee have scheduled over the course of the next two days. We hope that you will have fun, learn something new and most importantly make new friends and collaborators during your discussions over lunch, coffee, the hugely popular evening ceilidh and the wellbeing walk.

And finally, please join me in extending a heartfelt thank you to all of our students and EastBio Support Officer Hazel Harrop for their time, energy and hard work in making this symposium happen.

Kind regards,

Dr Attila Molnar and co-host Dr Sam Miller

Important information

Emergencies

Fire Alarm

There are no fire drills planned during our event, if the fire alarm sounds please make your way out of the building using the fire exits as guidance, and meet outside the front of the JMCC building.

Emergency Contacts

Hazel and Maria are your main points of contact on the day. We will monitor the bioenq@ed.ac.uk inbox during the two days of the Symposium. There will also be a representative from the venue available on both days.

Arrival

Travel and Parking

Edinburgh Waverley train station is less than 2 miles from John McIntyre Conference Centre with direct routes to and from many cities across Scotland. From there you can either walk 35 minutes to JMCC, or there are a number of Lothian Buses routes that will drop you a short distance from JMCC. Find out more here.

Edinburgh operates a Low Emission Zone (LEZ) to improve air quality in the city centre. This zone covers much of the city centre; there is a map of the zone on the City of Edinburgh Council website: Low Emission Zone (LEZ) boundary

There is free parking available at Pollock Halls on a first-come, first-served basis; we are unable to reserve spaces. Alternatively, charged on-street parking can be found throughout the city.

Storage

Luggage storage will be available in Boardroom 2, by the registration area of the symposium. Although the registration desk will be attended throughout the two days, items stored there are left at your own risk. Please ensure you collect all items by 5.30pm each day.

Registration

Registration will take place from 10:30am on the 24th of June in the foyer of JMCC. We understand that some guests may be attending later in the day and so will aim to have someone in this area at all times to provide your name badge.

You name badge pack will include traffic light cards to indicate whether you wish to be approached by other delegates, with a red stripe indicating that you wish to be left alone for the time being, and green indicating that you are open to socialising.

If you have your lanyard from the induction or previous symposia events, please bring that along to help us to save waste!

Photography consent

There will be a photographer present, capturing sessions and networking activities both to commemorate the event and to be used on the EastBio website, for news items by partner

institutions, and EastBio promotional activities. For further information about Edinburgh University's approach to data protection and your rights go to: https://data-protection.ed.ac.uk/data-protection-policy. If you do not wish to be photographed for these purposes, please complete this form https://forms.office.com/e/WgqHFgQE8K and be sure to collect a discreet sticker from the registration desk so that the photographer can identify you.

Accommodation check-in

Accommodation will be provided in Holland House, Pollock Halls. Find more information about the accommodation here: Holland House. Your allocation will be shared with you in the information email, but if you are uncertain please get in touch with bioenq@ed.ac.uk.

Check-in from 15:00 at the 24-hour Main Reception Centre, Pollock Halls Estate, 18 Holyrood Park Rd, Edinburgh, EH16 5AY. Tel: 0131 651 2001. Check-out is 10:30 AM. Please note that at check-in, you may need to provide a credit or debit card to guarantee any additional charges, but you will not be charged the cost of the stay.

Breakfast is served in the JMCC Restaurant between 7am – 10am.

If you have any queries relating to your booking, please contact the Central Reservations Team (Monday to Friday 0900 to 1700).

Venue

Toilets

There are gender-neutral toilets available opposite the Prestonfield room, as well as standard gendered toilets throughout the venue. An accessible toilet can be found in the Foyer.

Floorplan

A floorplan on the venue can be found at this link: https://drive.google.com/file/d/1CAzjLL-Dnzq6Q2-7lImzRHr-PlFhx4gQ/view?usp=sharing

Access

The venue is fully accessible. Please contact bioenq@exseed.ed.ac.uk to arrange any access requirements.

Student Reps

Look out for our students reps helping on the day who will be wearing EastBio t-shirts. We will do our best to have someone available at the registration desk throughout the event if you have any questions, either for the event or related to EastBio more generally.

Wi-fi

There is Wi-Fi available throughout the venue, both Eduroam and venue specific Wi-Fi. Delegates are welcome to bring a laptop or tablet if you wish.

Venue Food Statement

We would like to make you aware that we cannot eliminate or guarantee that cross contamination of food items will not happen, from within our kitchens or on food service stations.

Whilst we make every effort to limit contamination, and to accommodate dietary preferences and food intolerances (allergen specific, vegan or vegetarian) across our menu portfolio, our food may have come into contact with other food items and several allergens such as dairy, eggs, nuts or shell fish.

For those with severe allergies or food intolerances we advise it may be best for the individual to consider providing your own food options.

Our Wellbeing Portals display an allergen profile for each menu item, with additional dietary information such as nutrition, ingredients and calories to help customers make safe and informed choices:

Conferences and Events: conferenceandevents.mysaffronportal.com/

EastBio Catering and Sustainability Statement

EastBio is passionate about becoming a more sustainably minded DLA, and as part of these efforts we are trialling an entirely plant-based catering at the Symposium Lunch. At the dinner, there will be a meat-based main course, with all dietary requirements catered to. You can find out more about the carbon footprint of catering at the University of Edinburgh here: https://catering.ed.ac.uk/sustainability/carbon-footprinting.

We will also be providing QR codes linking to online versions of our Symposium booklet and schedule in order to reduce printing.

Wellbeing

Safe Spaces and quiet room

We want the Symposium to be as accessible, safe and inclusive as possible. If you need some space away from other delegates, you are welcome to use boardroom 1 as a quiet room. Please note that student reps may come in and out of this room every so often, but it will be less busy that the rest of the venue.

Mental Health First Aiders (MHFA) will be around throughout the event, and will be wearing green ribbon pin badges. If you would like to talk to someone, please either approach one of the MHFA or speak to Maria or Hazel (both MH First Aiders) at any point during the day.

Traffic light cards

In your lanyard pack you can find 2 ‘traffic light’ cards. You can use these to indicate whether you wish to interact with other delegates. If you are happy to be approached by others, you can display the green stripe card; if you are feeling less chatty at any time, you can display the red stripe card. Please be aware of other people’s traffic light colour.

Wellbeing walk

A 30 minute walk around Holyrood Park. Use this walk as an opportunity to chat with new people and get a breath of fresh air.

Feedback and complaints

There will be a feedback box at the registration desk where you can post feedback which will be considered as the event goes on. There is also a QR code linking to an anonymous feedback form should you feel more comfortable using this; this form can also be found here: https://forms.cloud.microsoft/e/pah7ZZiQ51 and be used to submit feedback after the event. Any immediate concerns or verbal complaints on the day can be directed to Maria or Hazel at any point, especially if a response by the team is necessary.

KEYNOTE – AGEING IN FREE LIVING ANIMALS - AND WHY IT MATTERS FOR THE GREATEST CHALLENGE OF THE 21ST CENTURY

PROFESSOR TOM LITTLE

My group studies the processes that lead to longer, or shorter, lifespan in wild vertebrates. Wild animals are much understudied compared to humans, but this is not just about filling a gap. To uncover the general causes of senescence, we need a range of approaches - lab, wild, observational, experimental – on a range of systems. Our work uses wood mice and birds, and the data is focussed on epigenetic clocks, molecular tools that measure both age and senescence. The world's human population is increasingly made up of the elderly, and with this comes innumerable health challenges. By uncovering general drivers of later-life declines, we hope to contribute to solutions to this global challenge.

PROFESSOR TOM LITTLE, UNIVERSITY OF EDINBURGH

Originally from Canada, Professor Little obtained a BSc and MSc from the University of Guelph in Ontario, Canada. In 1999, Professor Little moved to Basel, Switzerland, where he completed a PhD in Zoology. He first came to Edinburgh in 2000 on a NSERC of Canada Postdoctoral Fellowship. His current work focuses on the environmental drivers of senescence in wild animals, particularly mice, aiming to identify environmental factors that cause some individuals to have a fast-ticking epigenetic clock, and so are likely to die sooner.

SESSION LEAD: GHAZAL SHARIFIAN

Workshop: Pitching Your Research

Dr Sarah Jane Judge & Dr Edward Martin

In this hands-on workshop, we'll be exploring one of the most valuable skills you can develop as an early career researcher: how to talk about your work clearly, confidently, and in a way that leaves any audience understanding what it is you actually do.

First, we'll dig into the core tenets of science communication and look at what makes a message land. Using the principles of good public engagement, we'll explore how to identify the heart of your research, cut through the jargon, and think carefully about who you're speaking to — because the way you'd describe your work to a fellow researcher looks very different to how you'd explain it to a funder, a journalist, or someone you've just met at a conference. Through a series of hands-on exercises, you'll rethink how to present and communicate the most important parts of big scientific problems of today, before applying these skills directly to your own research.

This is a great opportunity to get hands-on with what good science communication actually looks like and reflect on where you can improve — then take those skills forward into your research, your public engagement, or even just a conversation over a pint with friends.

Dr Sarah Jane Judge

Sarah-Jane Judge has a background in Marine Biology and Ecotourism and has worked as a practitioner in the fields of science engagement and widening participation for over 20 years.

She joined the University of Edinburgh in 2020 after completing her PhD in Sociology. Her doctoral research, titled “Social Factors Influencing Children’s Experiences of School Trips to an Aquarium,” was an ESRC-funded collaborative project between the University of Warwick and The National Marine Aquarium in Plymouth.

From February 2020 to November 2024 Sarah-Jane served as the Public Engagement Manager for the Wellcome Centre for Cell Biology, playing a key role in shaping outreach and engagement activities and creating an engaged research culture. Since October 2023, she has also been a Teaching Fellow with the Biomedical Teaching Organisation and held a research fellowship with the Centre for Biomedicine, Self and Society (CBSS) at the Usher Institute, where she remains a visiting researcher. Her research interests focus on inequalities in non-formal science learning and the impact of research-adjacent activities, particularly public engagement and widening participation programs, on research culture.

In her spare time, she loves to cook, scuba dive, travel (she has visited 63 countries) and spend time with her two French Bulldogs. She is also a stand-up comic and especially enjoys hosting academic comedy nights such as the Bright Club and The Provocateurs.

Dr Edward Martin

Dr Edward Martin, an EastBio alumnus, is a Teaching Fellow in Science Communication and Public Engagement at The University of Edinburgh. With a background spanning bioscience, data analysis,

and creative research methods, he recently completed a PhD exploring the sonification of biological data, using sound to represent complex datasets and support new ways of understanding and engaging with science. His work brings together bioinformatics, research, and public engagement, driven by an interest in making scientific ideas more accessible through innovative and interdisciplinary approaches.

SESSION LEADS: JAKUB TEAHAN, PHOEBE SADLER, GHAZAL SHARIFAN

Researcher Speed Dating: Put Your Pitch to the Test

What are you researching? What is the key finding so far? Why are you doing what you're doing? Why does it matter? How would you ensure that someone outside of your field could keep up with you when you're explaining it?

And can you explain all of that..... in two minutes?

In this dynamic, fun session, you'll have the chance to put everything from our communication workshop into practice. Joining your fellow PhD students, you'll take part in a speed-dating–style event where each participant has two minutes to explain their research to a partner before moving on to the next person. Over a series of short, focused conversations, you'll practise adapting your message for different audiences, build your confidence, and get a feel for what's working in your pitch — and what might need a little more polish.

It's a low-stakes, high-energy session and a brilliant chance to make connections across EastBio while getting more comfortable with networking. Hopefully you'll leave with a fresh perspective on your own research too!

Session Leads: Jakub Teahan, Phoebe Sadler, Ghazal Sharifan

Poster Presentations

The poster session will be divided into three 30-minute sessions: Ecology and Sustainability; Understanding Cellular Mechanisms and Disease Biology; and Biomedical and Behavioural Research. The themes reflect shared research approaches and longer-term aims, bringing together projects from different disciplines and model systems. First-year students will present their research and progress to date.

