Introduction to the DLA and application process

DLA Team

What we will cover

Overview of the BBSRC Doctoral Training Partnership
- The team
- The partnership
- Our research areas
- Structure of the programme
- Cohort training outside the lab

Applying to the programme
- Eligibility
- Application process

Questions and answers from the audience

Meet the Nottingham BBSRC DLA team

Professor Zoe Wilson
DLA Director

Professor Sara Goodacre
Deputy DLA Director

Maria Richards
DLA Programme Manager

Gerry Tonks
DLA Project Support Officer

Mandy Gill
Project Officer

Sandra Rose
EDI and Welfare Officer

Alice Haslam
EDI and Welfare Officer

The Nottingham DLA Partnership

The Nottingham BBSRC DTP is funded by the Biotechnology and Biological Sciences Research Council (BBSRC) and has been training postgraduate researchers since 2012

- Programme Partners include Rothamsted Research, Research Complex at Harwell, Diamond Light Source, National Biofilms Innovation Centre
- CASE Partners are industrial settings that are attached to specific studentships

- A diverse community of over 180 PhD students
- An alumni community of over 280 graduates

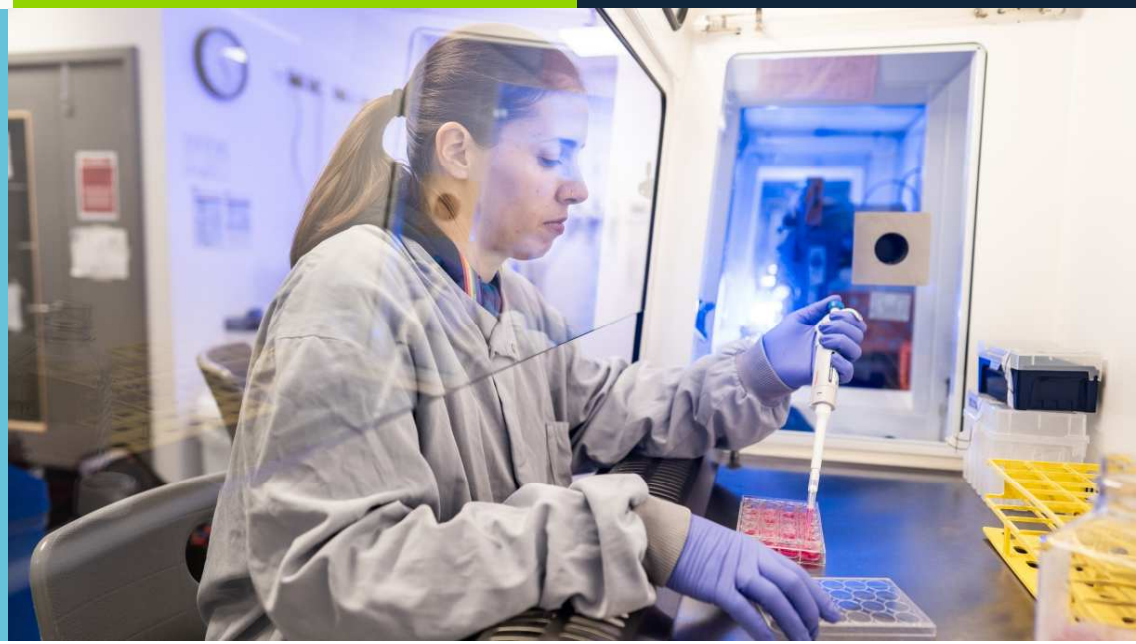
Led by the University of Nottingham in partnership with Nottingham Trent University

Our research themes

Bioscience for Human Health

Biotechnology for Sustainable Growth

Sustainable Agriculture and Food



Our Programmes

Standard Programme	CASE Programme
4 year programme	
Recruited to the programme	Recruited to a specific project
Mandatory induction	
1 x 10-week lab rotations	Start work on project immediately
Professional Internship for PhD Students (PIPS) - 3 month placement in year 3	Industry partner placement – you will spend 3-12 months of your studentship with your industry partner
Annual Training Week (year 1-3)	
Annual Conference	

You can apply to **either** the standard programme and/or the CASE programme, but it must be within the same cluster.

2026 CASE Projects currently open

Supervisor	Partner	School	Project Title
Hany Elsheikha	European Scientific Council Companion Animal Parasites	Veterinary Medicine and Science	Harnessing genomics, ecology, and behavioural data to unravel flea acquisition pathways in UK companion animals
Ian Mellor	Syngenta	Life Science	Identifying and characterising insecticidal neurotoxic peptides from the centipede, Scolopendra hardwickei, venom
Nicholas Girkin	Syngenta	Biosciences	Net Zero Rice: Unravelling the role of root exudates in rice for low emission protein consumption
Jonathan Hirst	Sygnature Discovery	Chemistry	Quantum computing applications in bioscience for human health
Vincenzo Di Bari	Adamo Foods	Biosciences	Designing Low-UPF Mycelium-Based Meat Alternatives: Linking Structure and Proteins Bio-Accessibility to Sensory Performance
Qian Yang	Magnum Ice Cream Company	Biosciences	Sweetness at Subzero: Sugar Reduction Strategies in Alternative Protein Ice Cream

Training

- You will be joining the DLA as a cohort of students – building a wide ranging personal and professional network

- You will have access to high quality training opportunities throughout your studies which will support your skills development, including:

    - Research technique development
    - Good research practice
    - Mathematical and computational skills
    - Career training
    - Entrepreneurship, Commercialisation and Innovation
    - Writing, Presentation skills, Thesis and Viva Prep

Training


Do you need to
know about
accessibility?


The
Nottingham
BBSRC DTP

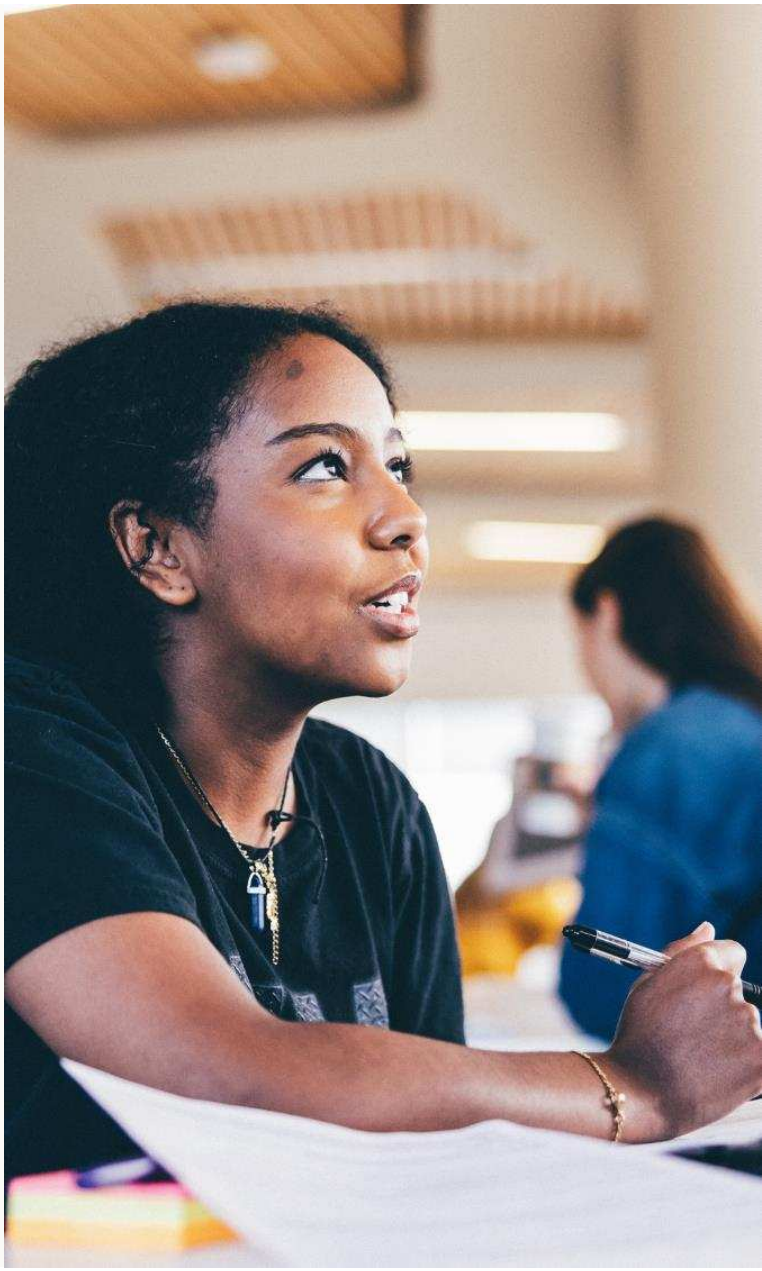

UKRI
Research Complex
at Harwell


University of
Nottingham
NOTTINGHAM
TRENT UNIVERSITY
UKRI
Welcome to
the Nottingham
BBSRC DTP


The Nottingham
BBSRC DTP

Training: Some Examples

- **Cohort based training throughout the PhD:**
- Cohort team building events and challenge days
- Excellence in Research Practice
- Data Science & Digital Research Skills training
- EDI-focussed training options such as Disability Awareness, Gender Awareness, Anti-Racism etc.
- Development needs analysis & reflective practice training
- Communication, presentation & project management skills
- Lab skills relevant to clusters
- Research Ethics and Responsible Research
- Researcher Academy training opportunities – short courses to support researcher skills and knowledge



Funding

- The four year programme is fully-funded
- The DLA studentship includes fees at the home level, a tax-free stipend and funding to support your research and training
- For 2025/26 the tax-free stipend is £20,780
- We can recruit up to 30% of the cohort from our international applicants and fee waiver scholarships will cover the difference between home and international fees.

University of Nottingham
UK | CHINA | MALAYSIA

NTU Nottingham Trent University

UKRI Biotechnology and Biological Sciences Research Council

Applying to the Nottingham BBSRC DLA - Eligibility

Nationality

- Applications are open to candidates with home (UK) fees status and international fee status.
- If English isn't your first language, you will also need to meet the relevant English language requirements. An IELTS score of 6.5 (no less than 6.0 in any element) is required, though we also accept alternative qualifications.

Applying to the Nottingham BBSRC DLA - Eligibility

Grades

- 2.1 or above in a relevant undergraduate degree from a UK university, or equivalent earned outside of the UK
- 2.2 in an undergraduate degree from the UK, or equivalent earned outside of the UK, plus a relevant Masters degree, or relevant work experience

Individual eligibility queries should be sent to bbdtp@nottingham.ac.uk.
We are not able to address these questions today.

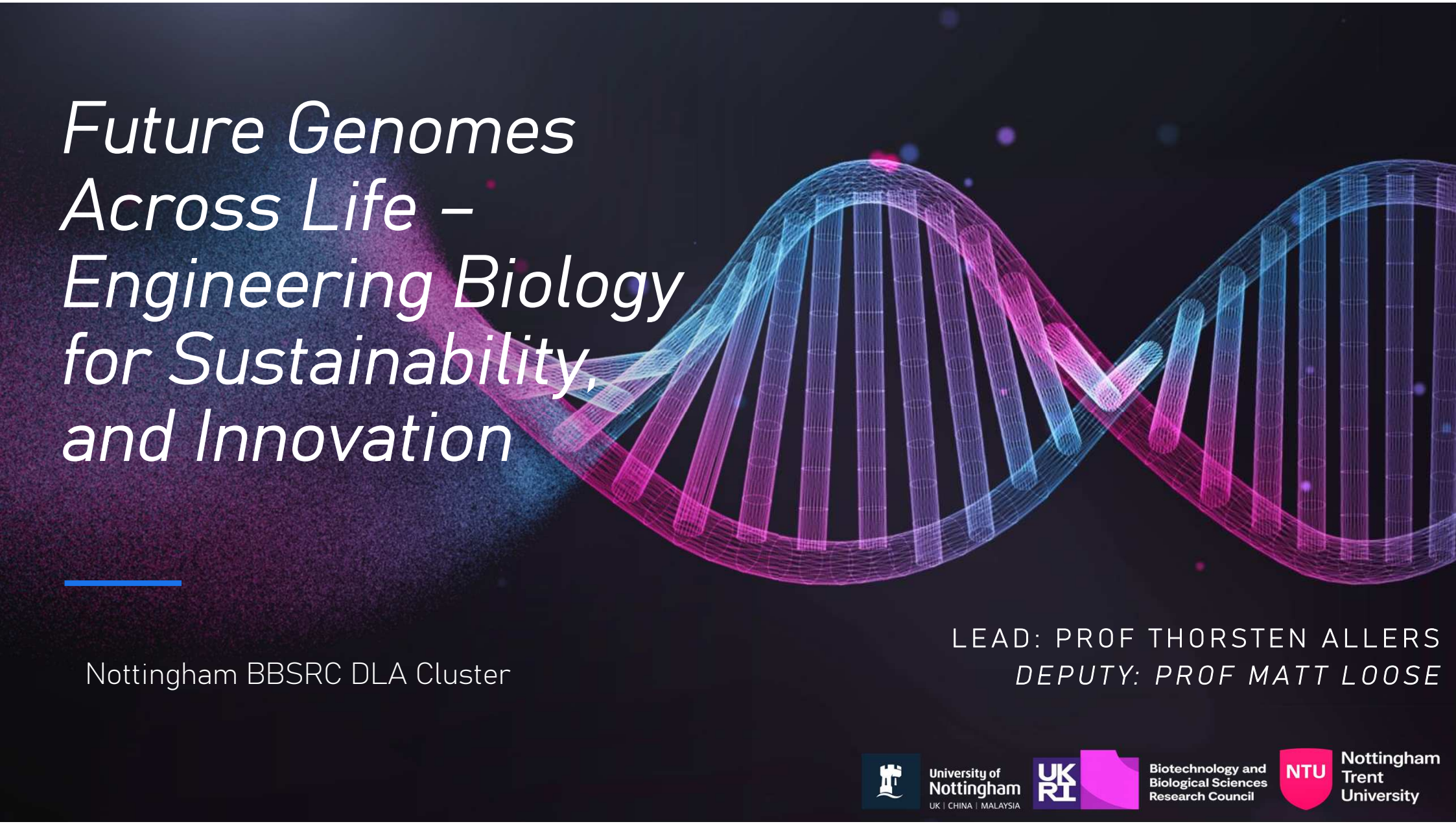
Applying to the Nottingham BBSRC DTP

- Go to https://www.nottingham.ac.uk/bbdtp/apply/apply-online.aspx
- Read all guidance notes
- Click on ‘Apply now’
- Complete online application form
- Remember to exclude any personal identifiable information in your cluster specific questions
- You can only apply once per academic year

Cluster presentation

Profesor Matt Loose

Future Genomes Across Life – Engineering Biology for Sustainability, and Innovation



Nottingham BBSRC DLA Cluster

LEAD: PROF THORSTEN ALLERS

DEPUTY: PROF MATT LOOSE

University of Nottingham
UK | CHINA | MALAYSIA

UKRI Biotechnology and Biological Sciences Research Council

NTU Nottingham Trent University

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

Engineering genomes and enzymes

- Exploiting Genomes
- Discovery Biology
- Engineering Biology

using bioinformatics and DNA/RNA sequencing technologies to interrogate the wealth of genomic dark matter from the three domains of life: archaea, eukaryotes and bacteria

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

using genetics, biochemistry, structural biology, and cell imaging to leverage genomic dark matter, and thereby uncover novel enzymes and biological processes

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

using synthetic biology and combinatorial biodesign to harness these novel enzymes and processes for sustainability and innovation

Engineering genomes and enzymes

- Exploiting Genomes
- Discovery Biology
- Engineering Biology

People

Lesley Hoyles
Matt Loose
Ruman Rahman
Keeley Brookes
Ylenia Chiari
Stuart Smith
Sarah Blott
Maria Rosa Domingo-Sananes
Bill Wickstead
Conor Meehan
Alasdair Hubbard
Hany Elsheikha (CASE)
Aditi Borkar
Ramiro Alberio

Engineering genomes and enzymes

- Exploiting Genomes
- Discovery Biology
- Engineering Biology

Training Skills

Bioinformatics and Genomics
DNA and RNA sequencing technologies
Data Visualization
Computational Structural Biology
R, Python and more
Machine Learning
Drug Development

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

Industry Connections

Oxford Nanopore Technologies
UKHSA
NHS
Ugenome
Compass Bioinformatics
Gates Foundation
Storm Therapeutics
Mars Petcare UK
ESCCAP

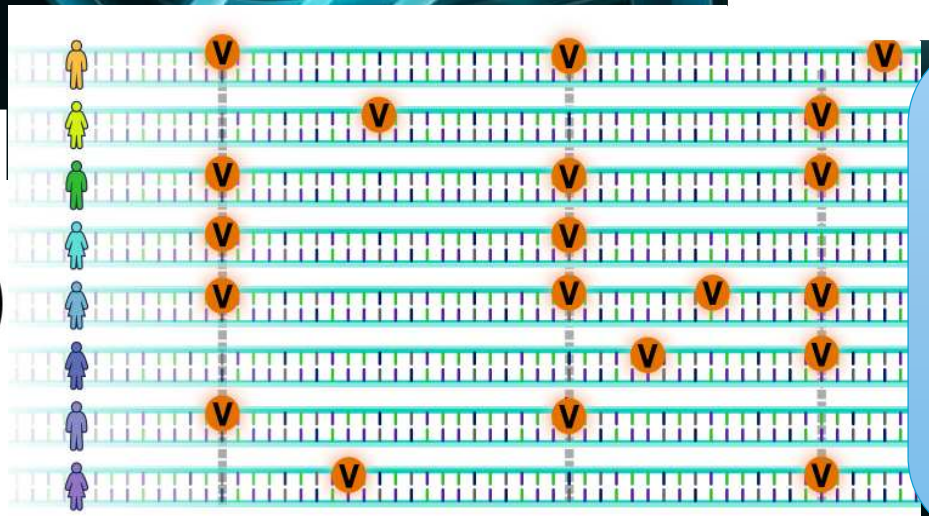
Exploiting Genomes

RESEARCH QUESTION:
Can we use the genome to predict aging traits?

Keeley Brookes

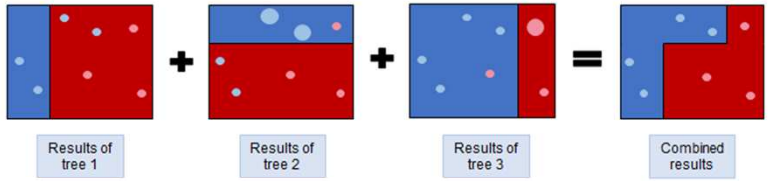
GATTACA
Genetics & Genomics Hub

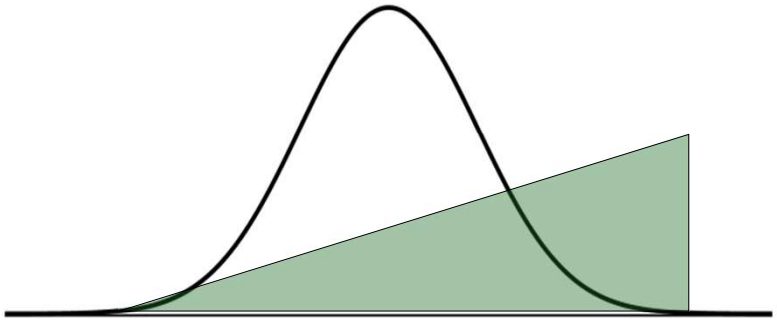
NOTTINGHAM TRENT UNIVERSITY



AdaBoost:

- Combining **weak learners** (decision trees)
- Assigning **weights to incorrect values**
- **Sequential tree growing** considering past mistakes





Polygenic risk scores

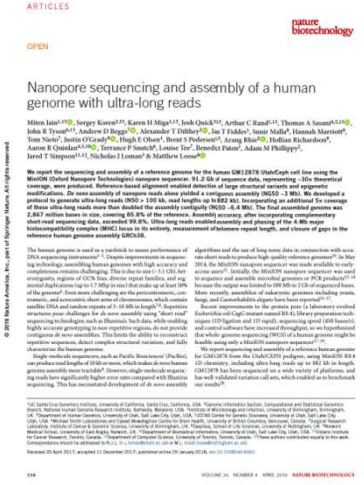
From Polygenic risk scores to machine learning classification algorithms can we determine gene paths to identify and differentiate between molecular heterogeneity for human traits.

#genotypingdata #ukbiobank #agingtraits #bioinformatics #modelling #RNAseq(?)

DNA Sequencing, Bioinformatics and Methylation

Matthew Loose

Research questions: How can Genomics answer challenging questions across biology?



ARTICLES

OPEN

nature biotechnology

Nanopore sequencing and assembly of a human genome with ultra-long reads

Neuro-Oncology

2035

ROBIN: A unified nanopore-based assay integrating intraoperative methylome classification and next-day comprehensive profiling for ultra-rapid tumor diagnosis

Key Points

- A single assay can provide intraoperative methylome classification and next-day comprehensive molecular profiling, including single nucleotide variants, copy number variants, and structural variants.
- In 50 prospective intraoperative cases, concordance with standard of care was achieved in 90% of cases.