A People's Choice Poster Award will be presented based on clarity of communication, understanding of the research, and poster aesthetics. Voting slips will be provided before the first session and collected at the end of the third session. Everyone attending the session is invited to vote.

Session 1: Ecology and Sustainable Systems

Time: 12:45 - 13:15

Presenters:

Poster 1: Gustaf Fredell - "Utilizing Endophytes for Improved Barley Agriculture."

Endophytes are a ubiquitous group of microorganisms that live inside plants. Both fungi and bacteria commonly occur as endophytes across plant species and can colonise a wide range of plant tissues. Their effects to their hosts are varied: some can increase nutrient acquisition by physically increasing root surface, others can increase tolerance to heavy metals, while some seemingly have no benefit at all. Endophytes can extend a plants genetic capacity by enabling access to traits associated with entirely different kingdoms of life. Because of their ubiquity and varied effects, a growing interest has been placed on using them for agriculture in an increasingly uncertain climate. Barley is one of the most cultivated crops in Scotland, however plant pathogens and environmental stressors can significantly impact yield. Despite this, endemic endophytic fungi associated with barley have been poorly studied. Here, we investigate endophytic fungi isolated from commercial barley, wild barley, and related species. Our aim is to understand more about the community of endophytes present within the aerial tissues of barley, isolate representative microbes, and evaluate their potential applications for agricultural use.

Poster 2: Charlotte Wood - "Invertebrate Communities: Measuring Nutritional Robustness in the Agricultural Landscape. "

Biodiversity is the variability of life on earth. Without it, ecosystems may lose resilience, species can disappear, and the essential processes that support life begin to break down, including invertebrate populations critical to ecosystem functioning through pollination, nutrient cycling, and food web support. When we measure biodiversity, we often use abundance and diversity metrics; but does this capture the full picture? Nutritional ecology explores how organisms acquire, balance, and utilise nutrients, linking individual physiology to population-level ecological processes. Insects are particularly sensitive to variation in macronutrients (proteins, lipids, and carbohydrates), which influence development, reproduction, and survival. Consequently, changes in plant nutrient composition, driven by agricultural practices, may affect insect communities in ways not reflected by these metrics alone. My project assesses invertebrate community nutritional robustness across agricultural habitats in north-east Scotland. It combines field sampling, controlled macronutrient-

manipulation experiments, and biochemical assays. I will quantify macronutrient ratios across trophic levels, from plants to apex predatory invertebrates, to assess how nutrient imbalances propagate through food webs.

Poster 3: Avalon Phillips - "Modelling missing pedigree and validating genomic predictions in local sheep breed. "

Genomic selection (GS), based on genome-wide single nucleotide polymorphism (SNP) markers, is standard across livestock breeding programmes. While GS improves prediction accuracy and accelerates genetic gain, implementation in small-scale breeding programmes is challenging. Specifically, lack of organised breeding infrastructure and incorrect or incomplete pedigrees limit effectiveness. An example is the Pag sheep, a Croatian breed locally adapted for milk and meat production. This study aimed to explore and validate modelling scenarios to optimise GS for Pag sheep. Data included 36,412 lactation records for 11,261 sheep, of which 2,826 were genotyped for 46k SNP after quality control. After correcting using genomic information and trimming to keep informative ancestors, the pedigree had 13,310 animals. We compared pedigree-based and genomic-based prediction models, with and without unknown parent groups (UPG) and metafounders (MF), to potentially reduce bias from missing pedigree. Genomic information improved model accuracy, while differences in bias and dispersion between the UPG and MF models were subtle. Results highlight the value of genomic information for correcting pedigrees and improving prediction accuracy, but future work is needed to justify the use of UPG and MF.

Poster 4: Nasir Mehmood Khan - "Are grasslands as important for soil carbon as we think?"

There is increased risk of soil organic carbon (SOC) loss in agricultural soils of Europe and UK, mostly evaluated by bulk SOC content or mineral-associated organic carbon (MAOC) saturation. Nonetheless, using such indices conceal the actual carbon distribution within various functional pools that hinder the mechanistic understanding of stabilization. Our study will utilize the archived soil samples from Tulloch organic trail (1995-2025) based in Aberdeen to assess whether fraction-based indicators optimize SOC risk assessment under arable-ley transitions. Analyses will be performed for total SOC and its fractions; particulate organic carbon (POC) and MAOC. Their ratios (POC: MAOC, POC: SOC, MAOC: SOC) will determine the changes in C partitioning and stability. Furthermore, amorphous (active) Fe and Al oxides and C: metals ratios will be quantified to bridge MAOC with mineral protection capacity. To measure the stabilized part of MAOC, subset of soil samples will be studied under NanoSIMS to determine organo-organic interfaces alongside organo-mineral domains. These outcomes strongly supporting enhanced modelling and MRV policies will be applied in rewriting SOC risk frameworks.

Poster 5: Muhammad Amanullah Jilani - "Cracking the code: Characterizing plant genes shaping microbiota composition at the root-soil interface."

This project aims at gaining novel insights into the genetics of plants and the microbial communities populating the roots-soil interface, designated the rhizosphere microbiota. Like the gut microbiota in vertebrates, the rhizosphere microbiota contributes to the growth, development and health of its host plant, which in turn controls the composition and function of these microbial communities. In my project I use barley, the world fourth's most cultivated cereal, and advanced genetic resources to gain insights into the host control of microbes art the root-soil interface. I used molecular markers to validate plant genetic material developed in the lab. Using aboveground biomass as a proxy for plant

growth, I determined plant's performance in soil with limited supply of mineral nitrogen, a rate limiting step for crop productivity globally. I obtained microbiota preparations from rhizosphere specimens and subjected to selective amplification of the 16S rRNA gene for high-throughput sequencing - aiming at generating a molecular census of the bacterial populations at the barley root-soil interface. In the poster I will further comments how plant genetics shape these interactions and the potential impact for sustainable agriculture.

Poster 6: Aoife Robertson - "One for all: Ecosystem service trade-offs in inland aquaculture agroecosystems."

Aquaculture offers a solution to the planet's growing demand for food production, and as such there is a need to research how to expand the industry sustainably. Although there is a body of research to select production sites, the focus is on optimisation and resilience to environmental fluctuations rather than understanding the changes in landscape ecological processes over time. This poster highlights the methods that will be undertaken in a PhD project to examine ecosystem service trade-offs for inland aquaculture, and identify the social, economic and environmental impacts of industry growth. The project uses a metasystem modelling framework to explore the impact of pond cover on ecosystem service trade-offs. Additionally, it will look at the effects of landscape heterogeneity and connectivity.

Poster 7: Helaena Fine - "Innocent Until Proven Gill-ty: Genomic Basis of Gill Immunophysiology in Atlantic Salmon in the Context of Scottish Aquaculture Pathologies."

Disease and pathology represent a substantial threat to the productivity of Scotland's extensive Atlantic salmon aquaculture industry, impacting fish health and survival. The salmon's gills lie at a critical interface between pathology and health, playing a crucial role in immune response to disease. These immunophysiological processes within the gill are characterised by a portfolio of diverse genes and proteins, which can be used as diagnostic biomarkers. My research aims to apply genomic & transcriptomic techniques to elucidate gill inflammation-associated immune biomarkers to detect early signs of gill pathology, helping to improve welfare & reduce mortality. Currently I am focused on angiogenin (ANG), a gene involved in pathology-induced vascularisation and inflammation, with high gill expression in previous salmon disease trials. In silico analysis revealed 8 nearly-identical tandem copies, or paralogues, making it unclear which aspect of the gene is controlling its high expression. I am designing and testing oligos to quantify paralogue-specific ANG expression using qPCR, which will be followed by adaptive long-read sequencing to confirm each paralogue and further downstream transcriptomic analysis, such as in vitro expression, cloning, in situ hybridisation, and RNA-seq.

Poster 8: Eve Sharples - "No Butterfly is an Island: Continental Gene Flow in the British Swallowtail"

Island populations can be reservoirs of genetic diversity against a backdrop of accelerating biodiversity loss. However, isolated populations and taxa face higher extinction risk, confronting conservationists with a trade-off between preserving island biodiversity and increasing resilience through connectivity. Understanding a species' demographic history, structure, and connectivity is crucial in informing conservation efforts. This project uses whole genome data to understand the population history of the British Swallowtail (Papilio machaon britannicus). We will analyse whole genome data from both britannicus and its continental sister taxon (Papilio machaon gorganus) to

quantify the demographic structure, history and extent of gene flow between populations. Both model based methods and diagnostic statistics will be used to build a demographic history and estimate a split time between island and continental populations. Secondly, we will investigate recent admixture and gene flow between populations using genome polarisation, which will be quantified using summary statistics. Together, these efforts provide new insights into the evolutionary history of Papilio machaon britannicus and its connectivity to the continent, which will inform reintroduction programmes.

Poster 9: Aoife Ong - "Unlocking potential mechanisms of Amoebic Gill Disease (AGD) resistance in Atlantic Salmon (Salmo salar)."

Atlantic Salmon (Salmo salar) production has a global value of approximately USD 20 billion as of 2023. Complex Gill Disease (CGD) is a multi-factorial disease whereby different pathogens and environmental factors negatively impact gill health. Among these pathogens, Neoparamoeba perurans, causes the specific condition of Amoebic Gill Disease (AGD) which can lead to a reduced gill surface area through lamellar fusion, excess mucus production, haemorrhaging and hyperplasia. This causes stress, reduced appetite, and suffocation in heavily infected fish. CGD is currently one of the greatest threats to the salmon production industry, with on-site mortalities of 5-20% when treated. Resistance against AGD has been shown to be heritable, though the underlying mechanisms are, as yet, not fully understood. This project seeks to identify potential heritable traits which may increase gill robustness by addressing the following aims: 1. To determine if external morphological characteristics related to genetic background impact AGD susceptibility. 2. To observe the stability of the gill microbiome throughout the production cycle within genetically distinct groups with known disease susceptibility. 3. To understand the role that associated microbial communities play in disease outcome.

Poster 10: Ianna Sonegheti Borloti - "Transcriptomic Signatures of Ageing in Wild Soay Sheep."

Ageing is characterised by a progressive decline in physiological function, driven by cellular damage and deterioration of maintenance mechanisms. Although studies in humans and laboratory models have advanced our understanding of ageing, how these processes unfold under natural ecological conditions remains less clear. Here, we investigate blood transcriptomic signatures of ageing in wild Soay sheep from St Kilda, one of the most intensively studied wild systems. We analysed gene expression across 100 individuals spanning four life stages: lambs, yearlings, adults and geriatrics. Differential expression analysis revealed substantial transcriptional shifts across the lifespan, involving developmental processes and immune system dynamics. Ageing was associated with a shift from early-life developmental, proliferative and adaptive immune-related processes towards increased innate immune activation and inflammatory signalling. These results indicate progressive immune remodelling across the lifespan, consistent with immunosenescence and chronic low-grade inflammation. Our findings provide insight into the molecular basis of ageing in the wild and highlight the importance of integrating transcriptomic data with long-term ecological studies.

SESSION 2: UNDERSTANDING CELLULAR MECHANISMS AND DISEASE BIOLOGY

TIME: 13:15 - 13:45

PRESENTERS:

Poster 11: Anna Rose Moelders - "GPR75: Why Sex Matters."

GPR75 is an orphan G protein-coupled receptor (GPCR) and potential target for obesity and metabolic disease, however its cardiovascular role and the influence of sex remain poorly understood. GPR75 knockout (KO) mice show reduced body fat accumulation on a high-fat diet, with a more pronounced female phenotype. This research aimed to characterise the cardiovascular consequences of GPR75 KO and investigate the presence of sexual dimorphism using data derived from previous GPR75 KO studies in 16-week-old wild-type and GPR75 KO mice on standard chow. Haemodynamic function was assessed by pressure volume loop analysis, vascular reactivity was measured by mesenteric artery myography, and glucose handling was assessed by oral glucose tolerance test. Male GPR75 KO mice presented a hypertensive phenotype, with elevations in several indices of systolic function and impaired glucose tolerance but no significant vascular effects. In contrast, female KO mice showed reduced body weight, preserved cardiac function and glucose homeostasis, but impaired mesenteric vasodilation. These data indicate notable sexual dimorphism in GPR75 function, highlighting sex as a key biological variable in pharmacological research and the need to move beyond one-size-fits-all approaches in drug development.

Poster 12: Adriana Cusi - "When Size Meets Stress: How TORC1 and PKA Regulate the Stress Response in Oversized Cells."

Cell size is a fundamental but poorly understood cellular property. Within a given cell type, cells maintain an optimal size range, where cellular processes can successfully scale with cell size. Beyond this range, biosynthetic processes deteriorate, leading to activation of the 'Environmental Stress Response' (ESR) (Neurohr et al. 2019, Lanz et al. 2022, Lanz et al. 2024). The ESR is a transcriptional program induced under a variety of environmental stresses and is known to be controlled by key signalling pathways, such as TORC1, PKA, Hog1 and Pkc1 in S. cerevisiae (Gasch et al. 2002). However, how these signalling pathways regulate the size-dependent ESR still remains to be understood. The aim of my project is to determine how S. cerevisiae cells induce the ESR when they grow beyond their optimal size. Specifically, the project will look at what signalling pathways contribute to the ESR induction and what molecular changes are being sensed by those signalling pathways, using a combination of RNA-seq with phosphoproteomics. More widely, this knowledge could be translated into a better understanding of physiological and pathological conditions, such as ageing and tumorigenesis, where cell size is known to be altered.

Poster 13: Destiny Docherty - "Investigating the acyl chain composition of phosphoinositides as a novel regulator of CD8+ T cell signaling and function."

CD8+ T cells from older human donors have reduced cytotoxic ability against infected and cancerous cells, contributing to increased disease burden in the elderly. During ageing, there is more memory CD8+ T cells and decreased signalling via the T cell receptor. The mechanisms responsible for this are incompletely understood. Phosphoinositides (PIPn) are key transducers of T cell signalling, and research has mainly focused on the regulation of cellular activity by the PIPn inositol head group.

The regulation of cells by the acyl chain composition of PIPn remains understudied. The aims of this project include elucidating how ageing impacts T cell PIPn acyl chain composition and dynamics, determining how acyl chain composition regulates PIPn-protein binding and signal transduction and determining whether PIPn acyl chain composition can be targeted to improve aged T cell function. Advanced mass spectrometry equipment can be utilised to analyse PIPn head groups and acyl chain compositions in a way which could not have been done previously. Results suggest CD8+ T cells of aged males and females have an increase in abundance of PIPn composed of 40 carbons and 6 double bonds. Future work includes measuring PIPn composition of young and old stimulated and unstimulated human CD8+ T cells.

Poster 14: Petra Lavay - "Maintaining a healthy blood-retina barrier to prevent age-related vision loss."

Older age is a major risk factor for vision loss, with 80% of people with significant visual impairment being over the age of 65. Understanding the cellular processes that occur during ageing may lead to interventions for this condition. The retina is the inner-most, light-sensitive layer of the eye and is responsible for visual processing. It relies on the blood-retina barrier (BRB) to maintain homeostasis. The BRB is composed of various specialised cells, including endothelial cells, retinal pigment epithelium, and multipotent mural cells called pericytes. Oxidative stress is known to drive age-related retinal diseases, where it compromises the BRB, leading to irreversible central vision loss. It is however unknown how oxidative stress impacts BRB cells, like retinal pericytes. Preliminary data has indicated that oxidative stress can induce differentiation in pericytes, leading to impaired BRB function. We therefore hypothesise that due to microenvironmental stress, the differentiation capacity of retinal pericytes is altered during ageing. During my project, I will assess the direct and indirect impact of oxidative stress on human retinal cells, build a standardised iPSC-derived co-culture model and advance our understanding of the pathology underlying age-related vision loss.

Poster 15: Jakub Teahan - "Malaria at the Intestinal Interface."

Malaria remains a major global health burden, classically defined by syndromes such as severe malarial anaemia and cerebral malaria. However, increasing evidence shows that Plasmodium falciparum infection also affects the gastrointestinal tract, with symptoms including vomiting, diarrhoea, and abdominal pain. Across human and mouse models, infection is associated with increased intestinal permeability, suggesting systemic infection drives local barrier disruption. Defining the mechanisms underlying this pathology is essential for understanding the full spectrum of malarial disease. To investigate this, we will use the Plasmodium chabaudi AS (PcAS) model of uncomplicated malaria. We will apply a dual-tracer approach using FITC-D and flow cytometric ovalbumin detection to define the severity and timing of acute permeability. Bulk RNA-seq of intestinal epithelial cells will identify molecular indicators of injury and assess the contribution of parasitaemia, inflammation, and haemolysis to barrier dysfunction. Finally, we will determine whether permeability defects and epithelial injury persist during recrudescence.

Poster 16: Gregor Fisher - "Directed modulation of TGF-β signalling using helminth derived TGF-β mimic anti-ST2 scFv fusion proteins."

Heligmosomoides polygyrus is a helminth parasite with extensive immunomodulatory capabilities allowing suppression and evasion of host type 2 immunity. One family of proteins important for this immunomodulation is the TGF-β mimic (TGM) family, with 10 known members found to have

diverse effects on TGF-β signalling including both agonistic and antagonistic interactions with the TGF-β receptor, TGFBR. TGF-β shows a high degree of pleiotropy, in part due to cell type specific co-receptors, which has made understanding of its roles complex. Similarly, TGMs have their own co-receptor interacting domains which allow distinct functions. TGF-β pleiotropy can be seen in the differing responses of fibroblasts and immune cells. In immune cells, TGF-β is generally immunosuppressive. ST2 is the ligand binding component of the IL-33 receptor and, by fusing an ST2 specific scFv to TGMs, TGFBR agonism or antagonism can be specifically directed to ST2 expressing type 2 immune cells, such as ILC2s. This could allow control of pathological cytokine responsivity and release, relevant to allergy and asthma, while avoiding unwanted activation of other cell types.

Poster 17: Fengqianrui Chen - "CTLH E3 ligase-mediated proteolysis of ETO2 in red blood cell development."

The production of red blood cells (erythrocytes), which are critical for oxygen delivery in the human body, is a precisely regulated multi-step process known as erythropoiesis. Its dysregulation can lead to severe human blood disorders such as anemia and leukemia. ETO2, a transcriptional corepressor, negatively regulates terminal differentiation of erythrocytes through associating with the transcriptional SCL complex. However, the mechanism of how ETO2-medited repression is alleviated to allow erythroid differentiation remains poorly understood. Our previous studies showed that the CTLH E3 ubiquitin ligase plays a functional role in human erythropoiesis and associates with ETO2. We hypothesize that CTLH E3 ligase targets ETO2 for proteasomal degradation to control ETO2 abundance and association with the SCL complex thereby promoting the transition of erythroid progenitor to terminally differentiated erythrocytes. The project aims to dissect the molecular mechanism of CTLH E3 ligase-mediated proteolysis of ETO2 and its functional role in human erythropoiesis. Deciphering the molecular bases for ETO2 participation in human erythropoiesis can lead to novel strategies for therapeutic intervention of blood disorders.

Poster 18: Dora Moffatt - "Long-range consequences of intestinal helminth infection."

Infections rarely strike alone, and immune responses shaped by one pathogen can alter host defence against another. Helminth infections induce strong type 2 and regulatory immune responses and can modulate immunity at distal mucosal sites. Helminth-driven changes in pulmonary immunity have been described, however the impact on the lung epithelium remains poorly understood. The lung epithelium is essential for barrier integrity, immune signalling and antiviral defence, meaning changes in epithelial composition or maturation may affect respiratory infection outcomes. This project investigates whether the gut-restricted helminth Heligmosomoides polygyrus alters the lung epithelial landscape and impacts secondary influenza infection. Using a murine model, epithelial changes will be characterised by spectral flow cytometry, transcriptional profiling and immunofluorescence imaging. Preliminary data suggest helminth-associated changes in the lung epithelium. Together, this work will provide insight into how intestinal helminth infection influences lung epithelial immunity and susceptibility to respiratory viral infection.

Poster 19: Holly Armstrong - "Investigating antiviral mechanisms during embryogenesis: The role of RNAi."

Mammalian cells rely on the innate immune response, the type I interferon response, to protect themselves from viruses. This response is conserved across nearly all cell types except embryonic stem cells (ESC) and oocytes which are unable to produce an interferon response. This suggests that

mammalian embryos may utilise alternative antiviral mechanisms in order to protect themselves from viruses. Some studies have suggested that RNA interference could be contributing to antiviral defence, reminiscent of the mechanisms that non-vertebrates use to defend against viruses. However, these results have been obtained from cells that have completely inactivated Dicer and Ago, meaning that not only RNAi is inactivated, but also miRNAs. To uncouple these two effects and investigate the relevance of RNAi in antiviral defence, I will mutate Ago2 to specifically only inactivate siRNA-mediated silencing. This approach will allow us to conclude if RNAi is providing effect antiviral defence but also if RNAi is a relevant post-transcriptional gene silencing mechanism in mammals. We expect to find novel mechanisms by which cells defend against viruses, especially important during intricate stages of embryonic development.

Poster 20: Suraya Fawcett - "From Bytes to Bioactivity: Data-driven Discovery of Novel Antifungal Peptides."

Invasive fungal infections pose a growing global health threat, causing an estimated 6.5 million infections and contributing to 3.8 million deaths annually. Despite this burden, antifungal drug development has been neglected, resulting in a limited number of effective drugs. Antifungal resistance is also rising, creating an urgent need to identify antifungal agents with novel mechanisms of action. Peptide-based therapeutics offer a promising alternative, due to high specificity and low host toxicity. Fermented products, like kefir, are a rich source of bioactive peptides that demonstrate a wide range of biological activities - including antibacterial, anti-inflammatory, and antioxidant effects. However, their antifungal potential remains largely unexplored. This project aims to identify and characterise novel kefir-derived peptides with antifungal activity. To date, 27 studies have characterised the kefir peptidome. Using an integrated informatics pipeline, I am performing in silico prioritisation of peptide sequences with unknown bioactivity, followed by synthesis and experimental antifungal screening. Ultimately, this work addresses a critical gap in antifungal research and contributes towards the development of next-generation antifungal therapeutics.

Poster 21: Ghazal Sharifian - "Looks Can Lie: Functional Divergence of Two Structurally Related Peptidase T in Staphylococcus aureus."

Staphylococcus aureus is an opportunistic pathogen for which antimicrobial resistance is a major healthcare concern. Methicillin-resistant S. aureus (MRSA) is the leading cause of antimicrobial resistance-associated mortality worldwide, highlighting the need for novel antimicrobial targets in this organism. SaPepT1 and SaPepT2 are two aminopeptidases involved in S. aureus virulence which are necessary for its survival in macrophages and in murin-coinfection models. Despite conserved catalytic motifs and predicted enzymatic functions, the two proteins differ in substrate scope, suggesting distinct biological roles. Both proteins contain a conserved dimerization domain, creating an interface for multimerization and potential target for inhibitor design. We used size exclusion chromatography and native mass spectrometry to determine the SaPepT1 and SaPepT2 multimeric states, revealing differences in dimer stability. Furthermore, despite both proteins being annotated as aminopeptidases acting on tripeptides, SaPepT2 does not demonstrate this activity and instead catalysed N-terminal self-cleavage. Future work will determine how the quaternary structure of these enzyme influences their catalytic function and substrate scope, as well as novel strategies for their inhibition.

Poster 22: Mash Bandouil - "Leveraging synthetic biology tools to characterise cell-cell interactions in organoid models of human skin."