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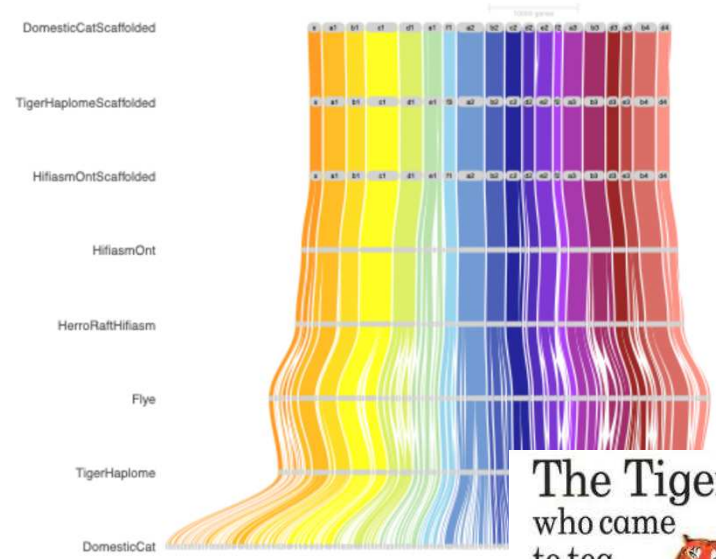
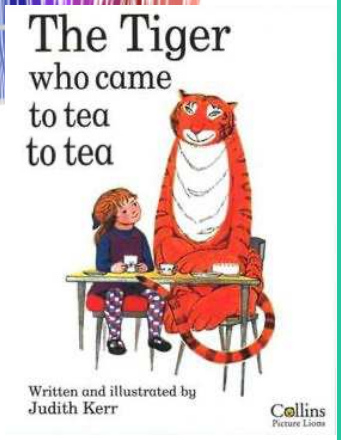
New brain tumour test a game changer, experts say

Gemma says the new test could have spared her daughter an extra surgery

Rob Sissons, BBC News, Nottingham and Dan Martin, BBC News, East Midlands

Techniques: DNA/RNA sequencing, Epigenomics, Real Time Data Analysis
DEEPSEQ – UoN NGS Facility

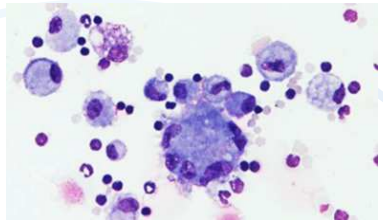




Sarah Blott – mechanisms of complex disease

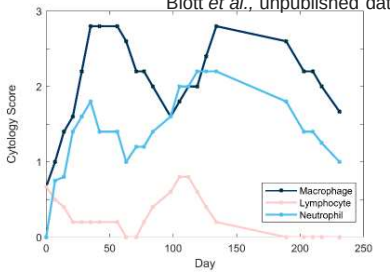
- Computational biology
- Genome-wide association studies (GWAS)
- Transcriptomics (RNA-seq)
- Whole genome sequencing (Nanopore)
- Genotype-by-environment studies
- Aim is to understand the mechanisms underlying complex disease and to identify key genes involved in disease risk
- Multi-species (including human and horse)

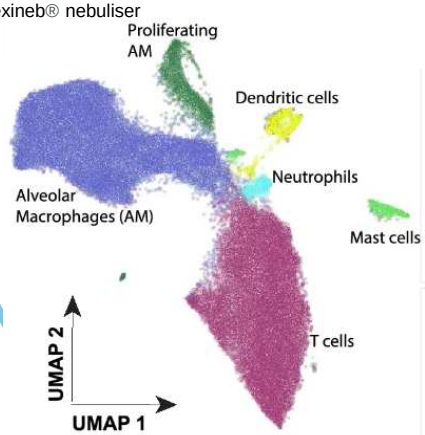
Flexineb® nebuliser



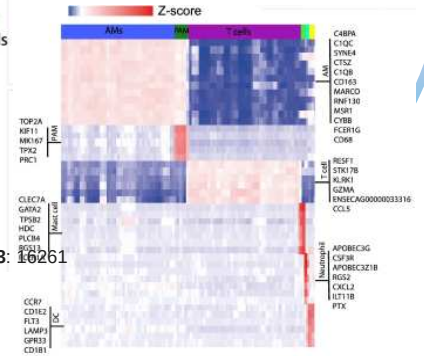
Morini *et al*. (2023) *Vet. Sci.***10**: 527

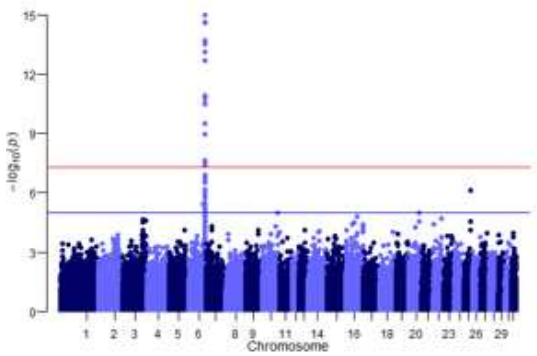
Blott *et al.*, unpublished data

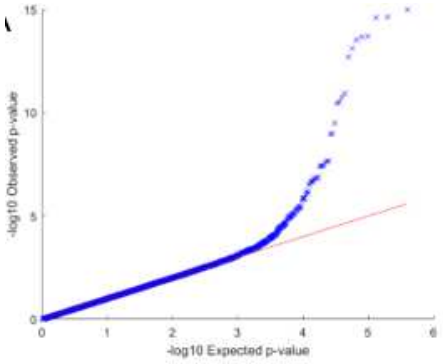




Riihimäki *et al. (2023) Sci Rep* **13**: 16261







Metabolic disease

Asthma and exercise-induced pulmonary haemorrhage

Maria Rosa Domingo Sananes

Evolution and Function of Cellular Networks and Genomes

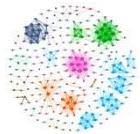
Work across the diversity of living organisms

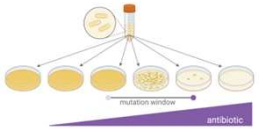
Key questions:

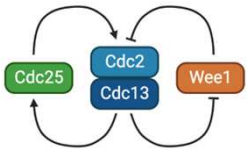
- How do genomes and networks change?
- How do complex functions evolve?
- Why are cellular networks the way they are?

Recent projects:

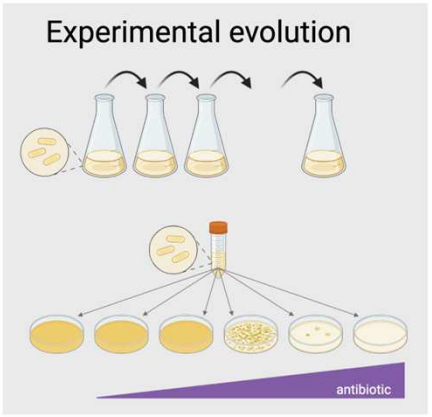
- Identifying genetic interactions in prokaryote pangenomes using machine learning (Beavan et al, PNAS, 2024)
- The importance of genetic background in the evolution of antimicrobial resistance (James et al, npj Antimicrobials and Resistance, 2024)
- Recovery of defects in mitotic entry through experimental evolution in fission yeast

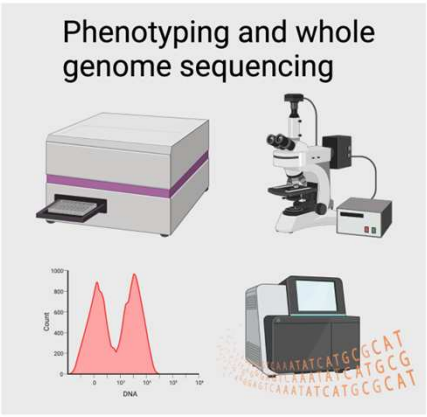


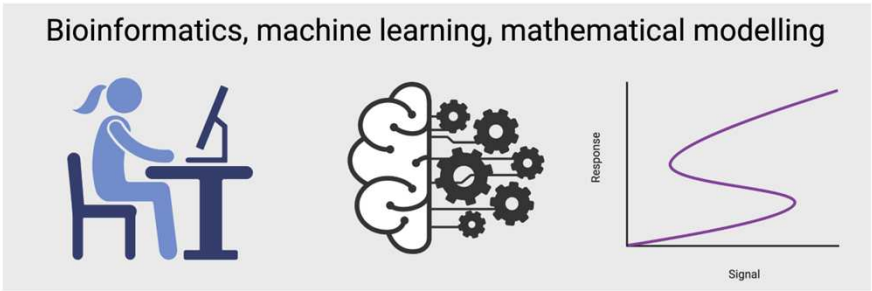




Techniques and research approaches:

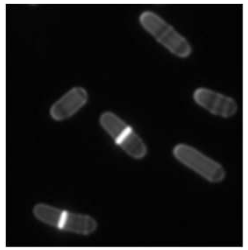






Experimental systems:

Fission yeast Bacteria

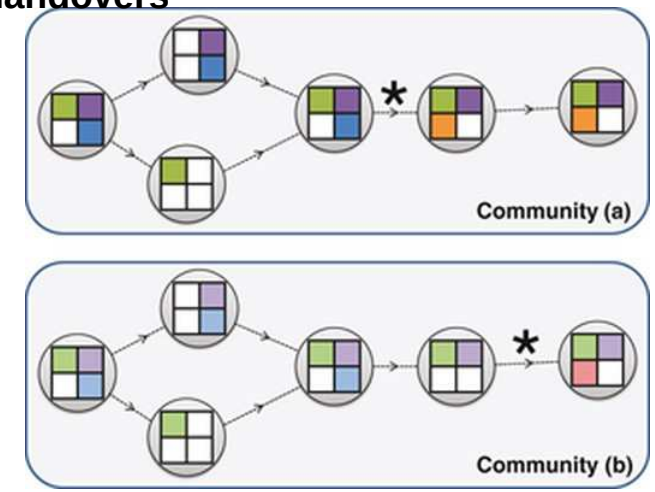


Nottingham Trent University

Community-level interactions and evolution in the microbiome

Conor Meehan

Community integration and metabolic handovers



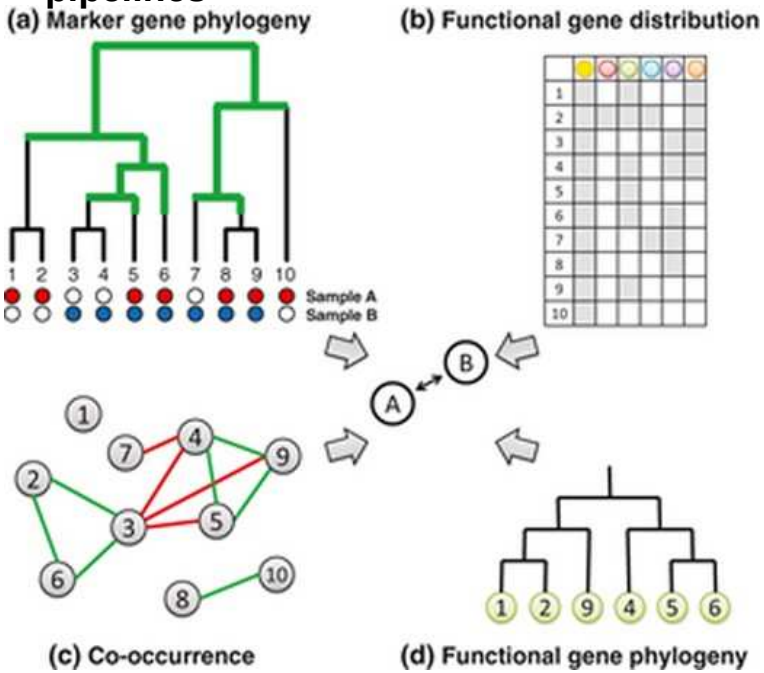
Research questions:

- What functional profiles define a microbial community?
- Can we manipulate the community to improve host health?

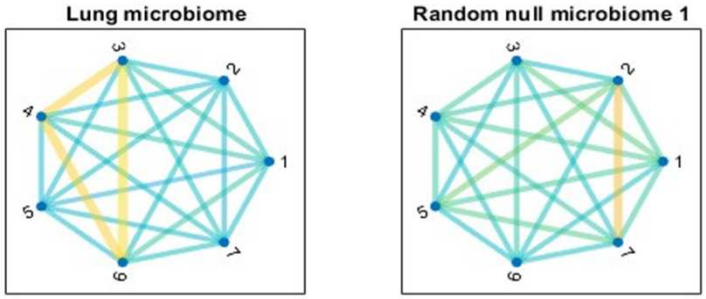
Key techniques:

- Bioinformatics/data analysis
- Microbiome profiling
- Comparative genomics & phylogenetics
- Network analysis and metabolic profiling

Functional community analysis pipelines



Network modelling of community members



Key papers

https://doi.org/10.1093/gbe/evu050

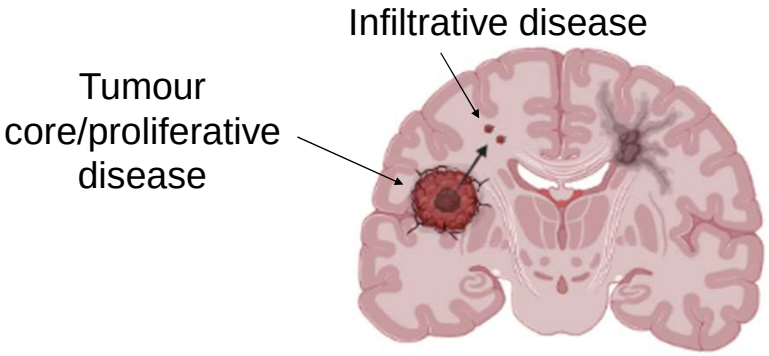
https://doi.org/10.1111/1574-6976.12035

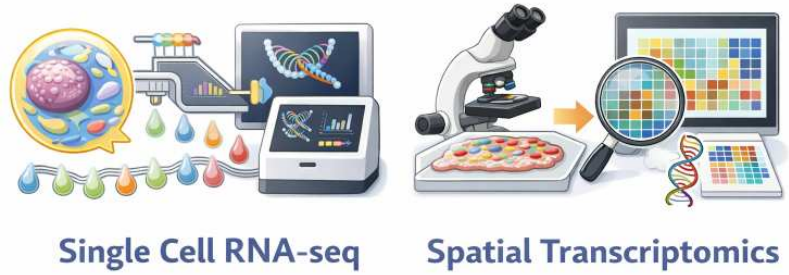
Genomic Profiling of Malignant Brain Cancer Invasive Phenotypes

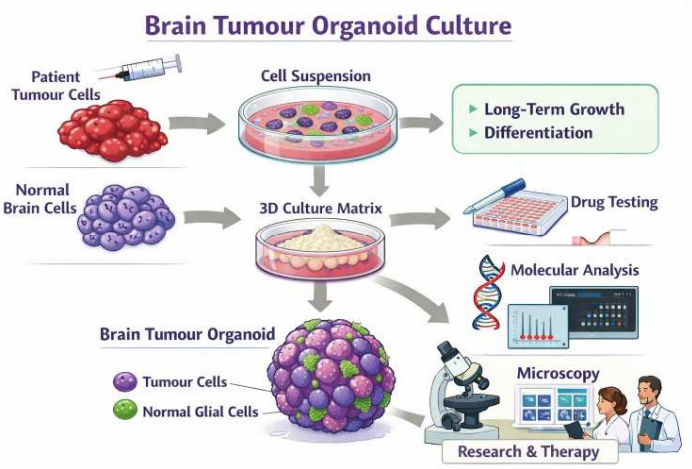
Ruman Rahman

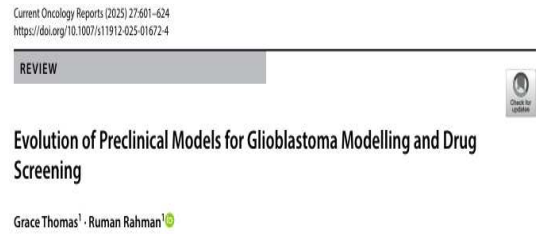
Research questions:

- Are genomic profiles of infiltrative disease distinct from proliferative disease?
- Is infiltrative disease characterized by sub-clonal variation?









Current Oncology Reports (2025) 27:601–624
https://doi.org/10.1007/s11912-025-01672-4

REVIEW

Evolution of Preclinical Models for Glioblastoma Modelling and Drug Screening

Grace Thomas[1] · Ruman Rahman[1]

https://doi.org/10.1007/s11912-025-01672-4

Andrieux et al. Genome Medicine (2023) 15:48
https://doi.org/10.1186/s13073-023-01207-1

Genome Medicine

RESEARCH Open Access

Spatially resolved transcriptomic profiles reveal unique defining molecular features of infiltrative 5ALA-metabolizing cells associated with glioblastoma recurrence

Geoffroy Andrieux[†], Tonmoy Das[1,2†], Michaela Griffin[3], Jakob Straehle[4], Simon M. L. Paine[3], Jürgen Beck[4], Melanie Boerries[1,5], Dieter H. Heiland[5,6,4,7], Stuart J. Smith[3], Ruman Rahman[3*] and Saijh Chakraborty[1,2*]

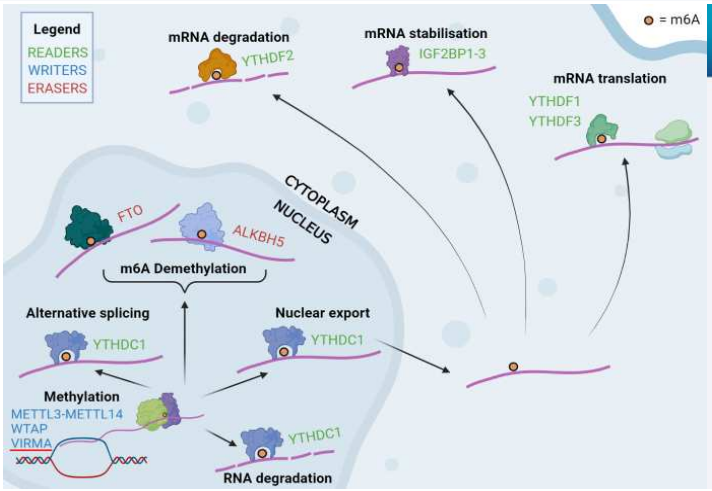
https://doi.org/10.1186/s13073-023-01207-1

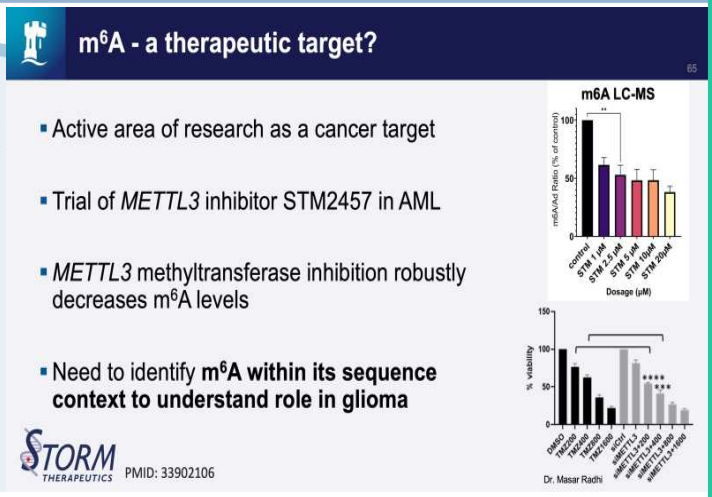
Techniques:
Patient-derived organoid culture; single cell RNA-sequencing; spatial transcriptomics; Nanopore sequencing; in vitro drug screening

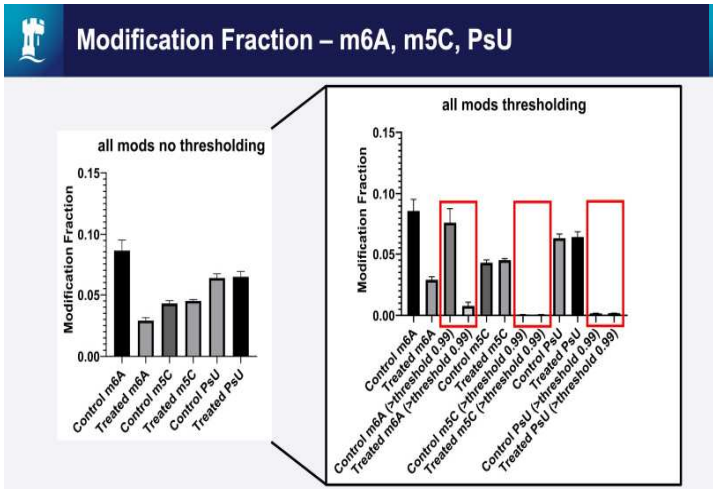
https://www.nottingham.ac.uk/medicine/people/ruman.rahman

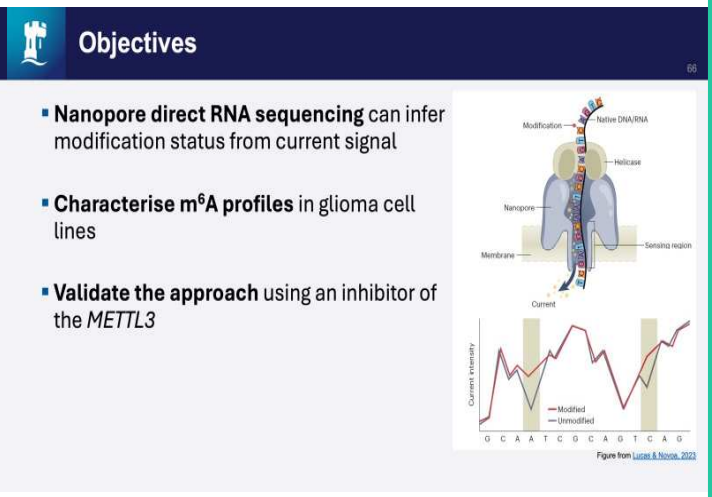
Regional Variation in Brain Tumour Genetics and Epigenetics – Stuart Smith, Clinical Assoc Prof, Neurosurgery

- Previous studies have shown regional transcriptional variation in malignant brain tumours
- DNA methylation a key factor in diagnosis and prognosis
- Seeking to understand variation and the influence of RNA methylation in high grade brain tumours
- Potential therapeutic avenue either through global alteration of RNA methylation or by targeting highly involved specific pathways







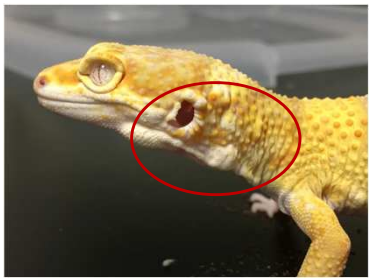


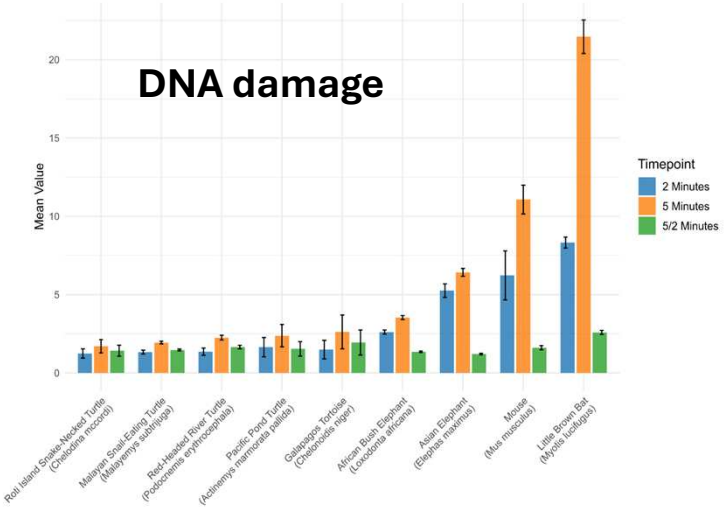
Molecular basis of variation in longevity and cancer rates

Dr. Ylenia Chiari

What are the molecular basis of variation in longevity across vertebrates?