Cell-cell communication governs a wide range of homeostatic mechanisms within the human body including Epithelial Defense Against Cancer (EDAC) wherein epithelial cells sense, suppress, and eliminate neighbouring transformed cells. EDAC might explain why cells do not always transform into a cancer, despite the accumulation of driver mutations. This is particularly important for understanding melanoma, since phenotypically normal melanocytes can have similar mutational profiles to cancerous ones, yet remain untransformed. Melanocytes are known to communicate extensively with neighbouring keratinocytes, but the exact mechanisms through which they regulate each other's behaviour is unclear. I hypothesize that keratinocytes utilize an EDAC-like mechanism to suppress melanocyte transformation and resist melanoma. To investigate this proposed mechanism, I will employ a contact-dependent neighbour-labelling system ('synNotch') and integrate it into organoid models of healthy and diseased human skin. This system will allow for keratinocytes interacting with melanocytes to be fluorescently labelled, isolated by FACS, and profiled using RNAseq to molecularly characterise how keratinocytes respond differently when in contact with healthy or mutant melanocytes.

Poster 23: Rosina Graham - "Investigating the Effects of Nuclear Envelope Protein Lamin A/C on Macrophage Functions."

Macrophages rely on rapid transcriptional and structural remodelling during inflammation and tissue repair, yet the role of nuclear architecture in these processes is not well defined. My project is examining how lamin A/C nuclear envelope protein influences macrophage activation and ability to clear dead/damaged cells during tissue repair. Using in vitro primary bone marrow derived macrophages (BMDMs) with targeted lamin A/C perturbations, I am assessing their cytokine responses following innate immune stimulation, and ability to clear foreign particles and apoptotic cells. In the near future I plan to test the effects of lamin A/C levels in macrophages in in vivo systems.

Poster 24: Hanhan Zhang - "Deciphering subcellular ion dynamics in the circadian clock."

Circadian rhythms are a fundamental characteristic of life on Earth. Organisms use an internal circadian clock to synchronize key biological processes, and disruption of this clock can lead to physiological and metabolic disorders. Our previous work revealed circadian rhythms in intracellular ion concentrations across several representative eukaryotic species. However, the physiological roles and functional consequences of these oscillations remain largely unexplored. It remains unclear whether these oscillations occur in the cytosol, in specific organelles, or in both. To address this knowledge gap, we aim to generate target highly sensitive fluorescent in vivo reporter proteins that will be targeted to specific cellular compartments, in order to visualise ion fluxes at the subcellular level. These tools would allow us to probe the functional roles of ion rhythms in sustaining robust circadian rhythmicity, which is critical to health.

SESSION 3: DRUG DISCOVERY AND BEHAVIOURAL RESEARCH

TIME: 15:15 – 15:45

PRESENTERS:

Poster 25: Joohwan Won - "Discovering inhibitors for glucokinase."
Glucokinase is an interesting target for treating diabetes. Here, we present our work so far towards the discovery of novel glucokinase inhibitors.

Poster 26: Megan Hine - "Optimizing Coiled-coil Protein Modelling."
Recent developments in protein structure prediction through programs such as Alpha Fold have led to the discovery of many previously unknown protein structures and their binding partners. Despite this, Alpha Fold and similar protein prediction programs have been shown to struggle with predicting coiled-coil proteins, whose structure varies widely depending on their composition. Vairo, a recently developed protein modelling program from the Uson lab, allows for flexible customization of protein query inputs, leading to a more diverse range of protein predictions. Thus far, results from the use of Vairo have highlighted it as a program which may be utilized to improve coiled-coil protein predictions. The aim of this project is to optimize coiled-coil protein modelling with Vairo, through fine-tuning and optimizing inputs to account for coiled-coil folding mechanics.

Poster 27: Hannah Mortlock - "New Chemical Matter to Enhance Mitophagy in Cells."
Parkinson's disease (PD) affects millions globally and remains a progressive disease with no cure and inadequate treatments. It is now understood that mitophagy, the selective autophagy of damaged and dysfunctional mitochondria, is impaired in PD. Enhancing mitophagy, therefore, has the potential to provide a new therapeutic modality for the treatment of PD and other neurodegenerative diseases. To enhance mitophagy, we aim to use bifunctional molecules that bring an effector and the damaged mitochondria into close proximity. Bifunctional molecules have been established as an effective strategy by targeted protein degradation. Typically, bifunctionals make use of the ubiquitin proteosome system, recruiting an E3 ligase to a POI. Expanding bifunctionals to recruit autophagy effectors opens the possibility of degrading whole organelles, such as mitochondria. My project aims to recruit ULK1, a validated autophagy-inducing effector to mitochondria to enhance mitophagy and provide bifunctional chemical tools that will help validate the therapeutic potential of this strategy.

Poster 28: Jacob Peatfield-Muter - "One-Pot Enzymatic Synthesis of Tryptophan Analogues: Gram-Scale and Outreach Applicable."
Tryptophan and its halogenated derivatives, hold a key position as a precursor to many potent bioactive compounds. In protein biochemistry it plays a central role in protein folding, fluorescence and structure. Synthetic approaches to access tryptophan analogues are multistep and generally include and enzymatic deracemization in the final step. Tryptophan Synthase (TrpS) enables simple preparation of a wide range of enantiopure analogues in a single step from serine and indole and shows excellent yields with high tolerance for substituted indole substrates. In this study, we outline a high school outreach project that allows us to generate tryptophan analogues formed using the cell free lysate of tryptophan synthase in a one-pot, single step reaction. Reactions were carried out

and products purified at low then gram-scale. A video was made, and published online, outlining the simplicity of the method which the Goss group has developed.

Poster 29: Nóirín Ní Ghiollagáin - "Does Anger Really Signal Aggression?"
Research has long recognised that facial displays of anger signal imminent aggression, but recent studies suggest other negative emotions may also play a role. It is still unclear how human observers integrate facial expressions of emotion to anticipate aggressive action in others. Here, we examine how observers use emotional expressions to predict behaviour during naturalistic interactions. Observers will view short video clips showing two people playing a face-to-face competitive reaction time game, where the 'winner' could administer a noxious sound blast to the 'loser', providing a quantifiable measure of behavioural aggression. The facial expressions of participants have been coded using the Facial Action Coding System, implemented through OpenFace 2.0. For each clip, observers will estimate how aggressively the participants shown behaved and rate the emotional composition displayed. We hypothesise that facial displays of disgust, as well as anger, will contribute to accurate predictions of aggression. This research will inform our understanding of how emotion perception contributes to the interpersonal dynamics of aggression. We aim to show that anger has been misrepresented as the sole driver of aggression, highlighting the hidden role of disgust.

Poster 30: Phoebe Sadler - "What's your type? A study into long-term partner preferences and the effect of career prospects and anticipated childcare responsibilities."
Men are commonly reported to prefer younger, nurturing partners, with women preferring older partners with financial resources. Rather than being fixed strategies, these preferences could be sensitive to expectations of future responsibilities. In this study, 617 UK-based adults (aged 18-29 years) completed a questionnaire assessing expected income contributions and childcare responsibilities, as well as their preferences for two partner characteristics: "parenting traits" (nurturing and good with children) and "provider traits" (career prospects and financial resources). Overall, we found support for different expectations in division of labour between the genders, along with a higher preference for provider traits in women compared to men. Regression data also suggested that expected contributions to a future household were in some instances correlated to partner preferences (especially in men). However, women's partner preferences seem less influenced by their expected contributions. These findings suggest that partner preferences could reflect flexible, role-based strategies rather than fixed gender specific differences, providing new insights into the evolution of human mating behaviour and the influence of shifting gender norms, and societal expectations on romantic choice.

Poster 31: Victory Ulamen - "Examining the Impact of Stress on Memory of Repeated Events: Using Virtual Reality and Generative AI to Develop Stimuli."
Eyewitness memory research traditionally uses videos or slideshows as stimuli, but these have limited ecological validity, hindering inferences about real eyewitnesses' experiences. To enhance real-world applicability, Virtual Reality (VR) can serve as an effective medium, yet developing VR stimuli to ensure effective manipulations is a complex process that requires validation. This project examines the impact of stress and the effectiveness of interviewing interventions on accurately recalling repeated events—similar events that occur over time—from long-term memory. Recalling a specific event is challenging and can lead to memory errors like misattributions or decreased recall

accuracy. Some repeated events are stressful (e.g., domestic abuse), and research in this area has relied on methods that manipulated stress levels of the subject rather than examined how stressful events are remembered. We use abusive and non-abusive scenarios and measures stress levels using physiological and self-report measures. In a preliminary validation study, participants evaluated perceptions of newly developed repeated event scenarios (using generative AI) involving abusive and non-abusive behaviours, showing that people gave higher abusive ratings to scenarios that contained abusive content.

Poster 32: Ana Belan - "When Timing Matters: Exploring Synchrony of Multisensory Signals in Real and Online Environments."

Multisensory integration allows the brain to combine information from different sensory modalities to guide perception and behaviour. This project investigates the timing aspects of audiovisual processing using various experimental paradigms. The first paradigm to be investigated is temporal order judgement (TOJ), where participants are presented with signals in different modalities at varying delays and are asked to respond which of two signals they have perceived first. Using computational modelling, my work focuses on whether TOJ responses can be predicted using unisensory reaction times. According to an adapted model, auditory and visual signals 'race' and whichever is processed first is therefore perceived first by the participant. Preliminary findings suggest that incorporating bias and noise free parameters to this model shows promising model fit to empirical TOJ data. The project also involves collaboration with Open Science Tools Ltd. As remote devices introduce uncertainty in audiovisual timing, the aim is to develop and improve tools that make the timing of multisensory experiments in online environments more reliable. This, in turn, would make it easier to recruit more participants and therefore increase the effectiveness of data collection in multisensory studies.

Poster 33: Zofia Farkowska - "A Model of the Presence of Self and Other Within Episodic Memory to Boost Cognitive Health of Older Adults."

Healthy ageing brings a quiet but consequential shift in how we remember our own lives. Personal priorities, environmental factors, and neurological changes within brain structures all individually add to a decrease in our ability to recall past events, which is further exacerbated by dementias. This substantially contributes to a lower quality of life. The self-prioritization effect, describing our innate draw towards our self, can boost healthy seniors' memory performance and other cognitive skills. The sense of self and its strength are overall maintained in older age, though its phenomenology may change across the lifespan. However, the self may start to depreciate in mild dementias, and this is presumed to be both a consequence and a contributing factor to long-term memory decline. This project proposes a novel model of the presence of self within episodic memory. Based on previous findings, we propose the self to remain stable in all episodic retrieval. Instead, a worsened episodic performance may be due to an increased inaccessibility of the self under certain conditions that additionally deteriorate with age. We propose that this model may be utilized to target self-related structures in dementia patients, with the aim of maintaining patients' performance over time.

Poster 34: Assunta Sansone - "Engineering landing pads in Pichia pastoris."

The methylotrophic yeast Pichia pastoris is an industrially relevant host for recombinant protein (RP) production. However, limitations in precise and stable heterologous gene (HG) integration hinder

consistent protein yields. Landing pads (LPs), engineered DNA sequences, can facilitate reproducible integration of HGs into highly expressed genomic loci, resulting in high RP titres. This project, in partnership with Fujifilm Diosynth Biotechnologies (FDBK), aims to engineer LPs in P. pastoris. Using genomic and transcriptomic analyses, optimal loci for LP insertion will be identified. LP constructs will then be integrated into these loci via classical integration and CRISPR, comparing the two methods. Ultimately, the system will be validated by employing model HGs, and the resulting strains will be assessed for genomic stability, fitness, and RP yield.

SESSION LEADS: GHAZAL SHARIFIAN & ZUNAIRA AMAN

Multimedia Presentations

A Framework for Assessing Antimicrobial Resistance in Seafood Supply Chains

Ava Drake

This short video outlines the impact of antimicrobial resistance (AMR) on aquaculture, presents how my research addresses this challenge, and discusses its wider implications.