Why do some species barely get cancer while others have extremely high cancer prevalence?





Hastings et al. (in review)
Bulls et al. (BMC Research Notes 2025)
Glaberman et al. (BioScience 2025)
Genome Biology & Evolution (2021)
GeroScience (2021)
Nature Ecology & Evolution (2019)
Nature Reviews Cancer (2018)

Genome sequencing and assembly → Comparative Analyses → Candidate Pathways and Genes → Cellular Phenotypes → Mechanisms

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Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

People

Thorsten Allers (CASE)
Yan Liao
Jasmine Ono
Stephen Gray
Ed Bolt
David Negus
Rian Griffiths
Sally Wheatley
Rob Wilkinson
Rachael Tarlinton
Jonathan Thomas
Cat Gadelha
Cuifeng Ying

Engineering genomes and enzymes

- Exploiting Genomes
- Discovery Biology
- Engineering Biology

Training Skills

Molecular biology and genetics
genomics
cell biology
protein expression and biochemistry
CRISPR genome editing
Microscopy
Transcriptomics
Proteomics
single-molecule label-free techniques

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

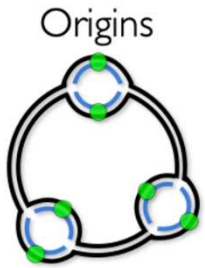
Industry Connections

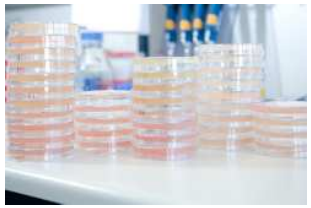
New England Biolabs
Oxford Nanopore Technologies
GALVMed
Phenotypeca
AHDB
European College of Veterinary Microbiology

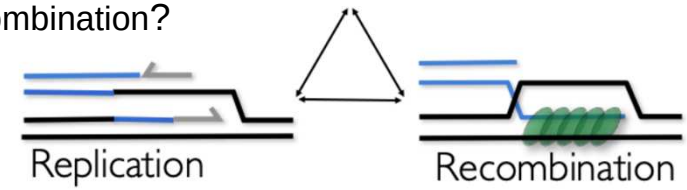
DNA Replication, Recombination, and Repair in Archaea

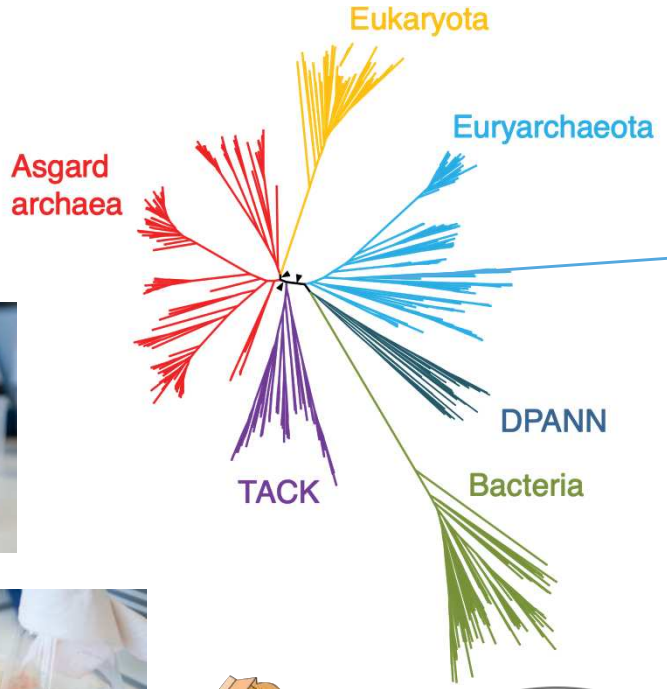
Thorsten Allers

Research questions: How does DNA replication operate in the absence of origins? How is replication linked to recombination?









Haloferax volcanii

OPEN BIOLOGY

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Review

Haloferax volcanii—a model archaeon for studying DNA replication and repair

Patricia Pérez-Arnaiz[1], Ambika Dattani[2], Victoria Smith[3] and Thorsten Allers

School of Life Sciences, University of Nottingham, Queen's Medical Centre, Nottingham, UK

Cite this article: Pérez-Arnaiz P, Dattani A, Smith V, Allers T. 2020 *Haloferax volcanii*—a model archaeon for studying DNA replication and repair. Open Biol. **10**: 200293. http://dx.doi.org/10.1098/rsob.200293

Received: 11 September 2020
Accepted: 9 November 2020

Subject fens: microbiology/molecular biology/genetics/biochemistry

Keywords: Archaea, *Haloferax volcanii*, DNA replication, DNA repair, homologous recombination

Author for correspondence: Thorsten Allers
e-mail: thorsten.allers@nottingham.ac.uk

†These authors contributed equally to this work.

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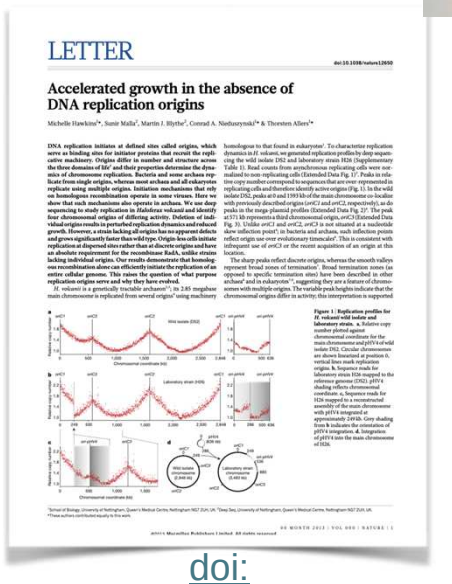
1. *Haloferax volcanii*

Pioneering work in the 1970s by Carl Woese and other microbiologists led to a profound reorganization of the tree of life. Woese's discovery of Archaea was initially based on small-subunit ribosomal RNA sequences [1], but was soon consolidated by work from Wolfram Zillig on RNA polymerase [2] and Otto Kandler on cell membranes [3]. Eventually, archaea took their place as members of a new *bla* domain, alongside Eukarya and Bacteria [4]. Archaea share morphological features with bacteria—both are prokaryotic cells—but they show dramatic differences at the enzymatic level. The information processing machinery found in archaea, which includes the enzymes involved in DNA replication, is strikingly similar to that of eukaryotes. In the decades since their discovery, archaea have been shown to be neither 'exotic bacteria' nor 'simplified eukaryotes'; instead, they display a mosaic of eukaryotic, bacterial and uniquely archaeal features. Furthermore, the recent discovery of Asgard archaea has provided support for a two-domain tree of life, where eukaryotes emerge from within the archaeal clade [5–7]. Thus, further study of archaea is needed to deepen our understanding of fundamental processes such as DNA replication and repair, and to shed light on our evolutionary history.

One of the model archaeal species is *Haloferax volcanii*, which is a member of the phylum Euryarchaeota. It is a halophile with disc-shaped cells and grows optimally at 45°C in 1.7–2.5 M NaCl, similar to the conditions found in the Dead Sea where it was first isolated in 1975 [8]. *Haloferax volcanii* cells do not possess a rigid cell wall but are instead surrounded by a glycoprotein surface (S-) layer, which can be a target for glycosylation [9]. *Haloferax volcanii* use a 'salt-in' mechanism to deal with the highly halophilic environment; this mechanism ensures that the internal salt concentration is maintained at the same molarity as the external environment [10,11]. The genome of *H. volcanii* is highly polyploid, with a copy number of approximately 20 copies per cell, as well as being relatively GC rich (approx. 65%) [12,13].

In the 1980s and 1990s, ground-breaking work from the groups of W. Ford Doolittle, Moshe Mevarech and Mike Dyall-Smith developed techniques for the transformation and genetic manipulation of *H. volcanii*, enabling researchers to



LETTER

doi:10.1038/nature12650

Accelerated growth in the absence of DNA replication origins

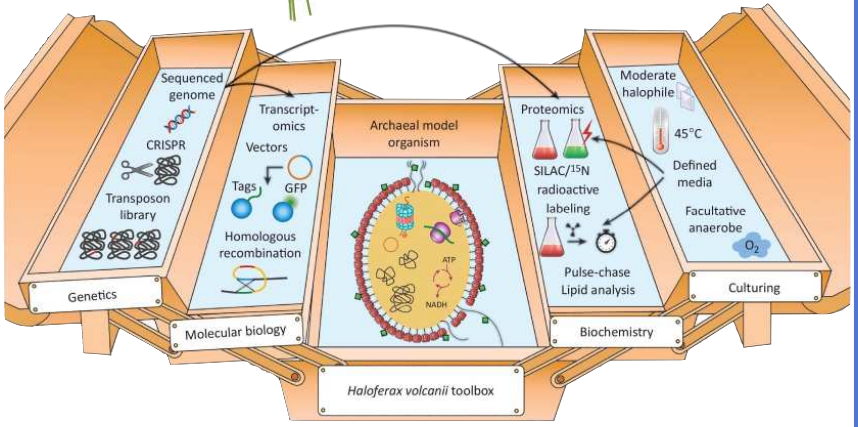
Michelle Hawkins*, Sunir Malla*, Martin J. Blythe*, Conrad A. Nieduszynski* & Thorsten Allers*

DNA replication initiates at defined sites called origins, which serve as binding sites for initiator proteins that recruit the replicative machinery. Origins differ in number and structure across the three domains of life and their properties determine the dynamics of chromosome replication. Bacteria and some archaea replicate from single origins, whereas most archaea and all eukaryotes replicate using multiple origins. Initiation mechanisms that rely on homologous recombination operate in some viruses. Here we show that such mechanisms also operate in archaea. We use deep sequencing to study replication in *Haloferax volcanii* and identify four chromosomal origins of differing activity. Deletion of individual origins results in perturbed replication dynamics and reduced growth. However, a strain lacking all origins has no apparent defects and grows significantly faster than wild type. Origin-less cells initiate replication at dispersed sites rather than at discrete origins and have an absolute requirement for the recombinase RadA, unlike strains lacking individual origins. Our results demonstrate that homologous recombination alone can efficiently initiate the replication of an entire cellular genome. This raises the question of what purpose replication origins serve and why they have evolved.

H. volcanii is a genetically tractable archaeon[9–11], its 2.85 megabase main chromosome is replicated from several origins[12] using machinery homologous to that found in eukaryotes[1]. To characterize replication dynamics in *H. volcanii*, we generated replication profiles by deep sequencing the wild isolate DS2 and laboratory strain H26 (Supplementary Table 1). Read counts from asynchronous replicating cells were normalized to non-replicating cells (Extended Data Fig. 1)[7]. Peaks in relative copy number correspond to sequences that are over-represented in replicating cells and therefore identify active origins (Fig. 1). In the wild isolate DS2, peaks at 0 and 1593 kb of the main chromosome co-localize with previously described origins (*oriC1* and *oriC2*, respectively), as do peaks in the mega-plasmid profiles (Extended Data Fig. 2)[9]. The peak at 571 kb represents a third chromosomal origin, *oriC3* (Extended Data Fig. 3). Unlike *oriC1* and *oriC2*, *oriC3* is not situated at a nucleotide skew inflection point[1]; in bacteria and archaea, such inflection points reflect origin use over evolutionary timescales[6]. This is consistent with infrequent use of *oriC3* or the recent acquisition of an origin at this location.

The sharp peaks reflect discrete origins, whereas the smooth valleys represent broad zones of termination[1]. Broad termination zones (as opposed to specific termination sites) have been described in other archaea[1] and in eukaryotes[14], suggesting they are a feature of chromosomes with multiple origins. The variable peak heights indicate that the chromosomal origins differ in activity; this interpretation is supported

Figure 1 | Replication profiles for *H. volcanii* wild isolate and laboratory strain. **a**, Relative copy number plotted against chromosomal coordinate for the main chromosome and pHV4 of wild isolate DS2. Circular chromosomes are shown linearized at position 0, vertical lines mark replication origins. **b**, Sequence reads for laboratory strain H26 mapped to the reference genome (DS2). pHV4 shading reflects chromosomal coordinate. **c**, Sequence reads for H26 mapped to a reconstructed genome of the chromosome with pHV4 integrated at approximately 2491kb. Grey shading from **b** indicates the orientation of pHV4 integration. **d**, Integration of pHV4 into the main chromosome of H26.



Techniques: molecular biology, microbial genetics, and genome editing

doi: 10.1098/rsob.200293

doi: 10.1038/nature12650

https://www.nottingham.ac.uk/life-sciences/people/thorsten.allers

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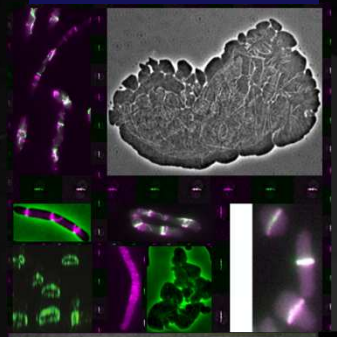
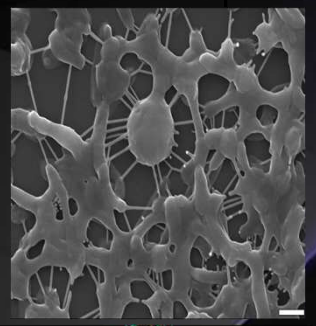
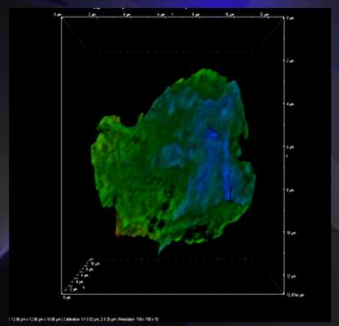
Extreme Habitats

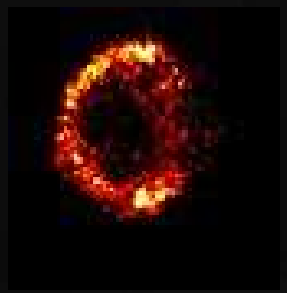
Understanding how life thrives at the edge to drive innovations in biotechnology and human health

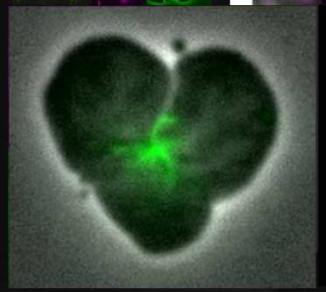
Genetic engineering	Microscopy imaging	Structural biology	Biophysical characterisation

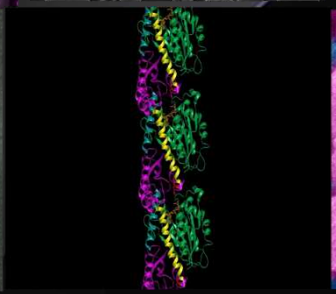


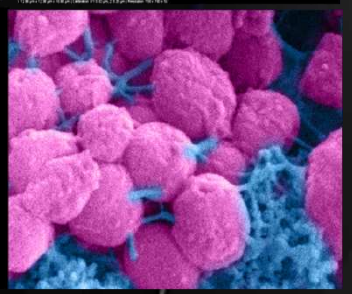












Liao et al *Nature Microbiology*, 2021
Hamm & Liao et al *Nature Communications*, 2024
Liao et al *Nature Communications*, 2025

Dr. Yan Liao

- Survival
- Dynamics
- Interaction
- Composition
- Diversity
- Bio-engineering

Join the Liao Lab to explore the edge of life: yan.liao@nottingham.ac.uk

Dr. Sally P. Wheatley*: Survivin, Cell Biology & Biochemistry

Work in my lab focusses on the multi-tasking adaptor protein, **Survivin,** which brings other proteins together to facilitate certain cellular functions. Most notably, it is essential for mitosis, can inhibit cell death (apoptosis) and is overabundant (and meddlesome) in cancer cells. Always collaborative, the survivin interactome has led us to explore many cell signalling areas involved in genomic regulation including, but not limited to:

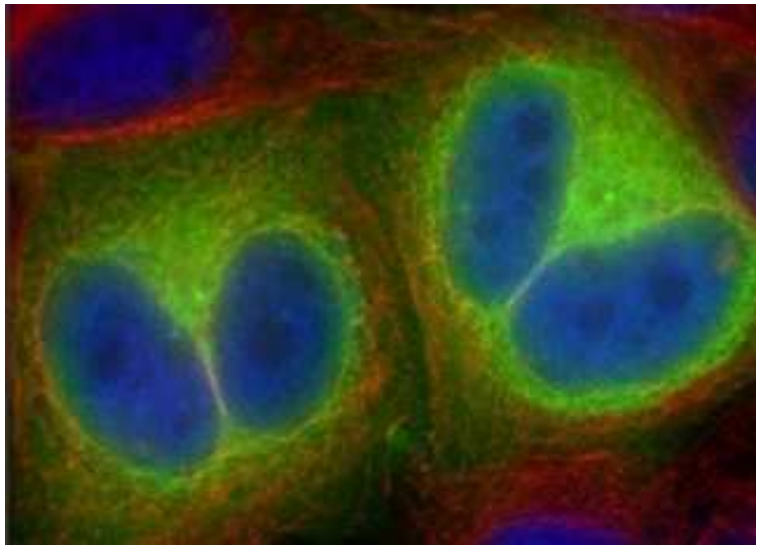
- **Mitosis and Cytokinesis**

  see Abdelkabir et al., 2025 doi:10.1002/1878-0261.70141
- **Transcriptional reprogramming** via the PRC2 complex in conditions of stress (hypopxia, starvation etc).

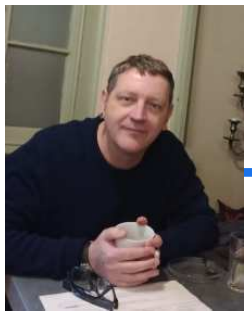
  see Vaidya et al., 2025 (JCS, in press)
- Genomic instability in **cancer** cells.
- Apoptotic and DNA damage response to oncotherapeutic agents.
- **Entosis**, a cellular form of “cannibalism”.

Techniques include, cell culture, advanced fluorescence imaging, protein-protein interactions, molecular biology/ cloning/ mutagenesis, and many more.

*Orcid ID: 0000-0002-9550-8979



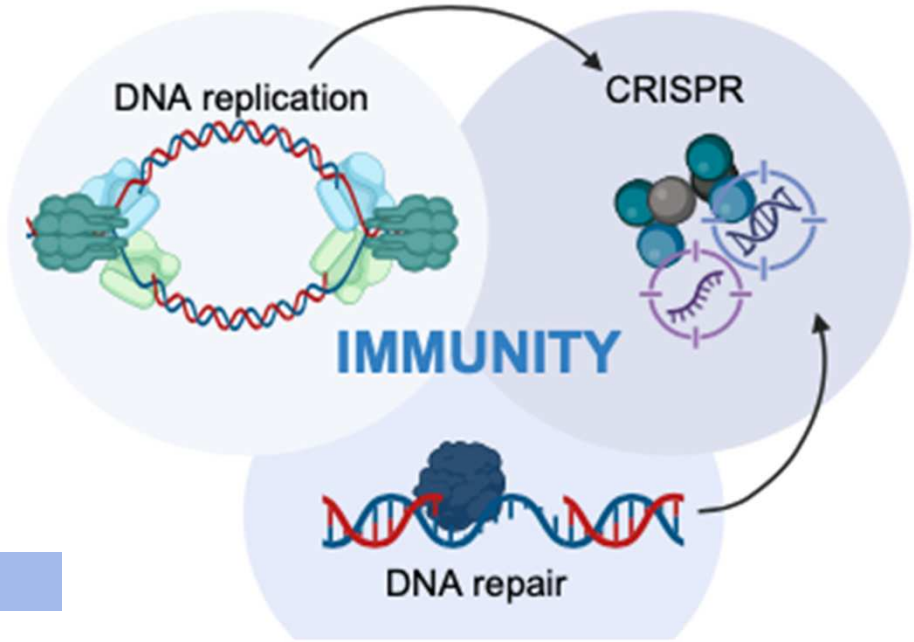
Binucleation in HeLa cells as a result of cytokinesis failure caused by expression of a mutant form of survivin.
Survivin-GFP mitochondria nuclei scale bar 20 microns.



Prof. Ed Bolt
Lab D58

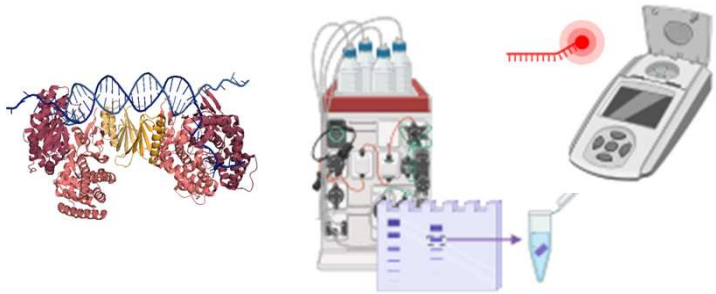
QMC Med School

What we do:

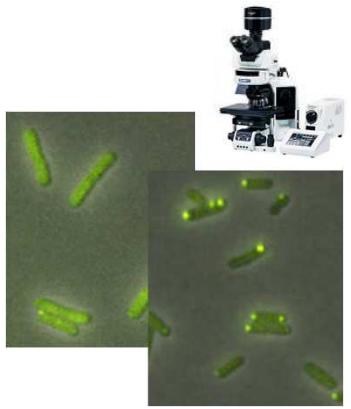


How we do it:

Protein-DNA Biochemistry & Biophysics

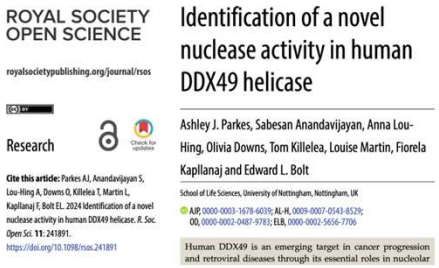


CRISPR/Cas9,
Prime editing of human genomes



Live cell imaging of proteins

Some recent papers:



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Research

Identification of a novel nuclease activity in human DDX49 helicase

Ashley J. Parkes, Sabesan Anandavijayan, Anna Lou-Hing, Olivia Downs, Tom Killelea, Louise Martin, Fiorela Kapllanaj and Edward L. Bolt

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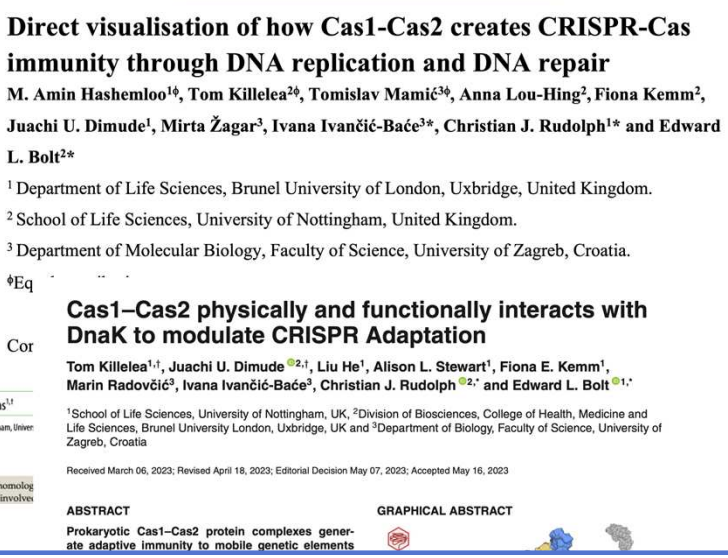
Research

The human HELQ helicase and XRN2 exoribonuclease cooperate i loop resolution

J. M. Pan, H. Betts, A. Cubbon, L. He, E. L. Bolt and P. Soultanas



Direct visualisation of how Cas1-Cas2 creates CRISPR-Cas immunity through DNA replication and DNA repair

M. Amin Hashemloo[1ϕ], Tom Killelea[2ϕ], Tomislav Mamić[3ϕ], Anna Lou-Hing[2], Fiona Kemm[2], Juachi U. Dimude[1], Mirta Žagar[3], Ivana Ivančić-Baće[3*], Christian J. Rudolph[1*] and Edward L. Bolt[2*]

[1] Department of Life Sciences, Brunel University of London, Uxbridge, United Kingdom.

[2] School of Life Sciences, University of Nottingham, United Kingdom.

[3] Department of Molecular Biology, Faculty of Science, University of Zagreb, Croatia.

Cas1–Cas2 physically and functionally interacts with DnaK to modulate CRISPR Adaptation

Tom Killelea[1,†], Juachi U. Dimude[2,†], Liu He[1], Alison L. Stewart[1], Fiona E. Kemm[1], Marin Radovčić[3], Ivana Ivančić-Baće[3], Christian J. Rudolph[2,*] and Edward L. Bolt[1,*]

[1]School of Life Sciences, University of Nottingham, UK, [2]Division of Biosciences, College of Health, Medicine and Life Sciences, Brunel University London, Uxbridge, UK and [3]Department of Biology, Faculty of Science, University of Zagreb, Croatia

Received March 06, 2023; Revised April 18, 2023; Editorial Decision May 07, 2023; Accepted May 16, 2023

ABSTRACT

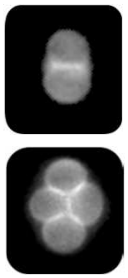
Prokaryotic Cas1–Cas2 protein complexes generate adaptive immunity to mobile genetic elements

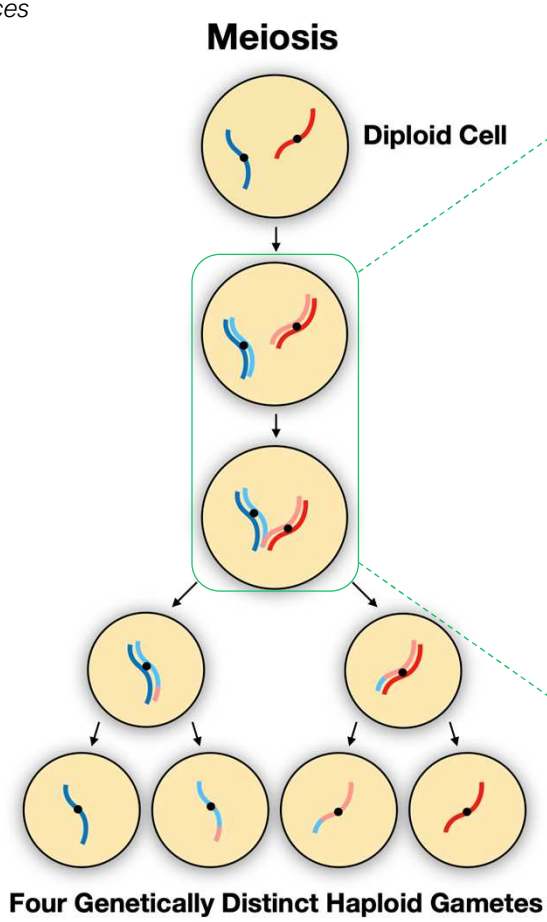
GRAPHICAL ABSTRACT

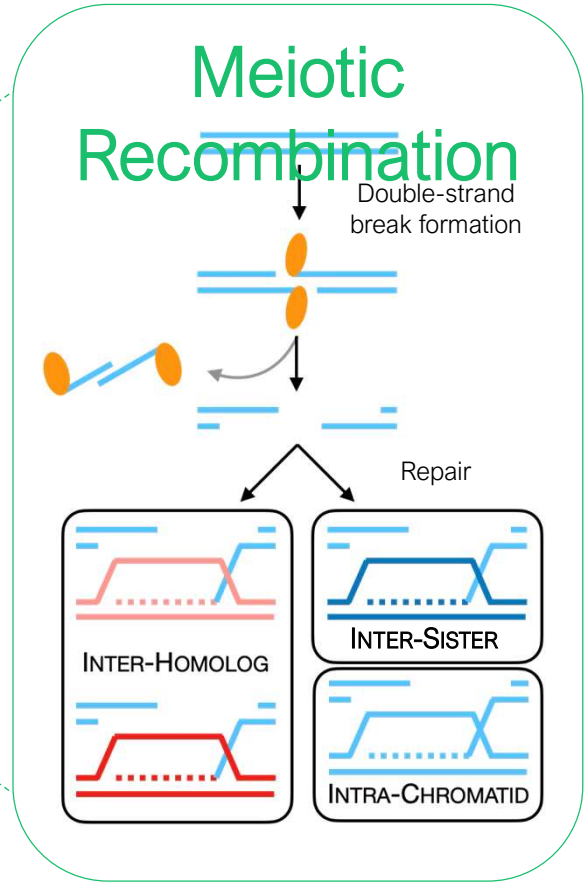
How is DNA repair regulated during meiosis to generate viable gametes?

Stephen Gray, University of Nottingham

Budding Yeast
Saccharomyces cerevisiae







Research Questions

Identifying genetic regulators of double-strand break repair

- Hundred of breaks occur in each cell during meiosis.
- When repair goes wrong, inaccurate chromosome segregation takes place leading to chromosomal aberrations

How does the cell ensure it repairs the break in the correct way?
How does the cell ensure it repairs the break from the correct template and locus?
https://doi.org/10.1098/rsob.130019
https://doi.org/10.1093/nar/gkad650

Regulating meiosis through ubiquitination

- Meiosis requires several unique and highly regulated processes to accurately divide the genome to produce viable haploid gametes
- Ubiquitination functions to degrade proteins at the correct developmental stage

How is ubiquitination regulated during meiosis?
https://doi.org/10.1016/j.celrep.2020.107858
https://www.biorxiv.org/content/10.1101/2023.07.24.550435v1

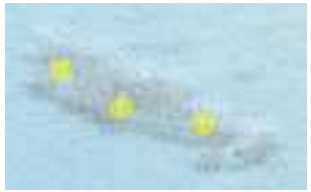
Techniques

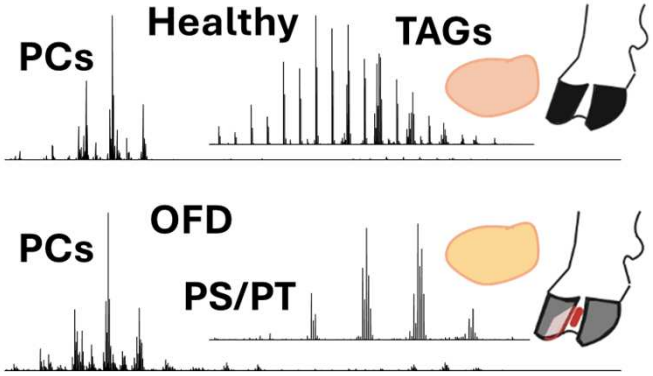
• Yeast Genetics • Molecular Biology • Cloning • Microscopy
• FACS • CRISPR Screens • Whole Genome Sequencing
• Bioinformatics • Genomics and Proteomics

stephen.gray@nottingham.ac.uk https://www.nottingham.ac.uk/life-sciences/people/stephen.gray www.genomedynamics.co.uk

Dr Rian Griffiths: Rian.Griffiths@nottingham.ac.uk **Surface Analysis and Imaging Mass Spectrometry** **Assistant Professor**

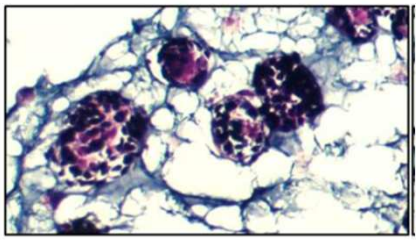
How I may be able to help you: **How could direct MS analysis of biomolecules from surfaces aid your research?**

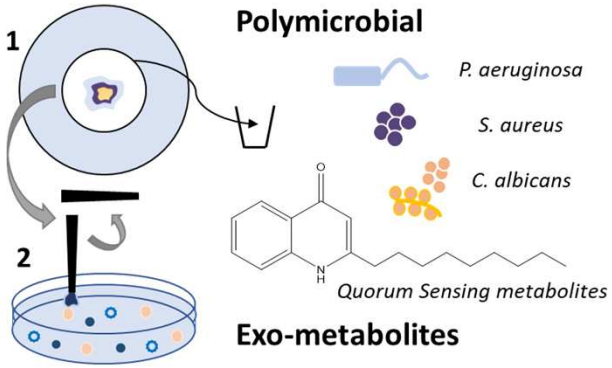


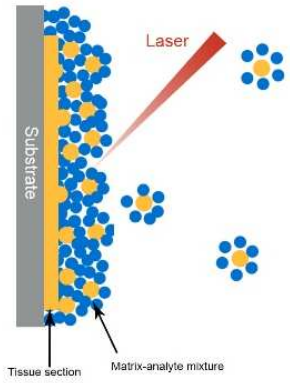


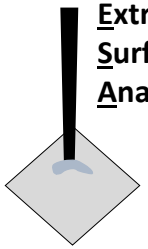
Sample surfaces examples:

- ***Tissue sections***
- ***Dried blood spot cards***
- ***Bacterial colonies***
- ***Biofilms***
- ***Hydrogels***









Secondary Ionisation Mass Spectrometry

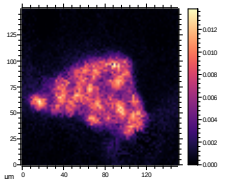
Matrix Assisted Laser Desorption Ionisation

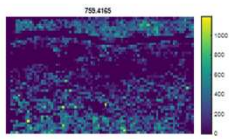
Liquid Extraction Surface Analysis

Spatial Resolution **Analytes/Biomolecules (mass)**

Typically 2 µm

1000 µm (1 mm)





Elements

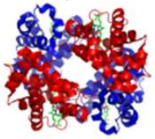
Amino Acids

Lipids

Peptides

Intact Proteins

Proteins Complexes



Rian.Griffiths@nottingham.ac.uk

University of Nottingham
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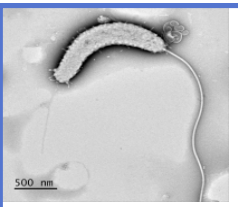


Developing the predatory bacterium *B. bacteriovorus* as a 'living antibiotic'

David Negus

Research questions:

- What are the underpinning molecular mechanisms which control of the predatory life cycle of *B. bacteriovorus*?
- How do prey bacteria escape predation and how can we overcome 'resistance' to predation?

npj | antimicrobials & resistance Review article

https://doi.org/10.1038/s44259-024-00048-1

How do Gram-negative bacteria escape predation by *Bdellovibrio bacteriovorus*?

Sourav Kumar Das & David Negus

Bdellovibrio bacteriovorus is a small predatory bacterium which reproduces by invading and killing Gram-negative bacteria. The natural antimicrobial activity of *B. bacteriovorus* has garnered interest for the potential to develop this predatory bacterium as a therapeutic agent. Transitioning *B. bacteriovorus* from 'bench to bedside' will require a complete understanding of all aspects of bacterial predation, including how prey species may escape predation. Here we discuss recent findings relating to how Gram-negative bacteria may escape predation.

doi.org/10.1038/s44259-024-00048-1

Staff Profile

@**davidnegus**.bsky.social

Nottingham Trent University

Annual Review of Microbiology ANNUAL REVIEWS

Predator Versus Pathogen: How Does Predatory *Bdellovibrio bacteriovorus* Interface with the Challenges of Killing Gram-Negative Pathogens in a Host Setting?

David Negus,[1] Chris Moore,[1] Michelle Baker,[1,2] Dhaarini Raghunathan,[1] Jess Tyson,[1] and R. Elizabeth Sockett[1]

[1]School of Life Science, University of Nottingham, University Park, Nottingham NG7 2UH, United Kingdom; email: David.Negus@nottingham.ac.uk, Christopher.Moore@nottingham.ac.uk, Michelle.Baker@nottingham.ac.uk, Dhaarini.Raghunathan@nottingham.ac.uk, Jess.Tyson@nottingham.ac.uk, Liz.Sockett@nottingham.ac.uk

[2]School of Computer Science, University of Nottingham, University Park, Nottingham NG7 2UH, United Kingdom

Keywords

bacterial predators, living antibiotics, antimicrobial resistance, predation

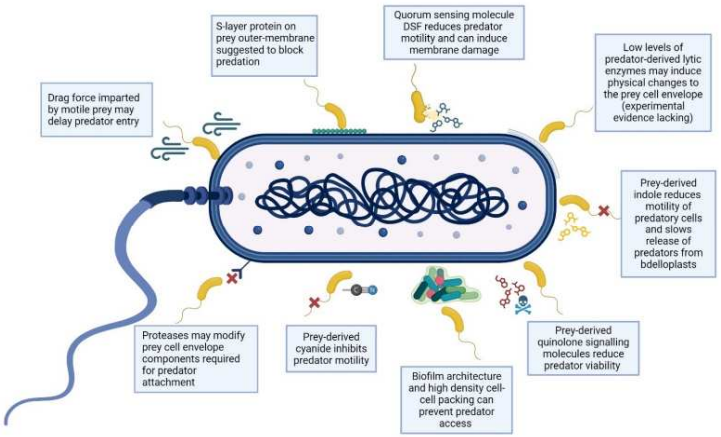
Abstract

Bdellovibrio bacteriovorus is a small deltaproteobacterial predator that has evolved to invade, reseal, kill, and digest other gram-negative bacteria in soils and water environments. It has a broad host range and kills many antibiotic-resistant, clinical pathogens in vitro, a potentially useful capability if it could be translated to a clinical setting. We review relevant mechanisms of *B. bacteriovorus* predation and the physiological properties that would influence its survival in a mammalian host. Bacterial pathogens increasingly display conventional antibiotic resistance by expressing and varying surface and soluble biomolecules. Predators coevolved alongside prey bacteria and so encode diverse predatory enzymes that are hard for pathogens to resist by simple mutation. Predators do not replicate outside pathogens and thus express few transport proteins and thus few surface epitopes for host immune recognition. We explain these features, relating them to the potential of predatory bacteria as cellular medicines.

doi.org/10.1146/annurev-micro-090816093618

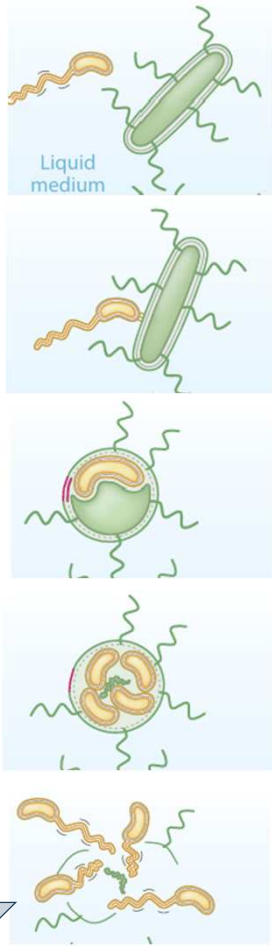
Methods / Techniques:

- Molecular biology / microbial genetics (cloning, gene tagging, gene deletions)
- Microscopy (fluorescence, TEM, SEM)
- Proteomics (protein expression, purification, mass spec)
- Genomics (genome sequencing, annotation, comparative genomics, RNA-seq)



How do prey escape predation?

Predatory life cycle



Genetics and Genomics of Adaptation

Jasmine Ono

University of Nottingham
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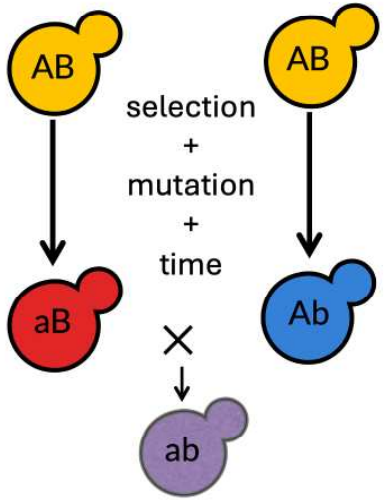
Key questions:

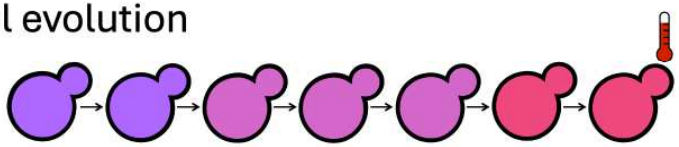
- Is adaptive evolution predictable?
- Why do species exist?

→What is the impact of genetic interactions.