Investigating the Effects of Lamin A/C on Macrophage Functions

Rosina Graham

Macrophages rely on rapid transcriptional and structural remodelling during inflammation and tissue repair, yet the role of nuclear architecture in these processes is not well defined. My project is examining how lamin A/C nuclear envelope protein influences macrophage activation and ability to clear dead/damaged cells during tissue repair. Using in vitro primary bone marrow derived macrophages (BMDMs) with targeted lamin A/C perturbations, I am assessing their cytokine responses following innate immune stimulation, and ability to clear foreign particles and apoptotic cells. In the near future I plan to test the effects of lamin A/C levels in macrophages in in vivo systems.

Eastbio Professional Internship Benefits & Challenges

Morag Clinton, BVMS PhD

mclinton@sitkascience.org

Dr Morag Clinton carried out her PIPS Placement in 2018 at the Ted Stevens Marine Institute (aka Auke Bay Labs) in Juneau, Alaska. She participated in the Southeast Alaska Coastal Monitoring survey onboard a trawl vessel and worked at the Little Port Walter remote Chinook salmon research hatchery on Baranof Island. In this video she outlines her experience and explains the benefits of this placement and the PIPS scheme in general.

YEAR 2 TALKS

During these sessions, we will break out into four smaller rooms to hear about the research being carried out by current 2nd year students. Please see the session details below so you can choose which session you would prefer to attend (but please be aware that space in each room will be allocated on a first-come-first-serve basis and if the room is full when you arrive you will be asked to go to another).

There will be 8 talk winners and runners up (1 per session), as judged by Dr Ahmad Al-Mrabeh, Dr Mihaela Crisan, Dr Noël Juvigny-Khenafou, and Professor Andrew Millar.

PARALLEL SESSION 1

ROOM: PRESTONFIELD
CHAIR: MELISSA RAMSAY

PRESENTERS:

John Girgis - Towards a Conotoxin-Based Fluorescent Probe for AMPA Receptors
AMPA-Receptor integration within synapses is essential for the molecular mechanisms that underlie memory formation. However, due to the diversity of binding co-partners and crowded synaptic compartmentalization, traditional genetic tagging and antibody-based methodologies provide limited utility in studying the dynamics of the receptor under neurophysiological conditions. I plan to investigate the potential for Con-Ikot-Ikot (CII), a toxin specific to AMPARs, to be repurposed as a fluorescent probe for the receptor. To help validate the specificity of the fluorescent probe, here I present an optimized neuronal primary cell preparation, and a comparison of the specificity of various AMPAR antibodies in delimiting synaptic structures.

Sarah Stevens - Characterising the Oocyst Wall Proteins at the Cryptosporidium suture
Cryptosporidium is a waterborne, protozoan parasite that is a leading cause of diarrheal disease. There is no vaccine or effective treatment options. Parasites are transmitted predominantly via water inside an eggshell-like structure called an oocyst. The shell provides protection against disinfectants and common water treatments, including chlorination. Upon ingestion, parasites emerge from a zipper-like opening in the oocyst wall called the suture. Although this structure was first described 40 years ago, how the suture is built and then 'unzips' is unknown. We have identified the first markers of the oocyst suture and will report image-based characterisation of these proteins.

Melissa Ramsay - The role of acoustic cues in multi-species scavenging aggregations in the intertidal zone
Scavengers support healthy ecosystems by recycling nutrients across trophic levels within a range of different habitats, including the intertidal zone. Carrion represents a high value yet ephemeral resource and attracts a range of foragers. I am investigating the dynamics of intertidal scavenging aggregations, and will present evidence for hermit crabs as primary scavengers. As an important keystone species, they produce cues across multiple sensory modalities which can be exploited by secondary scavengers to locate the resource. I am investigating a range of social cues, but here will present acoustic cues produced by hermit crabs during foraging aggregations.

Hannah Raddings - Investigating the Mechanisms of Salmonella Dublin Persistence in the Gallbladder

S. Dublin is a cattle-adapted serovar of Salmonella enterica and a leading cause of bovine salmonellosis. In calves, it causes systemic infections resulting in bacteraemia, meningoencephalitis with high mortality. It can also cause abortions in pregnant cattle, therefore significantly impacting dairy and beef industries. It can also persist asymptomatically in the gallbladder once symptoms resolve in older animals and be shed in faeces leading to undetected transmission within herds and contamination of food products. To identify bacterial mechanisms that play a role in gallbladder persistence, transposon mutant libraries generated in serovar-representative S. Dublin isolates are being screened in bile.

James Tang - Phylogenetically modelling mammal morphological evolvability under realistic sampling conditions

Evolvability is a concept increasingly invoked as a potential bridge between micro- and macro-evolution. Within phylogenetic comparative methods, the Fabric Model purports to identify shifts in evolvability for continuous traits. However, shifts identified by the Fabric Model are positioned on nodes in a phylogeny. As poor sampling or exclusion of fossil taxa will prune or expand a phylogeny, this could bias the Fabric Model relative to the 'true' evolutionary history. To test the Fabric Model prior to use with empirical measurements, we performed simulations under different sampling conditions to observe if the model could still correctly identify an evolvability shift.

Rosie Street-Jeakings - Profiling the Parasite: Integrating Computational Design into Chemical Probe Development for Antimalarial Targets

Rapid development of antimalarial resistance requires the rapid development of new antimalarial drugs in response. These new drugs should target different proteins in the parasite, which can be identified using chemical probes, tool compounds that inhibit or activate a specific protein so changes in phenotype and function can be observed. In this talk I will present the design and synthesis of chemical probes for malaria by applying computational approaches developed for drug discovery. By implementing these tools, I aim to create a robust workflow for developing chemical probes and ultimately accelerate the identification of new antimalarial targets.

Riona Datta-Savage - Expressing RVFV NSs filaments in situ for cryo-ET analysis

Rift Valley fever phlebovirus (RVFV) causes a viral infection which causes abortion storms within pregnant ruminant mammals, and febrile disease in humans, which, in severe cases, can lead to haemorrhage and encephalitis. It currently has no vaccine. The non-structural small (NSs) protein is its main virulence factor which oligomerises into filamentous structures in the nuclei of infected cells, forming complexes with nuclear proteins and inhibiting the transcription of proteins involved in the interferon response, thus suppressing host innate immunity. My project aims to express these filaments in mammalian cells and view them in their biological context using cryo-ET.

John Harvey - Environmental Impacts of Dog and Cat Feeding

We aim to assess the environmental impacts of dog and cat feeding. This is important because pet populations are growing and meat-heavy formats may increase resource pressures. A key challenge is allocating impacts to animal by-products versus prime meat. Using ingredient and nutrient label data, we built an open-source linear-programming model and applied it to 996 products. Footprints varied over 65-fold; prime meat drove higher intensity, and ingredient production contributed 0.9–1.3% of UK GHG emissions. Next steps are studying additional food formats and cat foods, reviewing allocation methods, and refining the model to support consumer and industry decision making.

Jamie Innes - A mechanistic in vitro approach to novel retinoid signalling across gut and brain barriers

Barrier dysfunction is increasingly recognised as a contributor to neurodegenerative disease pathology, particularly at the gut epithelial and blood–brain barriers. My project investigates

whether novel retinoids developed by industrial collaborators can modulate barrier integrity and inflammatory responses in staged in vitro models of gut epithelium and BBB endothelium. Cells are challenged with inflammatory cytokines and treated with candidate retinoids to assess transcriptional, protein-level and functional barrier responses, including retinoid pathway genes, inflammatory markers, tight junction proteins and permeability readouts. The overall aim is to define whether specific retinoid signalling mechanisms can influence barrier dysfunction in a neurodegeneration-relevant context.

Pratiti Nanda - Unraveling the Interaction Network Dynamics of Key Mitotic Regulators Critical for Accurate Chromosome Segregation
During mitosis, chromosome segregation enables equal transmission of genetic material through tightly regulated processes such as timely onset of sister chromatid separation and maintenance of centromere identity. Several phospho-regulated protein networks mediate these processes. Any defects these processes will lead to aneuploidy, causing cancers and genetic disorders. Hence, understanding the spatiotemporal dynamics of these protein interaction networks is crucial. In this work, we characterise the interactome of key mitotic regulators PP2A/B56 isoforms (PP2A/B56a and PP2A/B56g), the Mis18 complex and HJURP in a time-restricted manner. This analysis will provide new insights into the regulatory networks governing centromere maintenance and chromosome segregation.

Bea Atkinson - A Master Manipulator – does Phytophthora infestans use NLPs to evade plant host defences?
Phytophthora infestans is a plant pathogen which constitutes a major threat to global food security. As a result, understanding how P. infestans produces virulence in its hosts is essential for designing innovative solutions for preventing infection. Recent work has indicated that P. infestans enacts virulence through secreting effectors associated with vesicles which are then endocytosed via clathrin-mediated endocytosis (CME). However, the pathogen-derived molecules that facilitate CME are not yet known. Nep1-Like Proteins (NLPs), a group of pathogen-derived proteins that can cause plant cell death, have been suggested to be CME facilitators, as they can be recognised as microbe-associated molecular patterns (MAMPs) by plant cell surface receptors. NLPs have diverse yet unclear roles in pathogenesis. NLPs can be either cytotoxic or non-cytotoxic, but how either NLP type enacts their function is contested. By using various molecular and cell biology techniques, my project aims to determine whether NLPs, or other MAMPs, act as the key to effector-CME and to develop the understanding of what roles NLPs play in virulence.

PARALLEL SESSION 2

ROOM: DUDDINGSTON
CHAIR: HELAENA FINE

PRESENTERS:

Olivia Gray - Detecting Lichen Species in the Air
Airborne environmental DNA involves sampling particles suspended in the air; a promising method for monitoring biodiversity in the context of climate change and habitat loss. Airborne eDNA can be used to monitor the dispersal of organisms such as lichens, which reproduce via spores and reproductive propagules. Lichens are ecologically important species, and temperate rainforest habitat in West Scotland is a hotspot for UK lichen diversity, also hosting globally rare species. Once DNA is extracted from air samples, there are different methods available to analyse them – I present results from PCR and metabarcoding to evaluate the biases in each method.

Rebecca Hilgenhof - What shapes Leaves? The Interaction of Physiology, Defence and Escape in Passionflower Leaf Optimisation
Leaves are the primary photosynthetic plant organs optimised for light harvesting and gas exchange, whilst also protecting themselves against herbivores, using multiple strategies that include chemical and physical defence and avoiding recognition. Passionflowers possess great leaf diversity, occur in diverse habitats and are the sole host plants of Heliconius-butterflies, which have evolved resistance to cyanide-producing toxins in passionflowers. I am comparing Andean passionflowers that evolved in the presence of host-specific herbivores and Brazilian species in the absence of butterflies. Morphological, molecular and chemical analyses will test the extent to which their leaves have been shaped by biotic or abiotic factors.

Tablow Media - Determining the role of circular RNAs and extracellular vesicles during herpesviral infection
Herpesviruses are lifelong viral infections, and can lead to the development of cancer. Circular RNAs (circRNAs) are a type of noncoding RNA that have been found to play various roles in cancer and immunity, with some herpesviruses encoding their own circular RNAs. Extracellular vesicles (EVs) are particles used for transferring molecular cargo between cells. circRNAs have been found in EVs, important for shaping the tumor microenvironment (TME). In the context of herpesvirus infection, circRNAs, and circRNAs in EVs have not been thoroughly studied. This project aims to determine the significance of circRNAs and EVs on herpesviral infection and oncogenesis.

Megan Saathoff - Exploring the Population Fitness Dynamics of Avian Influenza
Wild waterfowl serve as the host reservoir species for all influenza viruses and are responsible for a majority of the genetic diversity. Therefore, understanding the fitness dynamics of influenza viruses in these avian species is key if we are to understand outbreaks. Phylogenetics allows us to evaluate virus fitness by assessing changes to the branching structure of phylogenetic trees. In this project, the population fitness dynamics of avian influenza clade 2.3.4.4b was evaluated using three methods. The H5N1 D1.1 lineage and the B3.6 lineage had the highest fitness, along with the co-circulating H5N5 A6 lineage. Additionally, fitness was geographically specific.