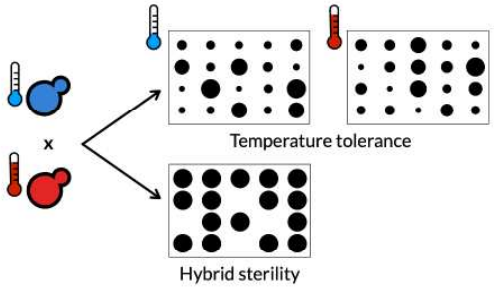


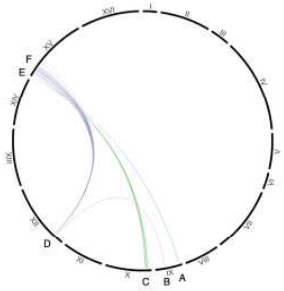
Main techniques:

Experimental evolution

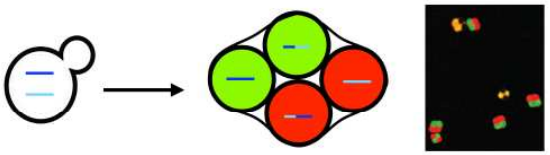


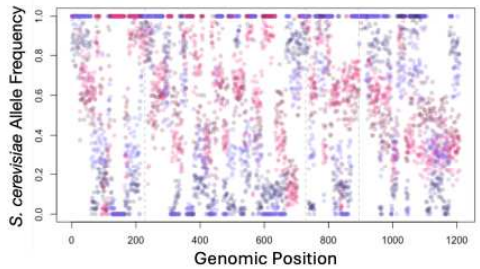
Whole-genome sequencing and trait mapping





Individual and population analysis





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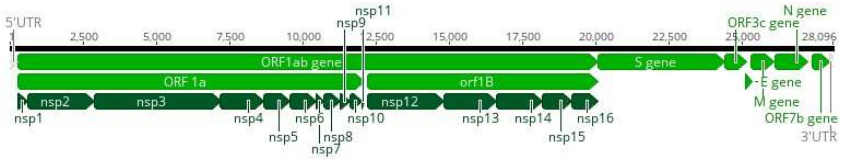
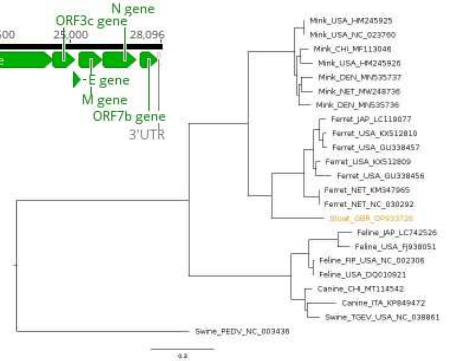
Rachael Tarlinton Research Interests Emerging viruses

- Anything from mice to elephants (literally)
- Tick borne diseases of Nigerian dogs
- Coronavirus (SARS-CoV-2) monitoring and sequencing in wildlife Social sciences work with small scale poultry holders and HPAI biosecurity measures
- Clinical specialist in Vet microbiology
- Bluetongue and Schmallenberg (ruminants)





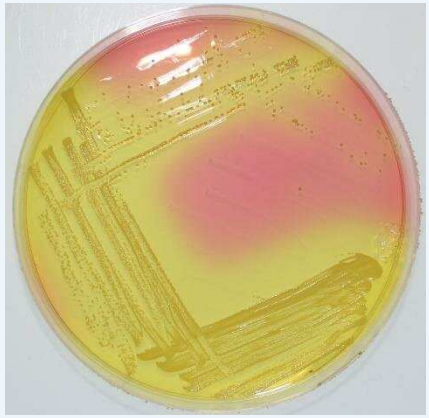
Population Genomics of Staphylococci

Nottingham Trent University

Jonathan C. Thomas

Research area: role of positive and balancing selection in driving genetic diversity and adaptation in *Staphylococcus* populations?

Investigation into how population structure among *Staphylococcus* species relates to their ability to cause disease versus persist as commensals



Techniques: whole-genome sequencing, qPCR, bioinformatics, RNA-seq

Relevant Publications:

- JC Thomas, L Zhang, DA Robinson Differing lifestyles of Staphylococcus epidermidis as revealed through Bayesian clustering of multilocus sequence types Infection, Genetics and Evolution 22, 257-264.
- CO Rimmer, JC Thomas Detection of positive selection driving antimicrobial resistance in the core genome of Staphylococcus epidermidis bioRxiv, 2024.09.30.615834

https://www.ntu.ac.uk/staff-profiles/science-technology/jonathan-thomas

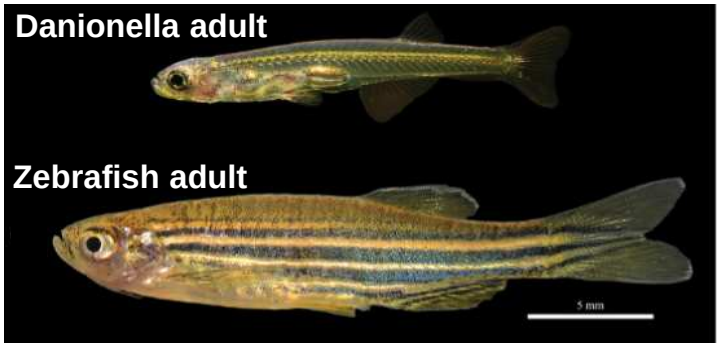
Rob Wilkinson

Rob.wilkinson@nottingham.ac.uk

Comparative Genomics to identify genetic regulators of Blood-Brain barrier (BBB) formation and function

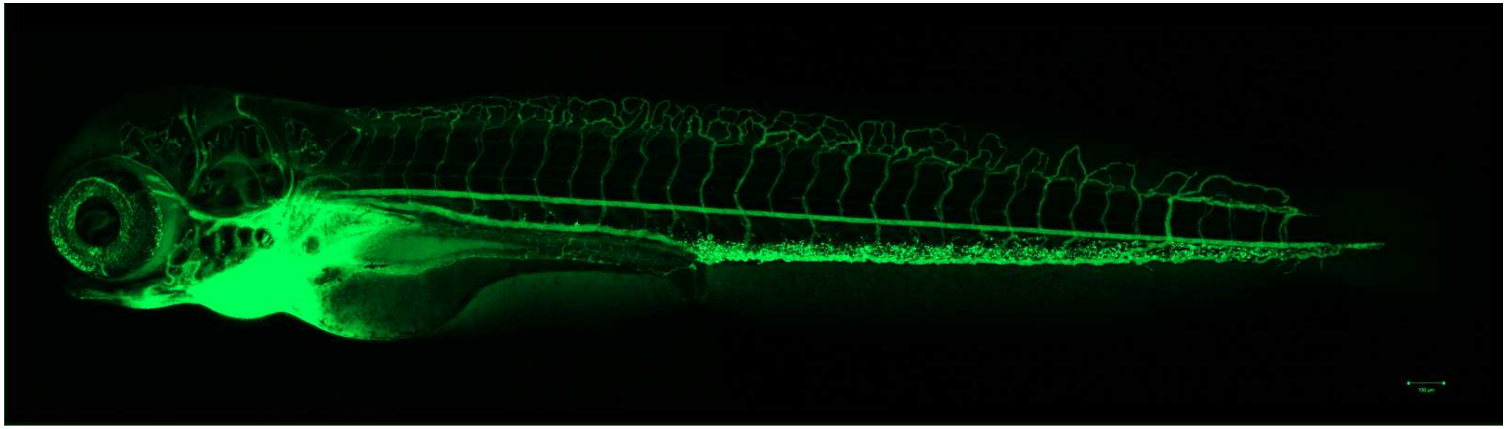
We use comparative genomics and genetic engineering to study how the BBB forms and functions. The BBB is a highly selective semi permeable barrier of specialised cells that acts as a gatekeeper protecting the brain from pathogens and toxins in the blood, while allowing nutrients to pass through.

We recently sequenced the genome of the transparent miniature glassfish ***Danionella cerebrum***, an emerging model in neurophysiology. *D. cerebrum* has the **smallest known vertebrate brain** (0.6mm^3). *Danionella* do not develop a skull roof, which means we can image the adult brain **non-invasively** throughout the life of the organism.

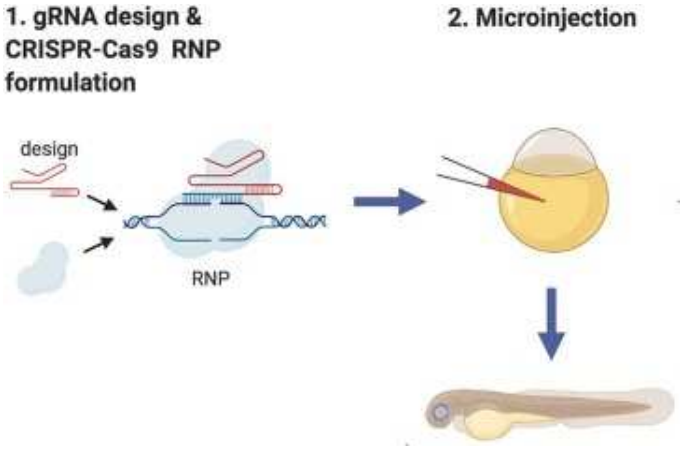


D. cerebrum and zebrafish are close evolutionary relatives, which means we can used establish genetic engineering approaches such as **CRISPR-Cas9** and transgenesis to knock out and fluorescently tag genes, this allows us to study the adult blood-brain barrier in *D. cerebrum* using live imaging.

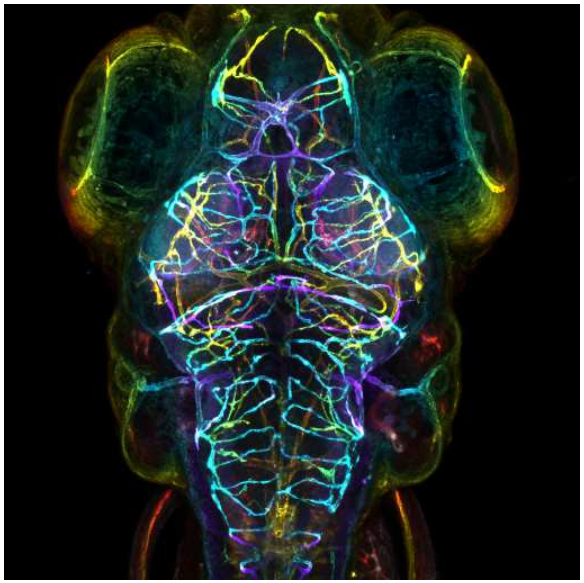
We want to identify genetic regulators of adult BBB permeability, which could provide therapeutic targets to modulate BBB function in human health and disease



Developing blood vessels in a 4 day *Danionella cerebrum* embryo



3. Genetically modified embryo (mutant/transgenic)



Blood-Brain Barrier in transgenic zebrafish embryo at day 5

Single-Molecule, Label-Free Insights into Enzyme Dynamics

Nottingham Trent University

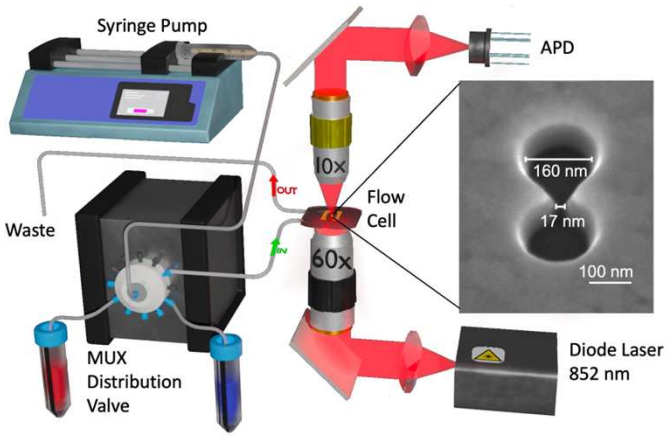
Advanced Optics & Photonics Lab

Cuifeng Ying

Department of Engineering

Nottingham Trent University

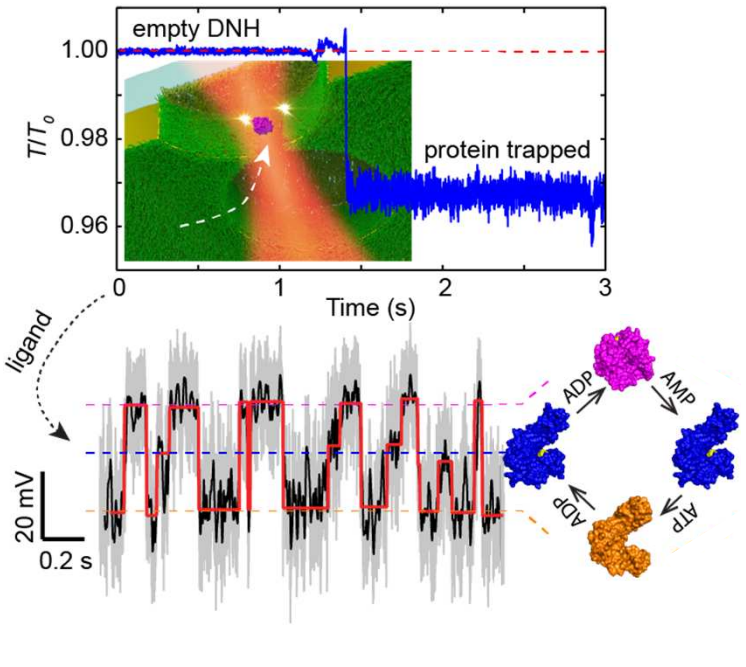
A **label-free, single-molecule** platform to characterise enzyme conformational dynamics in different solutions.

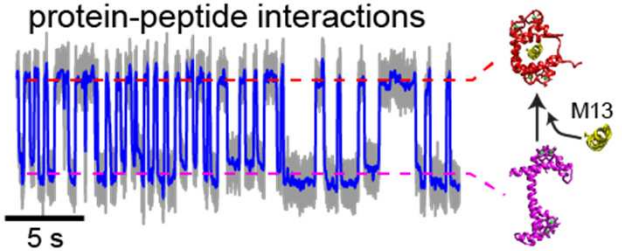


Plasmonic Nanotweezers can trap a **single, unmodified** enzyme in solution for hours, at the same

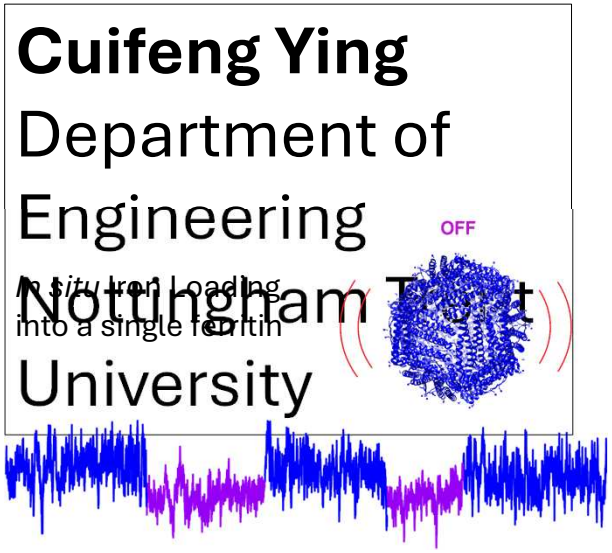
Application Examples:

Watching single enzyme at work

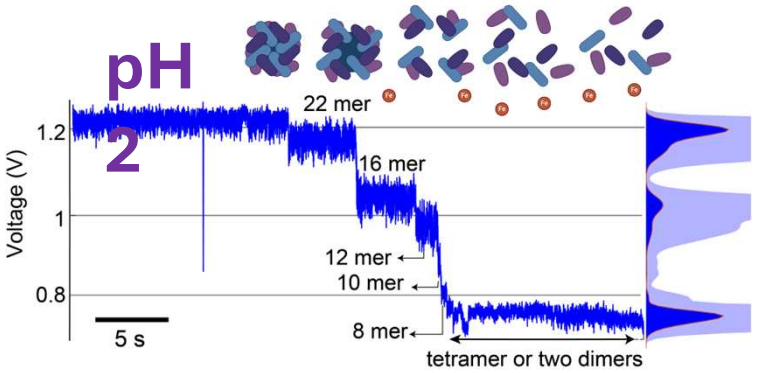




In situ iron Loading into a single ferritin



Disassembly kinetics of single ferritin



References:

Nanoletters 23, 3251-3258 (2023);

ACS nano 18, 15617-15626 (2024);

Inp Biosensing 1, 1-4 (2024)

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

People

John Heap
Ben Blount
Alex Faulds-Pain
Jack Leo
Rochelle Aw
Jack Bryant
Geoffrey Rivers
Andy Gill
Osvaldo Chara
Masaki Kinoshita
Ian Mellor
Sarah Kuehne

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

Training Skills

Combinatorial biodesign
synthetic pathways and chromosomes
high-throughput genetic tools and gene editing
mathematical modelling
fluorescent proteins and protein ligation systems
cell-free protein synthesis
tissue scaffolds and flow reactors

Engineering genomes and enzymes

Exploiting Genomes

Discovery Biology

Engineering Biology

Industry Connections

GlycoCell UKRI Engineering Biology Mission Hub
Pathfinder Bio
Iceni Glycoscience
Syngenta UK

Engineering genomes and enzymes

Exploiting Genomes

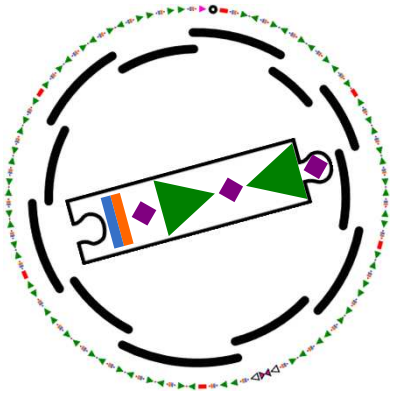
Discovery Biology

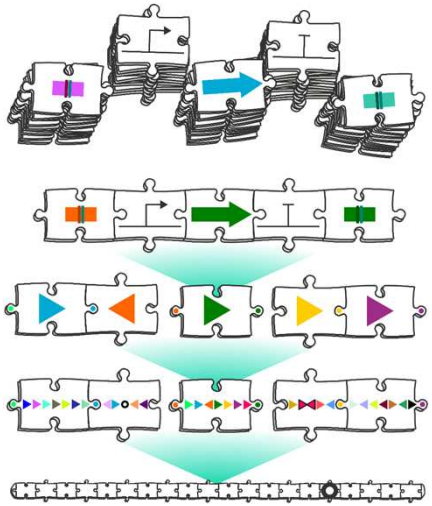
Engineering Biology

Ben Blount – Engineering Biology and Synthetic Genomics

NOTTINGHAM ENGINEERING BIOLOGY LABS

Advancing synthetic genome design and function to understand genome biology and allow bottom-up genome design





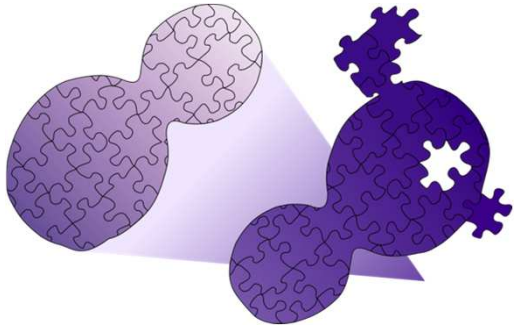
Developing news ways to build chromosome-scale DNA

GlycoCell
UKRI Engineering Biology Mission Hub

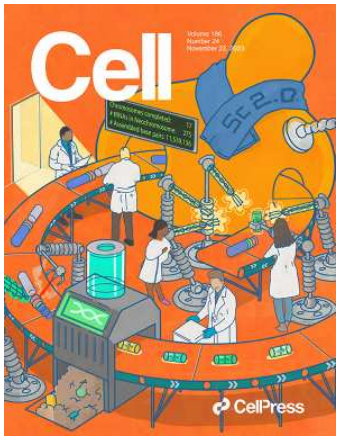
Engineering Biology to develop vaccines against fungal pathogens

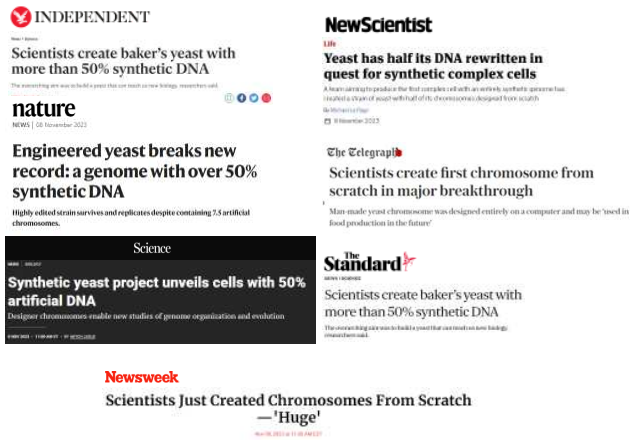
Visit from the UK Science Minister to announce GlycoCell

Evolving and engineering synthetic yeast strains for better biotechnology



Techniques: Synthetic biology, synthetic genomics, CRISPR genome engineering





Blount *et al*. (2023) Synthetic yeast chromosome XI design provides a testbed for the study of extrachromosomal circular DNA dynamics. ***Cell Genomics***

Xu *et al*. (2023) Trimming the genomic fat: minimising and re-functionalising genomes using synthetic biology. ***Nature Communications***

Blount *et al*. (2018) Rapid host strain improvement by in vivo rearrangement of a synthetic yeast chromosome. ***Nature Communications***

Schindler *et al*. (2023) Design, construction, and functional characterization of a tRNA neochromosome in yeast. ***Cell***

Blount. (2023) Synthetic bacterial genome upgraded for viral defence and biocontainment. ***Nature***