France Chaiyasut - Molecular responses of mesenchymal stromal cell lineages to mechanical wounds in Atlantic salmon (*Salmo salar*)
Skin wounding in Atlantic salmon is a common occurrence in aquaculture production and can lead to secondary infection, compromised welfare, and reduced productivity. One of the key cell types involved in skin regeneration is the mesenchymal stromal cell (MSC). MSCs are adult stem cells capable of differentiating into various cell types important for skin repair. A better understanding of the cellular mechanisms underlying MSC function during wound healing could enable the development of interventions to accelerate regeneration, thereby improving sustainability and animal welfare in aquaculture production.

Laina Langridge - Host associations in a multi-host system: next-generation sequencing insights into Leptospira in Madagascar
Multi-host disease systems pose a major challenge for understanding and managing infectious diseases, as transmission is shaped by complex interactions between hosts, pathogens, and environments. Leptospirosis is a globally important zoonotic multi-host disease, with rodents and livestock as potential sources of human infection. However, the roles of different hosts as reservoirs and the transmission of strains between hosts remain poorly understood. This project investigates Leptospira epidemiology in Madagascar using field sampling, next-generation sequencing, and sequence capture approaches. Four pathogenic Leptospira species have been detected, showing

varying host specificity. Further work will provide novel genetic insights into multi-host pathogen dynamics.

Emily Mahony - How mesenchymal cells coordinate intestinal elongation
Organ development relies on collective cellular activities, yet how they form consistent shapes is unclear. The intestine, changing significantly in length and structure during development, serves as an ideal study model. This research explores whether elongation arises from cell migration, differential proliferation, or mechanical influences. In chick embryos, intestinal elongation depends on coordinated mesenchymal behaviour. Mesenchymal cells align and divide along the growth axis, facilitating elongation through mechanical coupling and tension. This collective behaviour illustrates how cells generate form by interacting with their context. Understanding these dynamics offers insights into tissue development and morphogenesis as emergent processes.

Lauren Tribbeck - Impact of Vining Peas in the Crop Rotation on Soil Nitrogen and Soil Carbon
Vining peas are a valuable rotation crop for many UK farmers, with a known benefit of nitrogen fixation which can reduce artificial fertiliser requirements for peas and their following crop. This addition of fixed nitrogen, and decomposition of nitrogen rich residues may provide a benefit to soil carbon dynamics and lead to an increase in soil carbon sequestration. In my presentation I will focus on my initial fieldwork study that aimed to quantify the impacts of peas on total soil carbon and nitrogen across a range of commercial farms.

Max Leach - Investigating visually guided locomotion in Tribolium Castenum
Tribolium castaneum is a major stored-grain pest whose movement through dark substrates contributes to grain damage. We examined how illumination and social context affect adult locomotion. Beetles were recorded alone or in groups in arenas under light, darkness, or a split light–dark condition. Automated tracking quantified movement bouts, speed, distance, and use of open-field versus edge zones. In uniform arenas, light increased bout duration and open-field peak speed but had little effect on spatial occupancy or thigmotaxis. In split arenas, negative phototaxis was observed but overall kinematics between the two regions remained similar. Social context had minimal effect.

Katja Zumer - Cognition in the navigation of social chaos
This project investigated if cognitive ability predicts behavioural flexibility during aggressive contests in pigs (Sus scrofa). The reversal learning task assessed cognitive ability, and two measures of behavioural flexibility were extracted from contests. These measures were: repeated aggression against recent winners and changes in fight duration over time. The results found little evidence that reversal learning performance predicted contest flexibility, suggesting that aggression during mixing is influenced not only by cognition, but also by motivation, emotional state, and social context. This has implications for animal welfare and farm management.

PARALLEL SESSION 3

ROOM: SALISBURY
CHAIR: ZUNAIRA AMAN

PRESENTERS:

Sara Valkila - Modelling the effects of maternal inflammation on human brain development using 3D brain cultures

Inhibitory neurons play a critical role in human cortical development, and disruptions to their formation are linked to neurodevelopmental disorders. Maternal inflammation during early pregnancy is a known risk factor for these conditions, yet its effects on human inhibitory neuron development remain poorly understood. We have established a novel 3D ex vivo culture system of the human foetal brain, termed ventral cerebroids. Using immunofluorescence and microscopy, I investigate early development of the medial ganglionic eminence (MGE), a primary source of inhibitory neurons, and examine how exposure to pro-inflammatory cytokines associated with maternal immune activation (MIA) affects this process.

Felicity Wilson - In-Water Stunning Parameters Identified for European lobsters (Homarus gammarus) to Contribute to the Refinement of a Prototype Batch Crustacean Stunner
It is understood that DEFRA will soon publish guidance endorsing the electrical stunning of decapod crustaceans prior to slaughter in the UK; however, there is a lack of electrical stunning technology available to meet the needs of the shellfish sector, with a notable gap for an affordable, mid-range, in-water crustacean-stunning device. Partnering with Ace Aquatec Ltd., suitable stunning parameters were identified for such a unit using European lobsters (Homarus gammarus). Different electrical fields and stun durations were tested, revealing suitable parameters for reversible and irreversible stunning. Insensibility was identified using behavioural measures and verified with electroencephalograms to assess neurological activity.

Kingsley Warne - Evaluating treatments and disease progression in a novel ex vivo model of corneal inflammation and infection
Microbial keratitis is a severe infection of the cornea which can result in loss of vision. The main contributors to this are the pathogens themselves, the host immune response, fibrosis, and collagen degradation. Current models of the cornea are not able to capture the full complexity of the native collagen structure and cellular heterogeneity. We have worked to establish an ex vivo model of the cornea based on precision cut tissue slicing which would be suitable for studying fibrosis and collagen degradation.

Zachary Olsen Garza - Inducible Protein Degradation in Chicken Cell Lines
Traditional techniques for studying protein function during development target nucleotides and not the actual protein. Targeted protein degradation techniques, such as degron tagging, are an emerging alternative that allow for inducible depletion of a target protein. While degron tagging has been successfully utilized in mammals, it has not yet been adapted to chicken. Therefore, we systematically tested the efficacy of the most commonly used degron systems (OsTIR1-AID, BromoTag, dTAG) in 3 chicken cell lines. We found that these systems can efficiently degrade proteins in vitro. However, we observed chicken and cell type specific responsiveness to different degron tagging systems.

Zunaira Aman - Engineering Mammalian Cells as Last-Resort Therapies Against Drug-Resistant Bacterial Infections
Antimicrobial resistance is rapidly reducing the effectivens of conventional antibiotics, creating an urgent need for alternative therapeutic strategies. This project explores a novel cell therapy approach against multidrug-resistant bacterial infections by engineering mammalian cells to detect bacterial surface antigens and initiate localized antibacterial responses. As a first step, synthetic receptor platforms will be designed and tested for recognition of bacteria displaying GFP as a model antigen. Validated receptors will then be adapted to detect clinically relevant pathogen-associated antigens, such as outer membrane proteins from Pseudomonas aeruginosa. This work aims to establish a modular, high-specificity platform for targeted bacterial elimination.

Anna Rastedt - Hippocampal place cell activity in a rat model of GRIN2B haploinsufficiency

The *GRIN2B* gene encodes an NMDA receptor subunit, GluN2B, and heterozygous mutations in this gene are known to cause mild-to-severe intellectual disability and developmental delay. The NMDA receptor is essential for neural plasticity, learning and memory, yet little is known about the effects of specific subunit loss on neuronal and circuit function. NMDA receptors contribute to alterations in the activity of hippocampal place cells, neurons that support navigation by forming spatial representations of the environment. In this study, we use a Grin2b+/- rat model and record place cells to understand circuit-level consequences of *GRIN2B* haploinsufficiency.

Alex Wang - AI-driven Technologies to Differentiate Autoimmune Diabetes and Other Diabetes Subtypes

Autoimmune Diabetes including Type 1 has both genetic and environmental risk factors. After a triggering event, the body may start producing self-targeting antibodies. There are multiple other types of diabetes, some with similar presentations but requiring different treatments. However, these are often misdiagnosed, delaying effective intervention. Due to high costs of current autoimmune testing panels, population-wide screening has been limited to high-risk groups. As a result, many individuals remain undiagnosed until clinical onset, when significant β-cell destruction has already occurred. Machine learning approaches offer a solution by enabling the analysis of large-scale immunological and genomic datasets to differentiate subtypes.

Jacob Thomas-Hegarty - Neural information flow structure learning with dynamic Bayesian networks

Neural information flow describes how activity is communicated across biological neural networks. The structure of these networks can be inferred from simultaneous recording of neural activity, via methods ranging from electrophysiology to fMRI. However, current statistical methods for doing so can be unreliable. Learning these structures at a whole network level as dynamic Bayesian network models may overcome these limitations. To test this hypothesis we evaluate the ability of various methods for dynamic Bayesian network structure learning to correctly infer structures underlying simulated data. The performance of these methods are benchmarked against multivariate Granger causality and LASSO regression.

Talent Mabambe - Biofortified Rice: Exploring genetic variation within aus rice to increase grain micronutrient density

Rice is the primary staple food for over half of the global population and is essential for meeting daily caloric needs, particularly in developing countries where dietary diversity is limited. However, reliance on rice and other cereals, which are low in grain micronutrients, such as zinc, has contributed to micronutrient deficiencies in humans. This condition, referred to as “hidden hunger,” affects over two billion people, particularly in Asia, Africa, and Latin America. The rising prevalence of micronutrient malnutrition poses significant challenges to achieving sustainable development goals, including poverty reduction, improved maternal health, and decreased child mortality by 2035. Enhanced grain concentration of micronutrients offers a promising solution to combat hidden hunger among resource-poor communities unable to afford dietary supplements. This process aims to increase the concentration of essential micronutrients in grains through breeding and agronomic practices. This study investigates natural genetic variation in 243 Aus rice genotypes. Genome-wide association mapping will be used to identify genomic regions associated with micronutrient accumulation, and candidate genes will be identified for enhanced zinc accumulation. Controlled pot experiments will assess phenotypic variation under standardized growth conditions and evaluate the efficacy of micronutrient-enhancing soil amendments. This research aims to provide genetic targets for breeding zinc-rich rice varieties, contributing to biofortification programs targeting micronutrient malnutrition in vulnerable populations and improve health outcomes globally.

River McDonald - Understanding Owner Choice of Canine Walking Equipment in the U.K

Harnesses are an increasingly popular alternative to traditional collars and leads for exercising companion dogs. However, little is known about the factors influencing owners' choice of walking equipment, despite evidence from canine gait research suggesting that some harnesses may restrict movement and risk cumulative damage to joints and tissues. As part of a wider study applying machine learning to canine gait analysis, a survey of more than 2,000 U.K. dog owners investigated current trends in walking equipment use and owner motivations for equipment choice. Thematic analysis of free-text responses identified dog welfare as a primary consideration for many owners, highlighting the importance of further research into the physical effects of harness use on canine movement and musculoskeletal health.

PARALLEL SESSION 4

ROOM: HOLYROOD
CHAIR: LAURA ISABELLA ARBANAS

PRESENTERS:

Katrien Sutherland - Race Against Antimicrobial Resistance – Targeting Gram-negative bacteria with Peptides and Peptidomimetics
Antimicrobial resistance (AMR) is a growing public health emergency and presents a major threat to human health. Development of therapeutics against new targets is lacking and is urgently required; peptides are uniquely placed to inhibit 'undruggable' targets. The Gram-negative pathogen, Klebsiella pnuemoniae is a critical concern, due to increasing hypervirulence and multidrug resistance – RamA is transcription factor in K. pneumoniae that contributes to the AMR phenotype. This project aims to develop a high-throughput screening assay for identifying peptide binders against RamA, that will be used to evaluate RamA as a druggable target and to develop inhibitors using peptides and peptidomimetics.

Shravan Rathod - The nose knows: Structural insights into olfactory GPCR-G protein coupling in C. elegans
The sensory system enables organisms to detect and respond to environmental stimuli. Chemosensation, the ability to sense chemical signals, is the oldest sensory modality. In animals, G-protein coupled receptors (GPCRs), present in the nose, detect volatile molecules. We use Caenorhabditis elegans as a model to study olfaction. It has three pairs of olfactory neurons-AWA, AWB, and AWC housing ~550 olfactory receptors and 22 G-proteins. However, the rules for pairing between receptors and G-proteins remains unclear, in C. elegans or in other organisms. We combine computational and genetic approaches to investigate the structural and mechanistic aspects of GPCR-G protein coupling.

Jessica Reeves - Molecular control underpinning arm and leg size, development and regeneration
Limb development is a highly coordinated process that requires undifferentiated cells to form the limb bud, with interactions between several signalling centres (apical ectodermal ridge, progress zone and zone of polarising activity) and signalling molecules, to orchestrate limb outgrowth, and patterning across the positional axes. Knowledge of the sequential stages required for independent limb outgrowth has progressed substantially, however, knowledge of the mechanisms underpinning the symmetry of left and right limb outgrowth remain poorly understood. This project aims to investigate the complex processes that modulate the symmetry of limb length, and size, on opposing sides of the body.

Larissa Chicoski - Healthy Herds, Hidden Risks: Decoding Antimicrobial Resistance in British Cattle

Genomic surveillance of antimicrobial resistance (AMR) in healthy animals enables the monitoring trends of antimicrobial resistance genes (ARG). *Escherichia coli* isolates (n=270) were Illumina whole-genome sequenced and AMR profiles assessed with AMRFinderPlus. Sequence types (ST) were assigned using MLST, and phylogenetic tree was built with parsnp, visualized with iTol. Genotypically multidrug resistance was detected in 3% of indicator *E. coli* (7/200), higher (63%; 44/70) among ESBL-producing (20%; 61/70). ST58 and ST10 accounted for 8% (22) and 6% (16) of isolates, respectively. Genomic analysis can predict AMR dynamics, although it does not capture the phenotypic impact of the gene complement.

Sarah Rehman - Using host genomics to predict pathogen persistence in a fragmented metapopulation

Dispersal shapes population genetic structure and parasite transmission, yet quantifying host movement in fragmented landscapes remains a fundamental challenge. I use genome-wide SNP data from a water vole (Arvicola amphibius) metapopulation in Assynt, Scotland to reveal latent dispersal pathways and infer how parasites spread across a multi-host, vector-borne disease system with frequent extinction and recolonisation. A pilot RAD-sequencing study reveals two genetically distinct subpopulations connected by a narrow admixture corridor, with genetic differentiation deviating from isolation-by-distance expectations. Low-coverage whole-genome sequencing will be integrated with parasite community analyses to test whether inferred dispersal corridors predict pathogen persistence across the metapopulation.

Ellie Smith - Facultative parthenogenesis: why is the best of both worlds so rare?

Facultative parthenogenesis, the ability to reproduce both sexually and asexually, is theoretically the optimal reproductive strategy allowing organisms to gain the benefits of sex without paying the full costs. Yet facultative parthenogenesis is rare in animals. One hypothesis for this rarity is that sexual conflict constrains the evolution of facultative parthenogenesis. To test this hypothesis, I am exposing females of the facultatively parthenogenetic fruit fly, Drosophila mercatorum, to various numbers of males and comparing the fitness consequences between sexual and asexual females. These results will provide insight into the evolution of parthenogenesis and the persistence of obligate sex.

Megan Worsley - Who builds the nest?

Many animals care for their offspring, but why do the parents of some species cooperate, while in other species one parent does all the parental care? In birds, the nest is vital for offspring survival, and there is much interspecific variation in who builds the nest: biparental, female-only, and male-only building are all found. Despite this, nest building is often overlooked in the study of parental care. In this comparative study, I am investigating which conditions favour biparental nest building, to test whether theories about why parental cooperation evolves can explain this variation between birds.

Kai Zhou - Discovery of cryptic C-C bond forming activity within the pyridoxal-5'-phosphate (PLP) transaminase biocatalyst family

Pyridoxal 5'-phosphate (PLP)-dependent enzymes are widely exploited as biocatalysts for diverse chemical reactions. Here, we uncovered a cryptic activity within PLP-dependent transaminases (TAs), namely the ability to catalyse C-C bond formation. Following an extensive study of quinonoid intermediate, an engineered substrate screening revealed that simple activated aldehyde moiety, can act as electrophile and undergo cryptic C-C bond formation with the quinonoid, catalysed by TA. Further screening across multiple TAs showed that quinonoid formation is not unique to ATA1, but instead appears to be a more general and intrinsic feature of this enzyme family. These findings expand the catalytic repertoire of PLP-dependent TAs and open opportunities for engineering C-C bond forming biocatalysts.

Laura Isabella Arbanas - Uncovering the molecular mechanisms of spinal cord regeneration in the axolotl

Axolotls are uniquely able to regenerate the spinal cord after injury. Upon tail amputation, ependymal cells de-differentiate into an embryonic-like state to proliferate and differentiate into all spinal cord cell types. However, how ependymal cells reprogramme from a homeostatic to a regenerative state remains unknown. We hypothesize that this transition is governed by changes in gene expression and chromatin accessibility. Therefore, I am generating an RNA and ATAC-sequencing atlas of spinal cord regeneration to identify transcription factors and chromatin changes driving this process. Finally, perturbation of identified candidates will allow me to functionally assess their role in spinal cord regeneration.

Stefan Manolache - Mechanistic modelling and parameter inference of developmental gene regulatory networks

Developmental programs are classically represented as gene regulatory networks. Yet, in general, the behaviour of such a network cannot be read off its diagram, as the same topology can produce very different outcomes depending on the strength of its regulatory interactions. To this end, we are developing a computational framework that combines a mechanistic stochastic simulator of gene expression with Bayesian inference, to identify parameter regimes consistent with experimental data, using C. elegans endoderm specification as a case study. Ultimately, quantifying how gene expression dynamics respond to variation in network parameters can refine our understanding of developmental bias as a source of evolutionary constraint.

Paula Mora Rojas - Here you see me, here you don't: Genomic Insights into Island Colour Polymorphism in Oophaga pumilio

Oophaga pumilio is a neotropical poison frog exhibiting extraordinary colour polymorphism, particularly within Panama's Bocas del Toro archipelago, where populations range from cryptic to aposematic phenotypes. This system provides a natural framework for studying evolutionary interplay between natural and sexual selection. Genomic investigation has been hindered by the absence of a high-quality reference genome. We generated a chromosome-level assembly (6.98 Gb) using PacBio HiFi reads and Hi-C scaffolding, substantially improving contiguity and completeness. Using this resource, we analyse population structure, colonisation history, and gene expression differences associated with colouration, perception, and alkaloid metabolism underlying antipredator strategies.

SESSION LEADS: MELISSA RAMSAY, LAURA ISABELLA ARBANAS, HELAENA FINE, ZUNAIRA AMAN

EDI PANEL - INCLUSIVITY IN STEM

In this interactive panel session brought to you by the brand new EastBio Women in STEM network, we will be discussing what inclusivity means to various experts in STEM. First, we will hear from each panel member about their background and experience, and then we will open up to the audience for questions in the room and online. This will be a great chance to hear from a diverse panel about why EDI is so important in academia and industry, and what we can all do to make research environments more inclusive for all.

SESSION SPEAKERS: DR GWENETTA CURRY, DR ELEANOR GAUNT, PROFESSOR SRINJOY MITRA, HOPE OBASI, ALI SOMERVILLE

DR ELEANOR GAUNT

Eleanor (Elly) Gaunt is a Group Leader at the Roslin Institute, University of Edinburgh. She did her PhD at the University of Edinburgh on the molecular epidemiology of viruses, graduating in 2011. She moved to Cambridge University for a postdoc before returning to Edinburgh for two further postdocs. Elly started her lab in 2018 supported by a prestigious Wellcome Trust Sir Henry Dale Fellowship. She is a strong supporter of early career researchers, which she implements by serving on a number of committees, such as the Roslin's Postgraduate Student, the Roslin Fellowships, the Edinburgh Infectious diseases, and the Microbiology Society committees. Elly is particularly interested in supporting academics with neurodivergencies and caring responsibilities.

DR GWENETTA CURRY

Dr Gwenetta D. Curry is a Reader in the Usher Institute at the University of Edinburgh. Her research interests are Racial and Ethnic Health Disparities, Critical Race Theory, and Black Family Studies. Her present research analyses racial disparities in treatment and infection rates of Covid-19. She is the co-author of the UNCOVER Covid-19 Evidence review "What is the Evidence on Ethnic Variation on Covid-19 Incidence and Outcomes," and "Sharpening the global focus on ethnicity and race in the time of COVID-19" which has recently appeared in The Lancet. She is a member of The Royal Society's DELVE Initiative and a senior research associate in the Global Health Governance Programme at the University of Edinburgh Medical School. She is also a member of the UK Inclusive Data Taskforce and the Medical School Equality, Diversity, and Inclusion Alliance.

Professor Srinjoy Mitra

Based in the School of Engineering at Edinburgh University, Professor Mitra has two parallel research tracks.

His technological research interests are in low-power sensor interfaces, medical/neural electronics, neuromorphic systems and in engineering education. He is the Program Director for the MSc in Sensors and Imaging System. He is also a founding member of Edinburgh Neuroprosthetics Lab.

He is also deeply interested in technological innovation, its global implications, and its pedagogy. This includes a critical analysis of relentless growth in digital technologies and its impact on the planet and people, both historical and in future. He is the convenor of the Decolonisation Working Group in the College of Science and Engineering.

Hope obasi

Hope is a second year EastBio PhD student at the University of Dundee based in Dr Virginia De Cesare's Lab. Her project focuses on the innovative integration of Matrix-Assisted Laser Desorption/Ionization Time-of-Flight (MALDI-TOF) mass spectrometry with kinase inhibitor profiling. This aims to deepen our understanding of kinase activities, which are essential regulatory components in cellular signalling and numerous disease pathways.

Hope is also an EDI student rep for EastBio

Ali somerville

Ali is a third-year PhD student at The University of Edinburgh, whose research focuses on host-virus interactions using insect model systems. Since joining the EastBio doctoral training programme,he has served as an Equality, Diversity and Inclusion (EDI) representative, contributing to the development of student-facing documents and representing student viewpoints at management meetings. He is passionate about improving representation in STEM, particularly for LGBT+ identities and students from underrepresented backgrounds. He has been involved in a range of outreach activities, including delivering science workshops in secondary schools in disadvantaged areas and running public engagement stalls at Pride events to promote inclusive science. Through both advocacy and outreach, he is interested in how academic environments can become more inclusive and supportive for students and researchers at all stages of their careers.

Industry Placements: Lessons from the Front Line

This segment is a panel discussion exploring the lived experiences of both students and hosts following industry placements. It aims to equip students with the insights, practical knowledge, and confidence to undertake projects in a non-academic setting, allowing them to actively shape and maximise the value of their placements and their long-term career development.

Session Chair:

Dr Andrew Desbois | University of Stirling

Dr Andrew Desbois is Senior Lecturer and microbiologist at the Institute of Aquaculture, University of Stirling. He researches bacterial pathogens and has a special interest in antimicrobial resistance and ways to mitigate this global challenge. He has led projects in the UK, Europe, Africa and Asia, often collaborating with non-academic stakeholders including government agencies and businesses. Dr Desbois recognises the value of student placements having benefited from opportunities during his own undergraduate and doctoral studies. Moreover, when developing an innovative new European masters programme, he led the introduction of a major component of workplace-based learning where students spent 6 months in a non-University environment.