Awan *et al*. (2017) Biosynthesis of the antibiotic nonribosomal peptide penicillin in baker's yeast. ***Nature Communications***

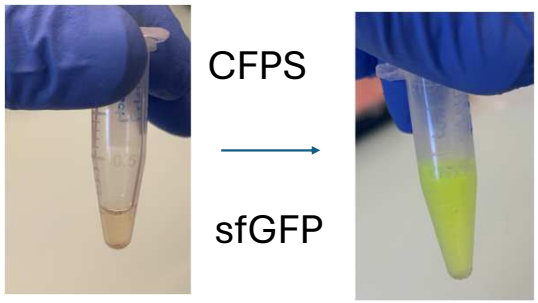
ochelle Av

Cell-free protein synthesis and in vitro glycosylation

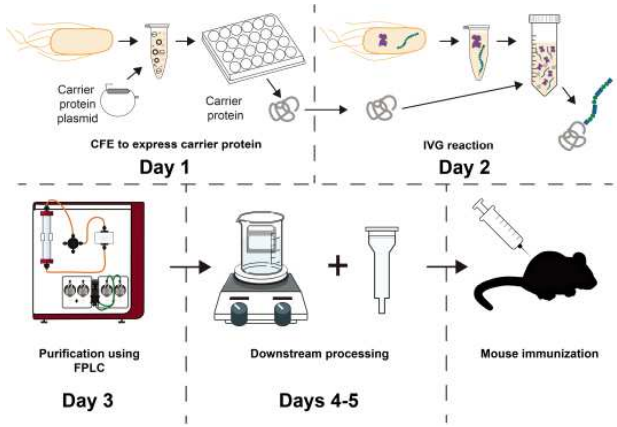
NOTTINGHAM ENGINEERING BIOLOGY LABS

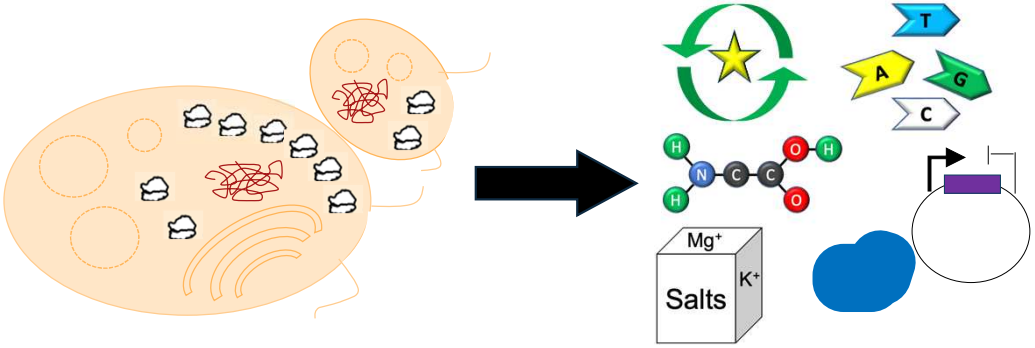
Can we engineer enzymes to improve sugar transfer using in vitro methods for biotherapeutic production

Cell-free protein synthesis can make proteins in hours with no specialised equipment



We can make vaccines in 5 days using in vitro methods





We can make different biotherapeutics using an in vitro method called cell-free protein synthesis and add sugars enzymatically to improve their activity

Techniques: cell-free protein synthesis, synthetic biology, glycoengineering, high throughput screening

Wong, Aw et al (2025) A Scalable Cell-Free Manufacturing Platform for Two-Step Bioproduction of Immunogenic Conjugate Vaccines. ***ACS Syn Bio***

Aw and Polizzi (2018) Biosensor-assisted engineering of a high-yield *Pichia pastoris* cell-free protein synthesis platform. ***Biotech Bioeng***

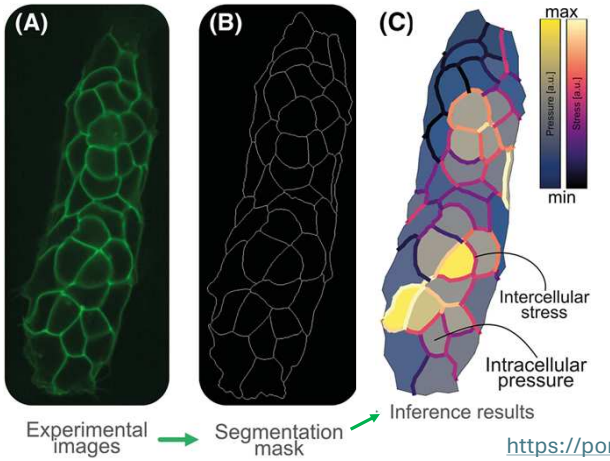
Spice, Aw et al (2020) Synthesis and Assembly of Hepatitis B Virus-Like Particles in a *Pichia pastoris* Cell-Free System. ***Front Bioeng Biotechnol***

Rezvani, Aw et al (2025) Scalable Cell-Free Production of Active T7 RNA Polymerase. ***Biotech Bioeng***

Modelling mechanical regulation of genetic programs

Osvaldo Chara

Research question:
How do genetic programs “read” and “use” mechanical cues during tissue development and regeneration?



Biochemical Society Transactions (2024) 52 2579–2592
https://doi.org/10.1042/BST20230225

PORTLAND PRESS

Review Article

Peeking into the future: inferring mechanics in dynamical tissues

Augusto Borges[1,2] and Osvaldo Chara[3,4]

[1]Unit Sensory Biology and Organogenesis, Helmholtz Zentrum München, Munich, Germany; [2]Graduate School of Quantitative Biosciences, Ludwig Maximilian University, Munich, Germany; [3]School of Biosciences, University of Nottingham, Sutton Bonington Campus, Nottingham LE12, U.K.; [4]Instituto de Tecnologia, Universidad Argentina de la Empresa, Buenos Aires, Argentina

Correspondence: Osvaldo Chara (osvaldo.chara@nottingham.ac.uk)

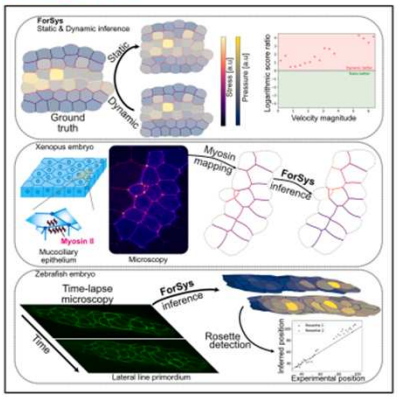
https://portlandpress.com/biochemsoctrans/article/52/6/2579/235363

iScience

Article

ForSys: Non-invasive stress inference from time-lapse microscopy

Graphical abstract



Authors

Augusto Borges, Jerónimo R. Miranda-Rodríguez, Alberto S. Ceccarelli, Guilherme Ventura, Jakub Sedzinski, Hernán López-Schier, Osvaldo Chara

Correspondence

osvaldo.chara@nottingham.ac.uk

In brief

Optical imaging

https://www.cell.com/iscience/fulltext/S2589-0042(25)01946-7

Techniques:
Mathematical ***/*** computational modelling **&** live image analysis.

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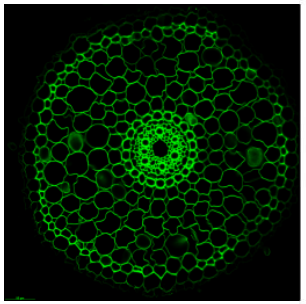
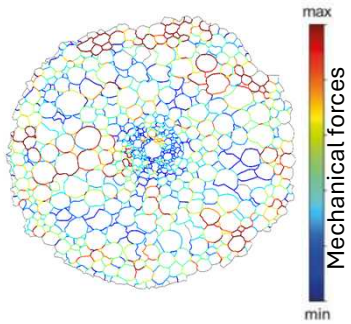
Article | Open access | Published: 26 November 2025

Ethylene modulates cell wall mechanics for root responses to compaction

Jiao Zhang, Zengyu Liu, Edward J. Farrar, Minhao Li, Hui Lu, Zhuo Qu, Osvaldo Chara, Nobutaka Mitsuda, Shingo Sakamoto, Feiyang Xue, Qiji Shan, Ya Yu, Jingbin Li, Xiaobo Zhu, Mingyuan Zhu, Jin Shi, Lucas Peralta Ogorek, Augusto Borges, Malcolm J. Bennett, Wanqi Liang ✉, Bipin K. Pandey ✉, Dabing Zhang & Staffan Persson ✉





https://www.nature.com/articles/s41586-025-09765-7

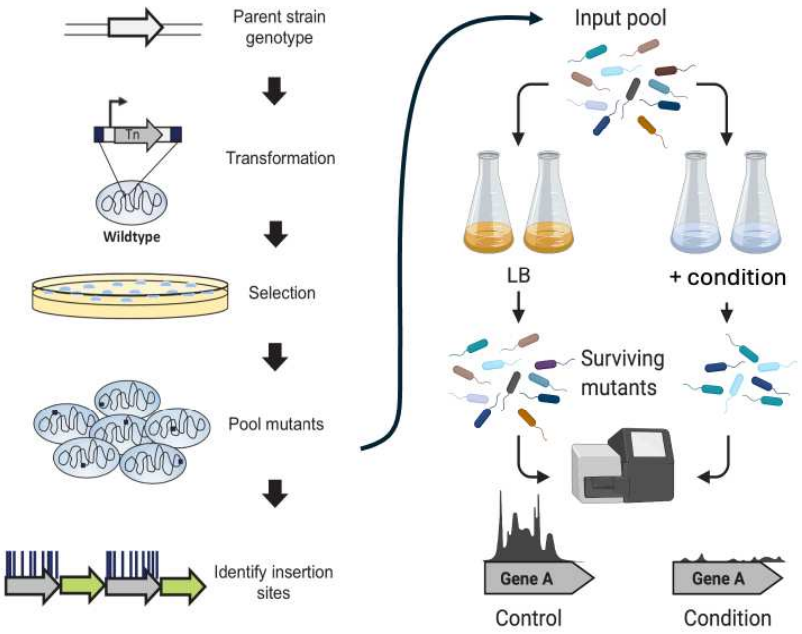
https://www.nottingham.ac.uk/biosciences/people/osvaldo.chara

National Biofilms Innovation Centre

High-throughput genetics to tackle bacterial AMR

Jack Bryant – NBIC Nottingham Research Fellow

Core methods used in our lab

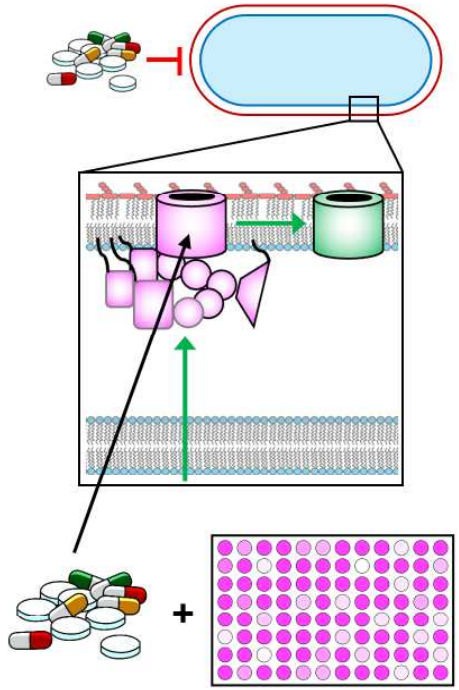


High-throughput genetics (TraDIS) –
Identify all important genes in relevant condition

+ Adaptive lab evolution, next-gen sequencing, fluorescence microscopy, biochemistry, protein structure modelling

Current projects

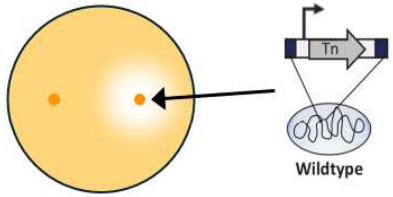
1) Understanding Gram -ve outer membrane protein quality control



2) Developing HT-screening tools for OM-targetting antimicrobial discovery

3) Novel antimicrobial / anti-biofilm surface technologies

4) TraDIS activation of cryptic antibiotic expression



Potential new projects

1) Leveraging synthetic biology for antimicrobial peptide production
2) Third-generation sequencing and TraDIS for secondary metabolite discovery

contact jack.bryant@nottingham.ac.uk to discuss

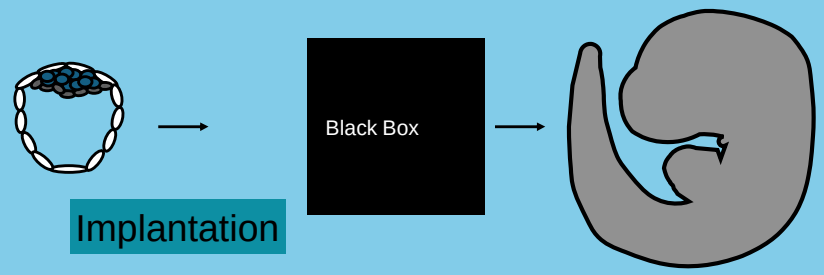
Embryonic stem cell research

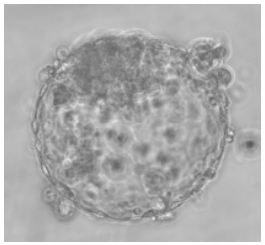
Masaki Kinoshita, School of Biosciences, University of Nottingham
(masaki.kinoshita@nottingham.ac.uk)

University of Nottingham
UK | CHINA | MALAYSIA

- How our body plan is made?
- How stem cells are regulated in the embryo or in the dish?
- Can we use stem cell to make embryos?

How human embryo implants and its body is formed?





Can stem cells model to understand

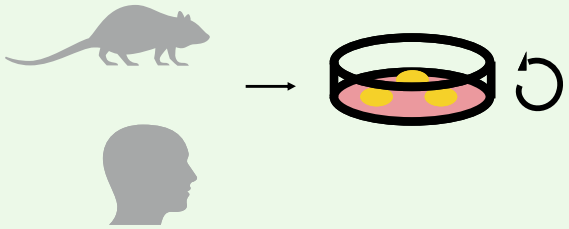
Implantation?
Organogenesis?

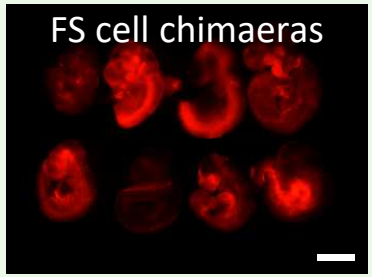
We use
- cell biology
- Omics
- Epigenetics
- Imaging
- Mathematical modelling
- Engineering

Image: Human embryo-like structure made from human ES cells

Past achievements

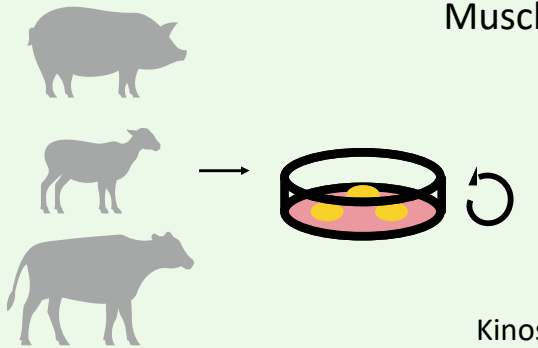
1. Established novel embryonic formative stem (FS) cell lines from mouse and human embryos



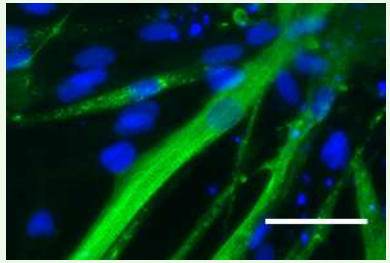


Kinoshita M et al *Cell Stem Cell* 2021

2. Established novel embryonic disc stem cell (EDSC) line from pig, sheep and cattle embryos



Muscle fibres from cattle EDSCs

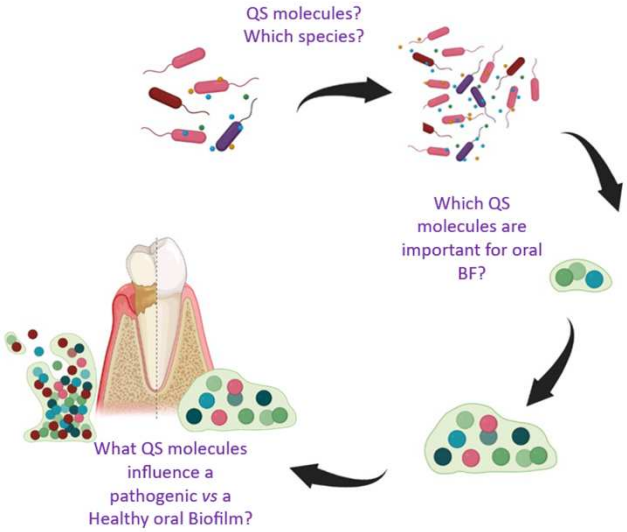


Kinoshita M et al *Development* 2021

Microbiomes in health and disease

Sarah Kuehne

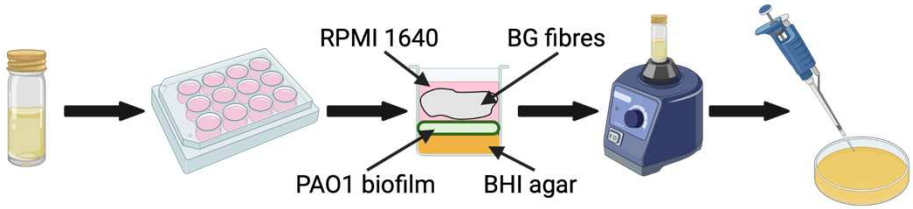
Bacterial communication
In the oral cavity and beyond



Key techniques:

- Anaerobic bacterial culture
- Adherence and invasion assays
- Multispecies biofilms
- Genetic engineering of (anaerobic) bacteria
- Antimicrobial testing

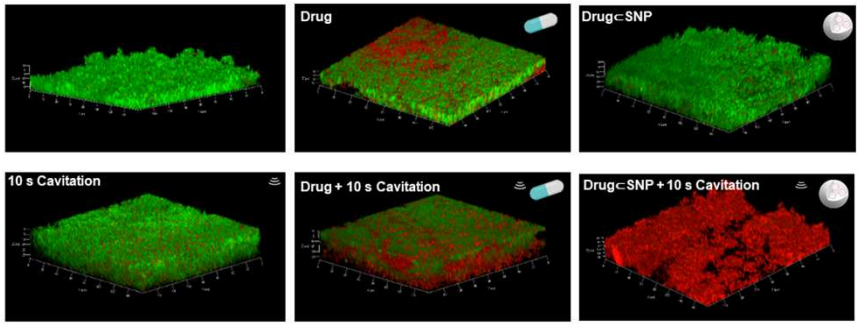
Chronic wound biofilms



Biofilms treated with bioactive glass fibres

Anaerobic microbiology

Biofilms



Biofilms treated with nanoparticles

NTU

Antimicrobial Resistance Omics & Microbiota

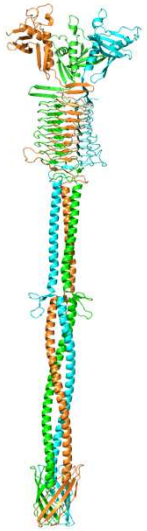
Nottingham Trent University

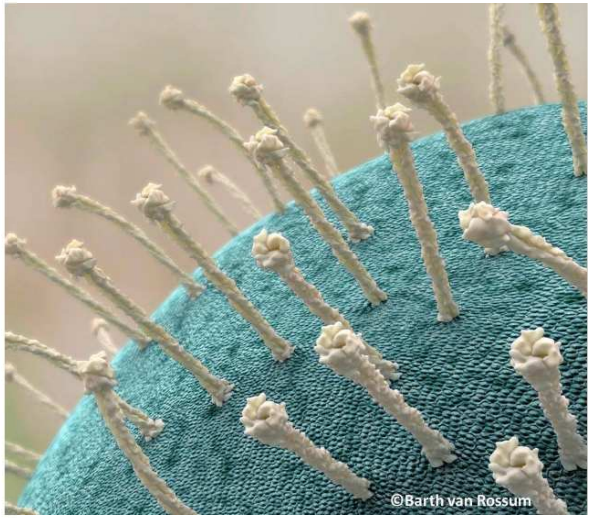
Jack C. Leo, PhD

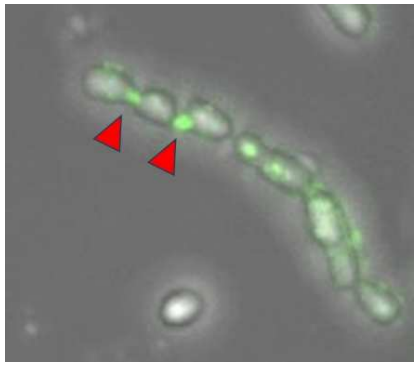
Antimicrobial Resistance Omics & Microbiota

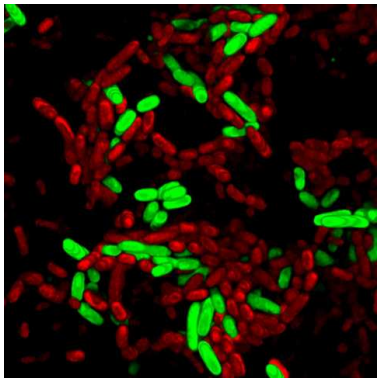
Areas of interest:

- Bacterial adhesion, autoaggregation and biofilm formation
- Protein secretion and surface display
- Outer membrane biogenesis and homeostasis





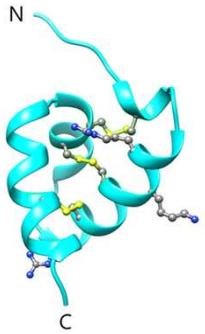


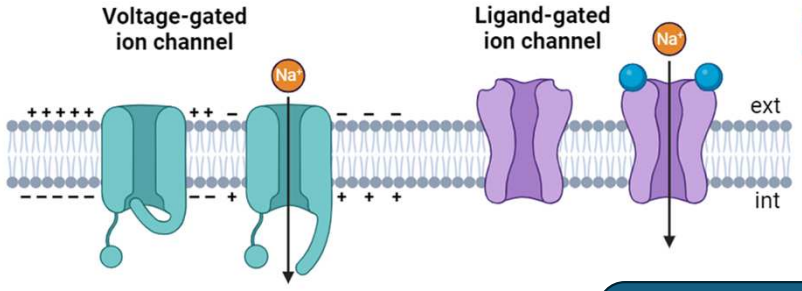


Main techniques:

- Molecular cloning, protein expression and purification
- Subcellular localisation, protein labelling and detection
- Adhesion and biofilm formation
- Biophysical methods (interaction assays, structural biology)

Bioprospecting in centipede venom gland transcriptomes: discovery of ion channel targeting peptides





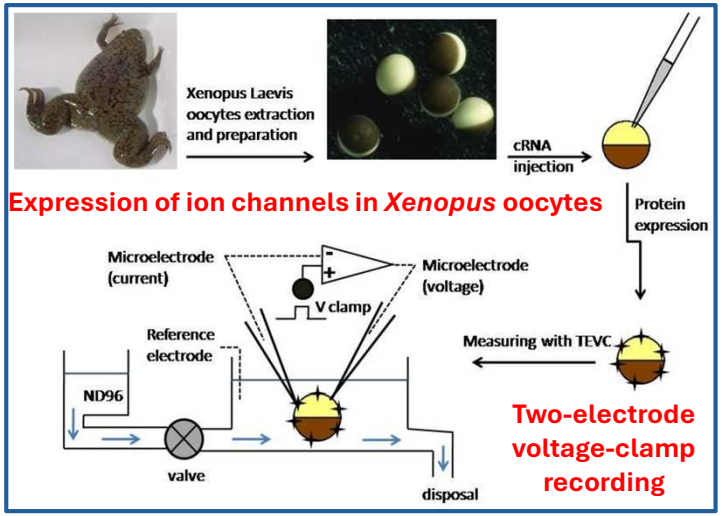
Ian Mellor

Bioinformatics

Peptide synthesis

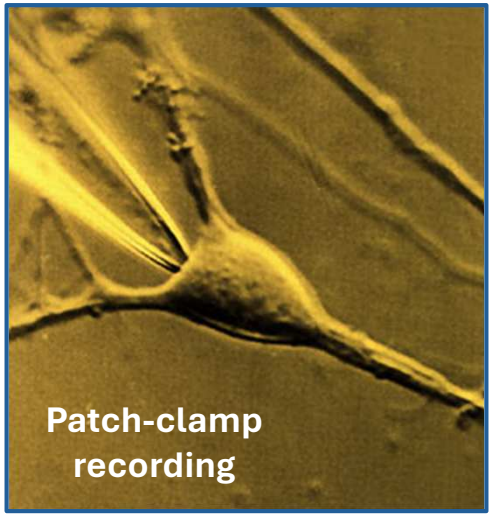
Pesticides?
Drugs?
Tools for neuroscience?

Techniques:



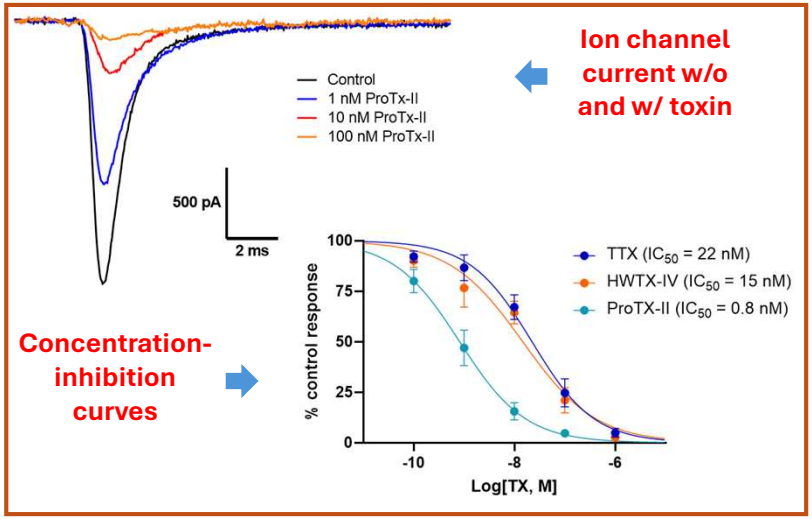
Expression of ion channels in *Xenopus* oocytes

Two-electrode voltage-clamp recording



Patch-clamp recording

Data:




Future Genomes Across Life –
Engineering Biology for Sustainability, and Innovation

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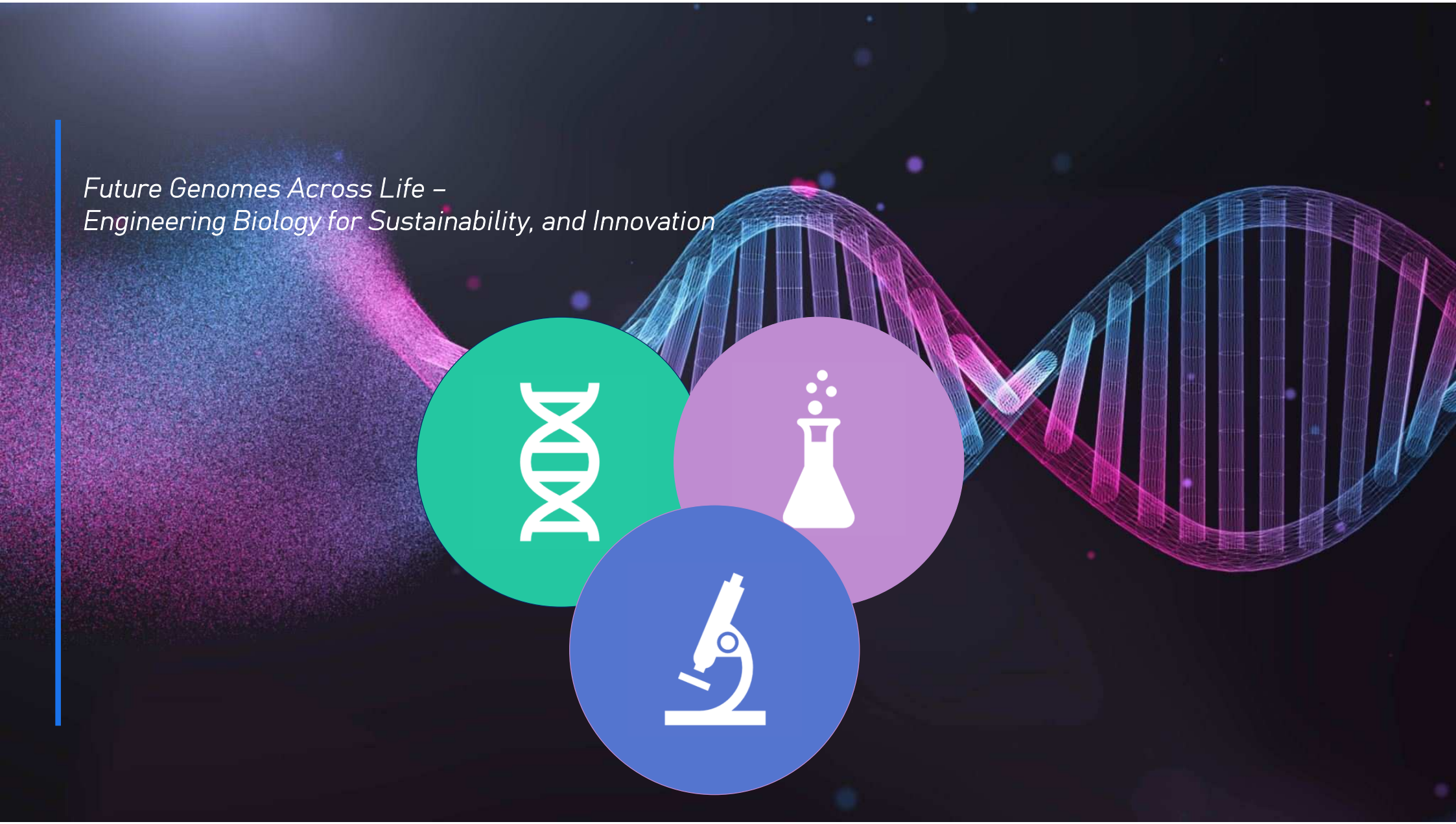
Engineering Biology for Sustainability, and Innovation



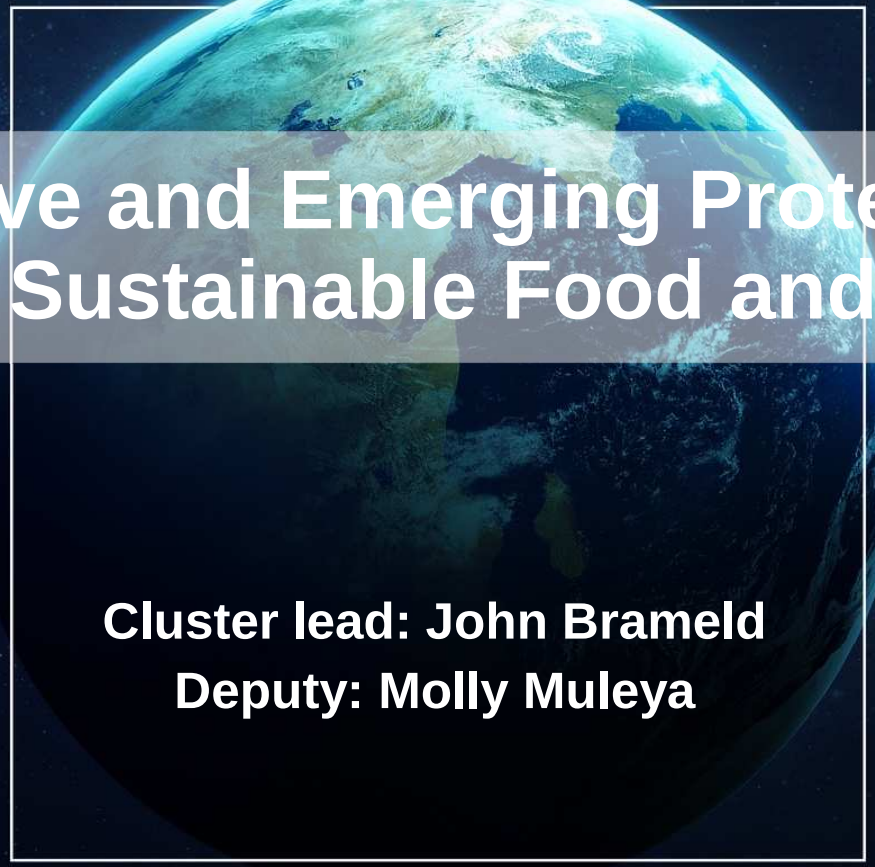
Cluster presentation

Dr Molly Muleya

University of Nottingham
UK | CHINA | MALAYSIA

Nottingham Trent University

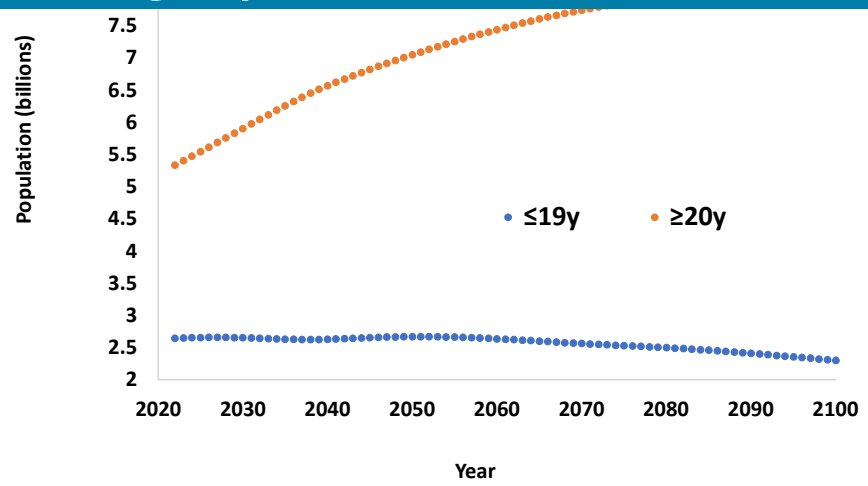
Alternative and Emerging Protein sources for Sustainable Food and Feed



Cluster lead: John Brameld
Deputy: Molly Muleya

Why do we need alternative proteins

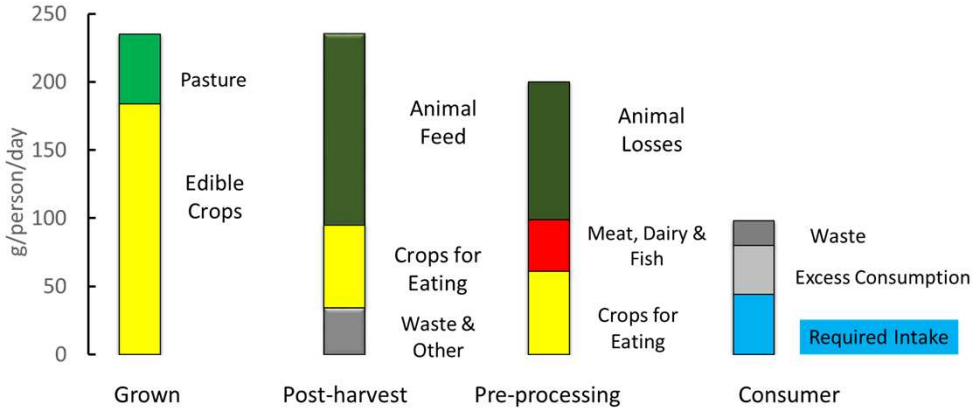
Global Population Demographics



Year	Total Population (billions)
2022	**7.98**
2050	**9.71**
2100	**10.35**

https://population.un.org/wpp/

Global Protein Balance Sheet



Based on data from Berners-Lee *et al* (2018)
DOI: https://doi.org/10.1525/elementa.310

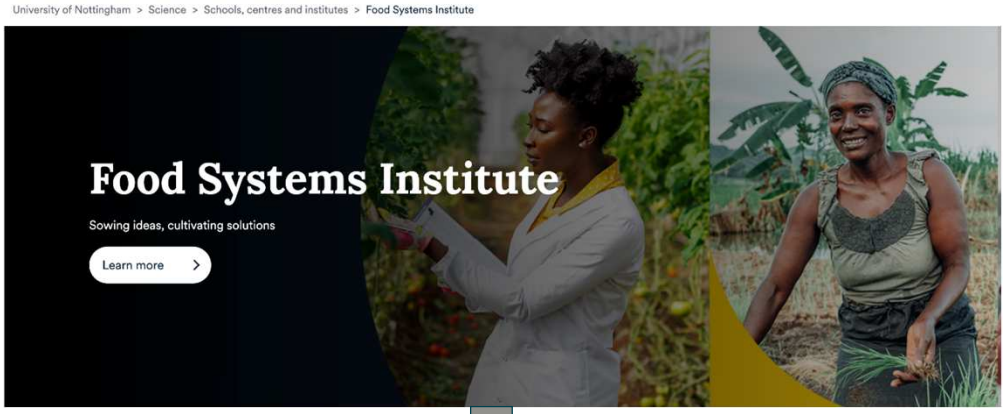
How do we sustainably meet the protein requirements of future generations?

- Reduce excessive consumption of animal-derived protein

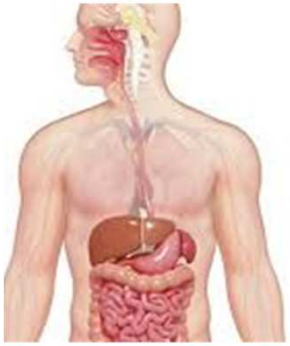
- Where appropriate, replace animal-derived protein with alternative sources
  - Increase the diversity of protein sources for humans

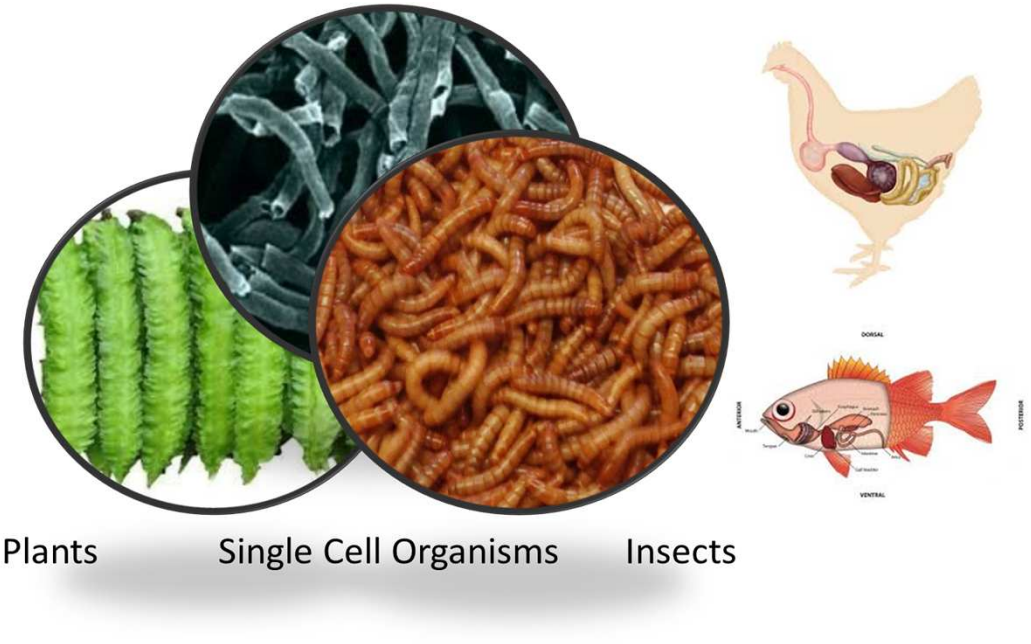
- Feed livestock with more sustainable protein sources that, ideally, are not appropriate for direct human consumption
  - Increase the diversity of protein sources for animals

Future Protein Hub



Evaluate novel plant and non-plant protein sources to develop the most suitable for animal feed and/or human food.





Future Protein Hub

Evaluate novel plant and non-plant protein sources to develop the most suitable for animal feed and/or human food.