Session Speakers:

Christoph Wagner | University of Edinburgh - Year 4 | Singapore Institute for Manufacturing Technology A*STAR

My placement was about the design, fabrication and testing of a digital microfluidics (DMF) platform for automation and miniaturisation of next generation sequencing (NGS) library preparation. The manual preparation of NGS samples is tedious, lengthy, error-prone and uses expensive reagents. DMF enables automation and miniaturisation, enabling faster, cheaper, high-throughput assays. During my internship, I worked at the interface between engineers and genomics experts at A*STAR to determine the properties of a useful DMF device, translate those properties into a viable design, have that device manufactured and carry out preliminary testing of the associated library preparation protocol in the wet lab.

Jed Hawes | University of Dundee - Year 3 | Drug Discovery Unit, University of Dundee

During my placement in the Drug Discovery Unit I transitioned from my molecular biology background to explore the application of artificial intelligence in drug design. My project focused on developing an automated pipeline to test a new computational tool for predicting drug resistance. By

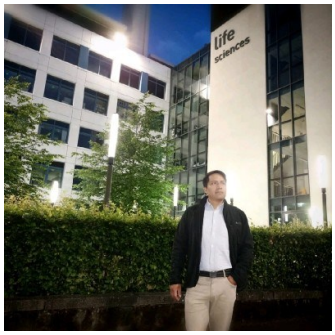
simulating the effect of hundreds of specific protein mutations on drug binding I was able to evaluate the tool's effectiveness. This approach streamlined a time-consuming manual process transforming weeks of analysis into a fast automated workflow. The placement allowed me to gain valuable computational skills while directly contributing to the evaluation of emerging AI methods for improving drug design.

Hope Obasi | University of Dundee - Year 2 | Singer Instruments

My internship focused on the PRISM project, a cloud-based microbiology platform that uses AI to improve routine lab tests such as colony counting, antimicrobial susceptibility testing (AST), and total viable count (TVC) analysis. PRISM is designed to help laboratories work faster and more accurately by automating image analysis. I contributed to developing and testing the AI models behind the platform, making sure they worked reliably on real lab images, including plates with uneven lighting, background noise, and overlapping colonies.

Eleanor Swift (she/her) | Scottish Government

Eleanor is an analyst in Corporate Analytical Services (CAST), the Scottish Government's HR analytics function. The team provides insights on topics from employee experience and wellbeing to workforce planning and organisational design. Their analysis informs both strategic and day to day decision making across government. CAST have hosted four EastBio interns. Their projects have included developing new reporting on training uptake, creating dashboards for the Scottish Government Executive Team, and analysing differences in employee experiences through the lens of demographic characteristics. Eleanor develops new project ideas and is one of the line managers for interns



Dr Cesar Mendoza Martinez | Drug Discovery Unit, Dundee

Dr Cesar Mendoza is a Senior Computational Chemist at the DDU. Before joining, he worked at the University of Edinburgh as a Newton Fellow and in industry as a Research and Development Manager. His work sits at the interface of experimental and computational methods, spanning computational chemistry, medicinal chemistry, and structural biology. He contributes to the innovative targets portfolio using computational approaches, including AI. He has supported student placements by defining projects, providing day-to-day guidance, and supervising computational and data analysis tasks. He offers regular feedback and helps students connect their work to broader scientific questions, while ensuring projects are engaging and valuable for both training and research.

Industry Workshop & Debate: Hot Skills for Graduates Moving to Industry

This session brings together alumni and industry stakeholders to discuss and debate the key skills needed to transition into industry, while giving students insight into what employers value and how organisations benefit from engaging high-calibre graduates.

Session Chairs:

Skills Session Chair: Dr Mary Doherty

Dr Mary Doherty is a cross-sector leader in biotechnology and education, with experience spanning academia, industry, and programme management. She is Head of Skills at IBioIC, where she leads initiatives linking skills development with industry needs and emerging technologies. Her career includes senior academic roles at the University of the Highlands and Islands, alongside leadership in R&D and programme delivery within industry. She also contributes to national strategy through advisory roles with organisations such as UKRI BBSRC, supporting talent development and innovation across the life sciences sector.

Debate Session Chair: Dr Raquel Arribas

Dr Raquel Arribas is a structural biologist and Teaching Lecturer in Biochemistry and Biophysics at The University of Edinburgh. Her background spans research and teaching across molecular life sciences, with expertise in structural biology, biochemistry, drug discovery and the study of DNA repair mechanisms. Prior to her current role, she held research positions at the University of Sussex and the Institute of Cancer Research (London), contributing to research on genome stability through a structural lens. Her industry-funded PhD was at the Institute for Research in Biomedicine (Barcelona) exploiting the potential of prokaryotic replicative helicases as drug targets. Her current work combines scientific research with a strong interest in innovative and research-lead approaches to teaching and learning in biochemistry and biophysics

Session Speakers:

Dr Ian Archer

Dr Ian Archer is a senior leader in industrial biotechnology, with experience across research, development, and commercialisation. He currently serves as Commercial Director at James Hutton Institute Scientific Services, following leadership roles including CEO of the BioConnect Innovation Centre and Technical Director at the Industrial Biotechnology Innovation Centre. Beginning his career in chemical development at organisations such as Ingenza

and Zeneca, he has consistently worked across science and industry to bring innovation into real-world application.

Dr Jennifer Harbottle

Dr Jennifer Harbottle is an EastBio alumna who completed her PhD at the University of Aberdeen and has developed her career at the interface of academic research and the biotechnology industry. Now Associate Director of Nonclinical Safety for Cell Therapy at AstraZeneca, she focuses on the safe development of next-generation cell and gene therapies, with expertise in gene editing technologies such as CRISPR and base editing, and the assessment of genomic integrity. Her work is underpinned by a strong grounding in bioscience and experience translating research into practical, innovation-driven applications.

Dr Edward Martin

Dr Edward Martin, an EastBio alumnus, is a Teaching Fellow in Science Communication and Public Engagement at The University of Edinburgh. With a background spanning bioscience, data analysis, and creative research methods, he recently completed a PhD exploring the sonification of biological data, using sound to represent complex datasets and support new ways of understanding and engaging with science. His work brings together bioinformatics, research, and public engagement, driven by an interest in making scientific ideas more accessible through innovative and interdisciplinary approaches.

Dr Samuel Gibbon

Dr Samuel Gibbon is a Research Fellow at the Centre for Medical Informatics, where he uses retinal imaging to investigate brain health and neurological disease. He completed his PhD in Clinical Brain Science at The University of Edinburgh as part of the EastBio programme, taking a multidisciplinary approach that combines computational methods, artificial intelligence, and biomedical science to identify early indicators of conditions such as dementia. Alongside his academic work, he has contributed to research at University of Cambridge and explored the potential of AI-driven medical imaging through innovation and entrepreneurship initiatives

Session Leads: Industry Engagement Manager Lizzie Leigh

Dinner Table Plan

There is a table plan for dinner so that the venue can manage dietary requirements and to encourage you to speak to other EastBio students and supervisors who you may not have met.

Table 1	**Table 2**	**Table 3**	**Table 4**
Geraint Thomas	Adriana Cusi	Anna Råstedt	Aman Jilani
Gregor Fisher	Charlotte Wood	Aoife Robertson	Andrew Desbois
Hannah Connor	Hannah Mortlock	Destiny Docherty	Delma Childers
Jamie Innes	Hannah Raddings	Eleanor Gaunt	Kasidis Chaiyasut
John Harvey	Nik Copeland	Ghazal Sharifian	Katja Zumer
Nasir Mehmood Khan	Phoebe Sadler	Gustaf Fredell	Katrien Sutherland
Nóirín Ní Ghiollagáin	Raquel Arribas	Hanhan Zhang	Lauren Tribbeck
Paula Mora Rojas	Rob Kelly	James Tang	Megan Hine
Prerna Vohra	Rosina Graham	Larissa Melo Chicoski	Sarah Rehman
Samuel Gibbon	Talent Mabambe	Lizzie Leigh	Temitayo Ademolue
Table 5	**Table 6**	**Table 7**	**Table 8**
Benjamin Clokie	Angus Comerford	Jakub Teahan	Ahmad Al-Mrabeh
Edgar Huitema	Eve Sharples	Kai Zhou	Anna Moelders
Eileen Clemens	Indra Warr	Riona Datta-Savage	Attila Molnar
Haya Al Siyabi	Jack Hearn	Sara Valkila	Jack Horne
Kingsley Warne	Maheshika Sandaruwanie Kurukulasuriya	Shravan Rathod	Jacob Thomas-Hegarty
Max Leach	Megan Worsley	Stefan Pulver	Mash Bandouil
Petra Lavay	Samantha Miller	Steve Whisson	Sarah Stevens
Rebecca Atkinson	Stefan Manolache	Suraya Fawcett	Tablow Media
Sandra Maria Sajan	Steven McPherson	Talal Hossain	Vito Margaritondo

Table 9	**Table 10**	**Table 11**	**Table 12**
Amaya Albalat	Cristina Ponce	Ana Belan	Ann Van Eetvelt
Assunta Sansone	Dora Moffatt	Dominic Campopiano	Avalon Phillips
Ellie Smith	Ewen Calder	Dylan Torrance	Felicity Wilson
Gerben van Ooijen	Leo Yin	Federico De Filippi	Hazel Harrop
Ianna Borloti	Matt Broadbent	Irina Guliaeva	Helaena Fine
Jed Hawes	Melissa Ramsay	Jessica Montoya	Matthew Swaffer
Pratiti Nanda	Rosie Street-Jeakings	Katie Hendrick McCrone	Mihaela Crisan
Rose Parsa	Victory Ulamen	Lara Dasar	Olivia Gray
Zofia Farkowska	Zunaira Aman	Laura Arbanas	Sezny Gall
		Maria Filippakopoulou	Taylor McCarthy
Table 13	**Table 14**		
Ava Drake	Alex Wang		
Holly Armstrong	Aoife Ong		
Ivan Pocrnic	Cesar Mendoza Martinez		
Jacob Peatfield-Muter	Fengqianrui Chen		
Jennifer Harbottle	Hope Obasi		
Joohwan Won	Megan Saathoff		
Joy Edwards-Hicks	Sander Granneman		
Peter Ashdown	Stephen Jenkins		
Rebecca Hilgenhof	Sujith Surendranath		
Rosie Gallagher	Zachary Bloxham		

CONCLUSIONS AND ACKNOWLEDGEMENTS

Our student reps, supported by Symposium academic hosts, Dr Sam Miller and Dr Attila Molnar, and the EastBio team, have worked with dedication and enthusiasm to deliver the 2026 Symposium on research in an evolving world you'll be attending in June 2026.

We have had a lot of fun planning the Symposium and we are confident that you'll have a lot of fun taking part in it! The planners – first and second-year students representing the EastBio partner institutions and our EDI student reps – addressed the complex brief comprehensively, giving you much more than its essential element, research presentations by first and second-year students (oral, via poster or a video). They brought together academic and non-academic experts to discuss careers in research and industry, the value of a placement as part of the PhD journey and workshops on communication and networking. Our fabulous EDI student reps have worked with commitment to ensure a fascinating panel of speakers on equality and inclusion with a focus on women in STEM. We are, finally, delighted that so many former EastBio students have returned to share with you insights from their current stage of their careers - in academia, industry or third sector.

We're proud of all our students whose work is on display these two days as they navigate a research environment that keeps changing but remains focused on shared values and goals; we're thankful for the generosity of organisers and guests that make this event a genuine opportunity to interact on the challenges and the potential of authentic collaboration across disciplines and sectors that shores up the necessary evidence-based, human-centered research and understanding that improves all our lives.

Have a wonderful day or two with our community of students and academics!

Dr Maria Filippakopoulou (she/her)

EastBio Partnership Manager

EASTBIO STUDENT REP ORGANISERS

Many thanks to our student reps who worked so hard to organise this symposium.

Zunaira Aman

Laura Arbanas

Helaena Fine

Melissa Ramsay

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Ghazal Sharifan

Jakub Teahan

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