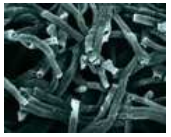
Biology **Engineering** **Food Science** **Nutrition**

Novel primary sources

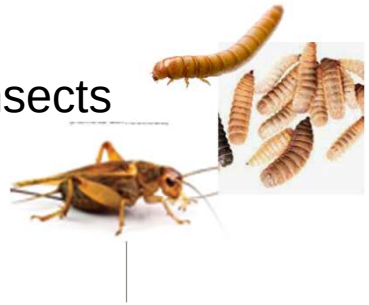
Alternative plants

Single cell

Fungi



Insects



processing

Human

Production animal

The Future Protein Hub evaluates and compares different novel protein sources via cross-discipline collaborations

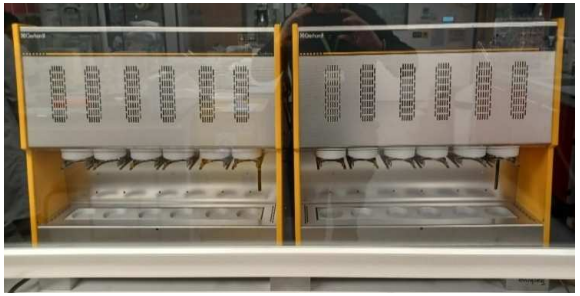
Nutritional Composition & Digestibility Lab

Freeze Dryer

Bomb Calorimeter

Nitrogen Analyser (protein)

Soxhlet Lipid Extractor



ICP-MS

Mineral analysis

TSQ Altis QQQ with Vanquish Flex binary LC

Amino Acid Analysis

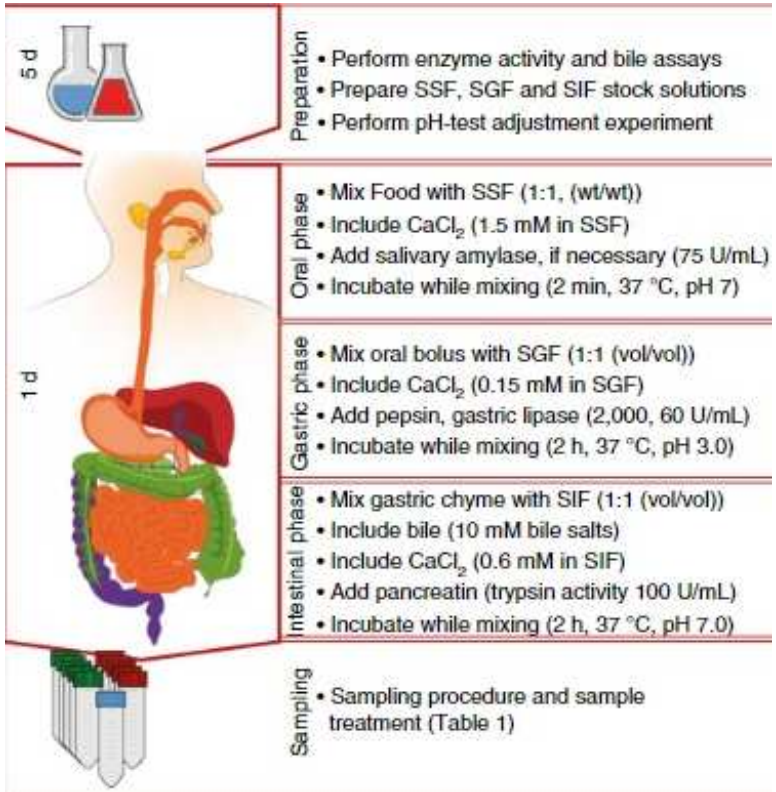
Thermo Scientific™ ISQ™ 7000 GC-MS system

Fatty Acid Analysis

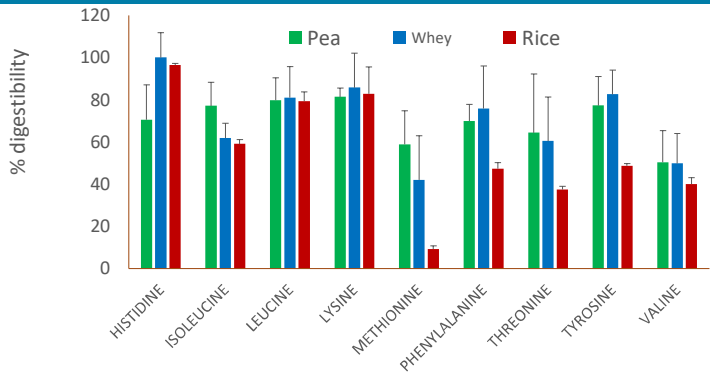
Thermo Scientific ICS-6000 Ion Chromatograph

Mono/oligo - saccharides

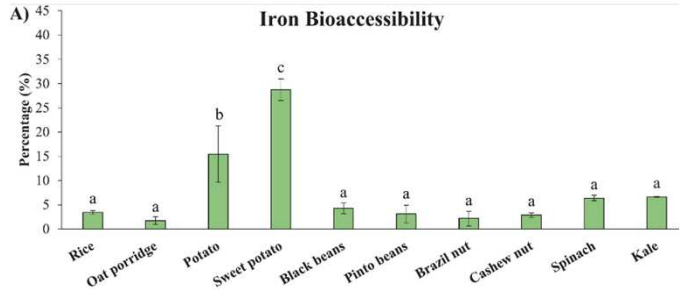
INFOGEST in vitro digestion model



Amino acid digestibility platform



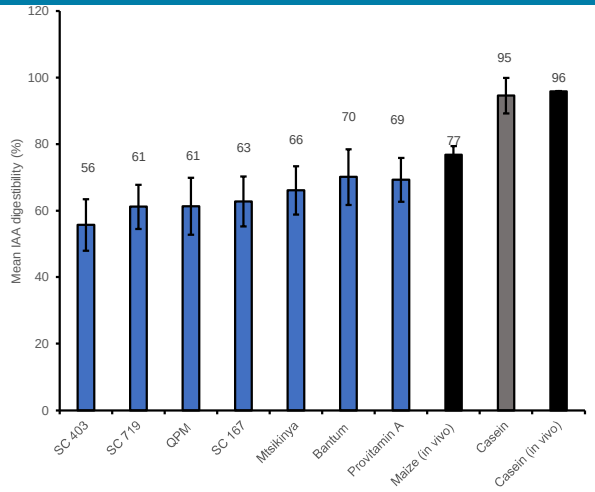
Mineral bioaccessibility platform



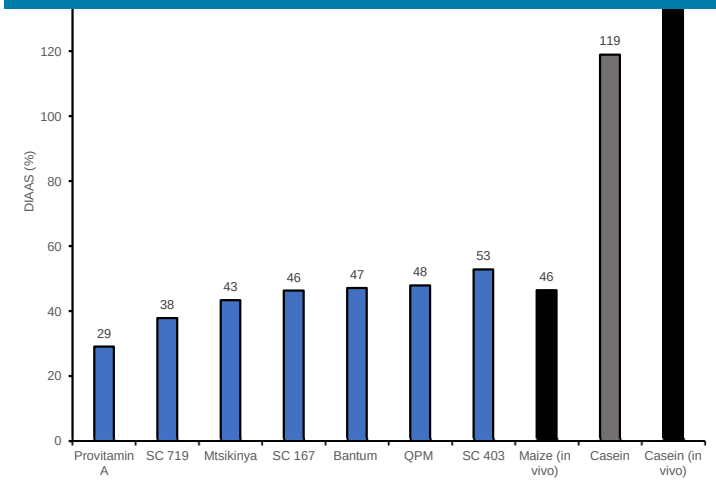
Comparison of maize varieties in Malawi using INFOGEST in vitro digestion model

- Cereals such as maize, are important sources of protein in most sub-Saharan countries
- Identifying varieties to bridge the protein/lysine gap is important
- As expected, lysine was identified as the limiting AA

Indispensable amino acid digestibility



Protein quality measured using the DIAAS metric



Muleya et al, 2023 http://dx.doi.org/10.1016/j.heliyon.2023.e19797

Underutilised crops – important sources of protein

Winged/Goa Bean

(*Psophocarpus tetragonolobus*)

Strengths:

- Annual or perennial vine
- Grows in hot humid tropics
- Nitrogen fixing
- Leaf & pod: rich source of vitamin minerals, fiber
- Seed & tuber: high in protein, carbohydrate

Challenges

- Anti-nutritional factors
- Indeterminate growth habit
- Photoperiod sensitive
- Variability within landraces

Bambara Groundnut

(*Vigna subterranea*)

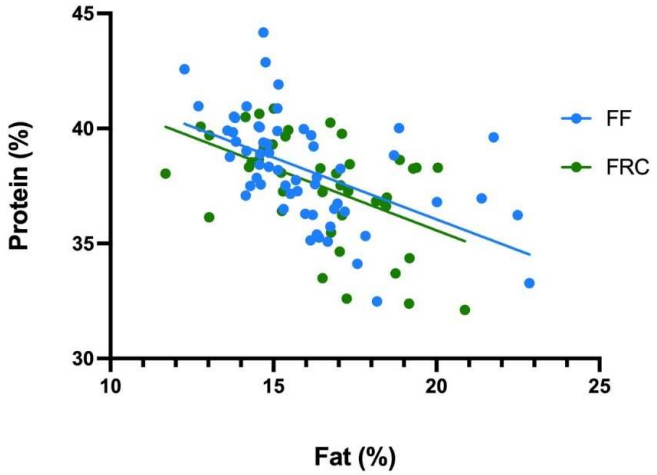
Strengths:

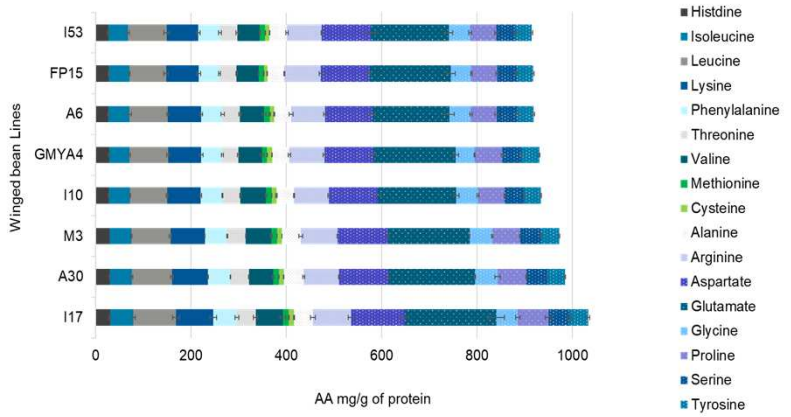
- Drought tolerance
- Grows in semi-arid & tropical environments, marginal soils
- Nitrogen fixing
- Fast growing (4-5 months)
- 3rd most important nutrient legume in sub-Saharan Africa

Challenges

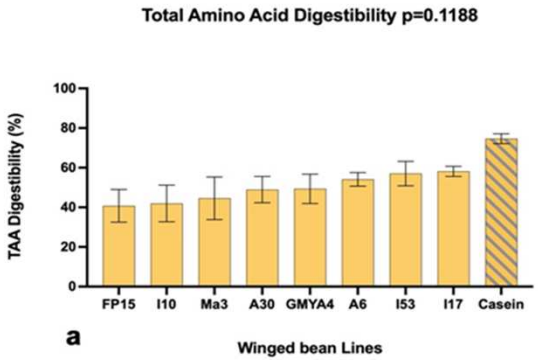
- Antinutritional factors
- Photoperiod sensitive
- Variability within landraces
- Lack of commercial varieties

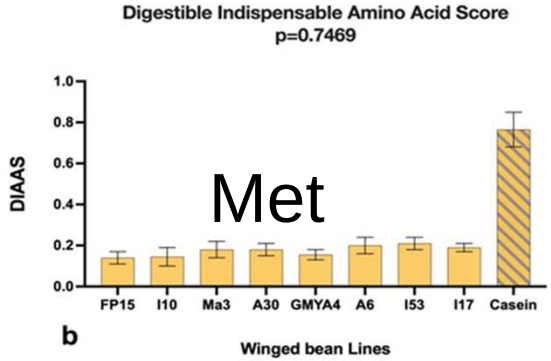
Winged Bean – identifying QTLs for nutritional value





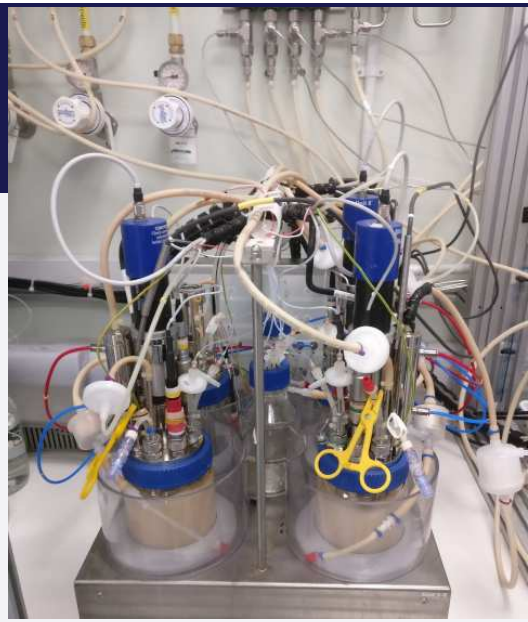
WB Line	Protein (%)	Fat (%)	Phytic acid (g/100 g)	Total Phenolics (mg/100g)	Colour
GMA4	42.67	14.54	1.768	7.093	CREAM
A27	39.76	14.15	1.402	-	CREAM
A35	39.16	17.38	1.205	-	BROWN
A10	39.08	14.56	1.303	-	BROWN
A30	38.73	15.41	0.842	6.765	CREAM
*I17	38.56	14.38	1.308	7.802	BROWN
*FP15	38.47	20.61	1.424	8.281	PURPLE
A57	38.41	15.14	1.177	-	BROWN
A4	38.3	15.79	1.371	-	BROWN
A15	38.29	14.69	1.296	-	BROWN
A11	38.16	14.65	1.348	-	LIGHT BROWN
A13	38.08	15.55	1.433	-	DARK BROWN
A56	37.91	14.52	1.05	-	DARK BROWN
*I53	37.3	15.94	0.832	7.833	BROWN
A7	37.05	15.04	1.186	-	BROWN
A6	36.38	17.18	1.472	8.214	PURPLE BLACK
A21	36.33	16.06	1.094	-	BROWN
*I10	36.3	16.09	1.088	7.687	BROWN
*MA3	35.44	21.78	1.244	7.700	BROWN



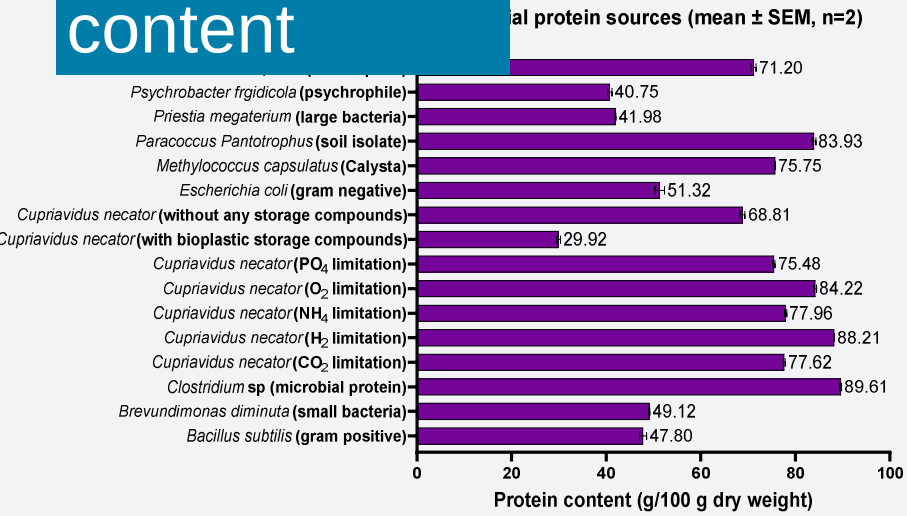


Tsoutsoura et al, unpublished

Bacterial protein sources

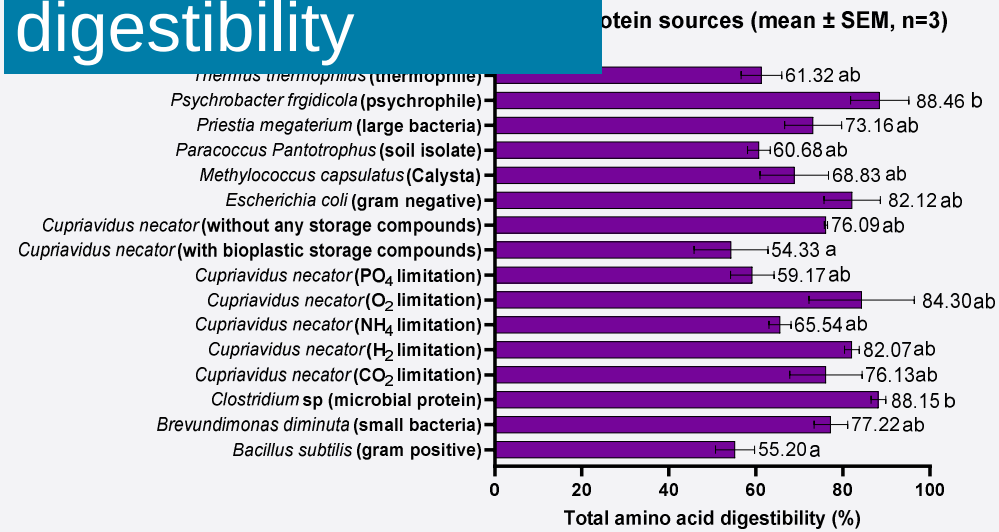


Total protein content



- Wide variation in protein content and amino acid digestibility
- Majority of the candidates have potential applications as feed ingredients

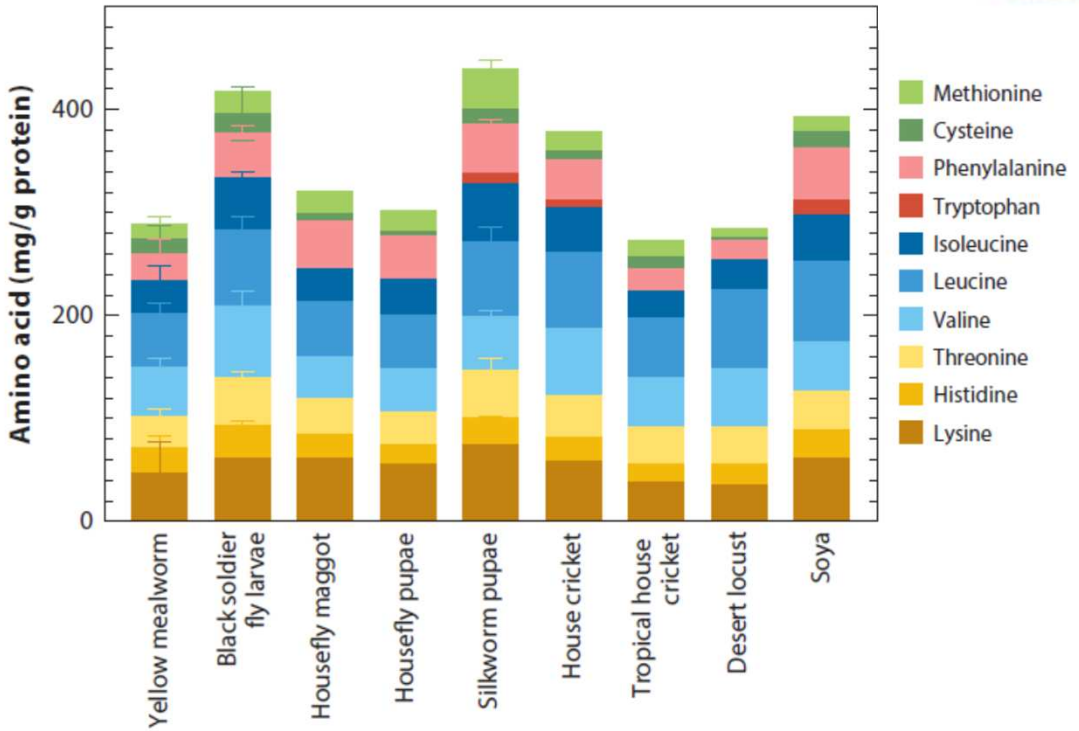
Total amino acid digestibility



Cochetel et al, unpublished

Edible insects as protein sources

Species	Protein (% dry matter)
Yellow Mealworm	46-54
Black Soldier Fly Larvae	34-42
Housefly Maggot	51-60
Housefly Pupae	71-76
Silkworm Pupae	23
House Cricket	59-72
Tropical House Cricket	70
Desert Locust	76
Soya	55



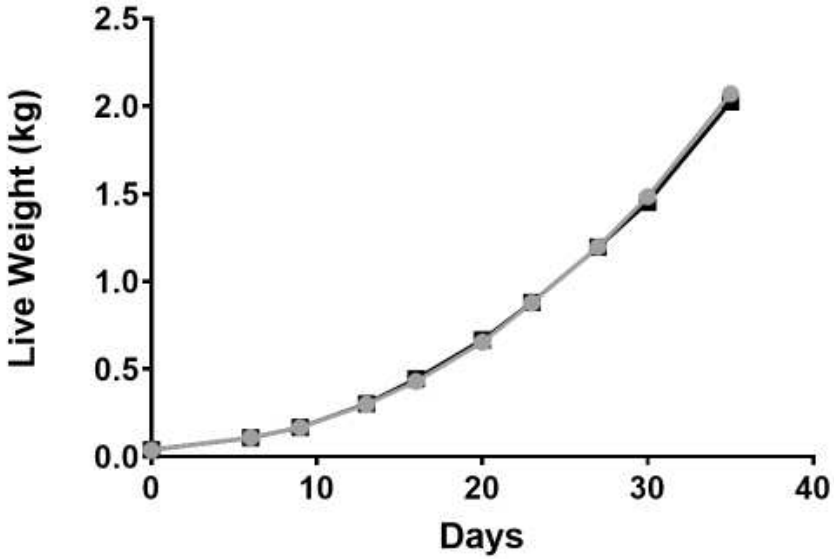
Challenges – protein functionality in various food formats, consumer acceptance

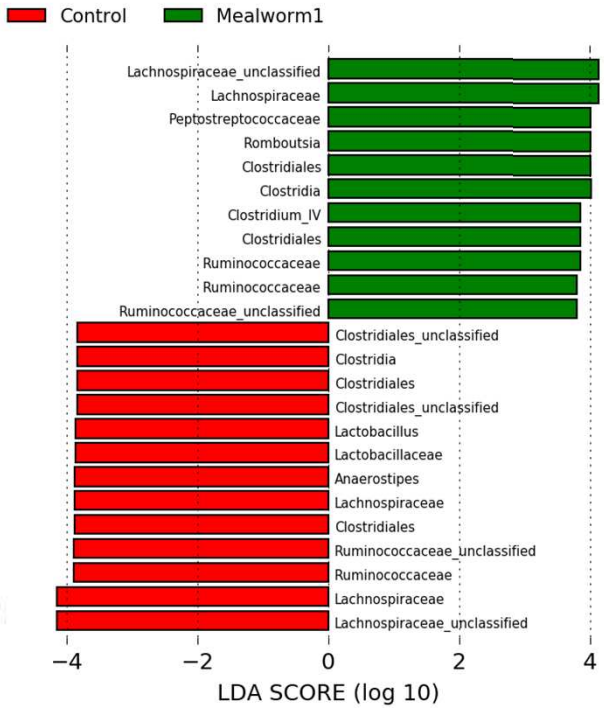
Hawkey et al (2021) https://doi.org/10.1146/annurev-animal-021419-083930

Impact of Replacing Soya with Mealworm Protein on Growth of Broiler Chickens

10% Soya replaced with dried mealworms (reformulated to balance lipid content)

No significant difference in live weight gain

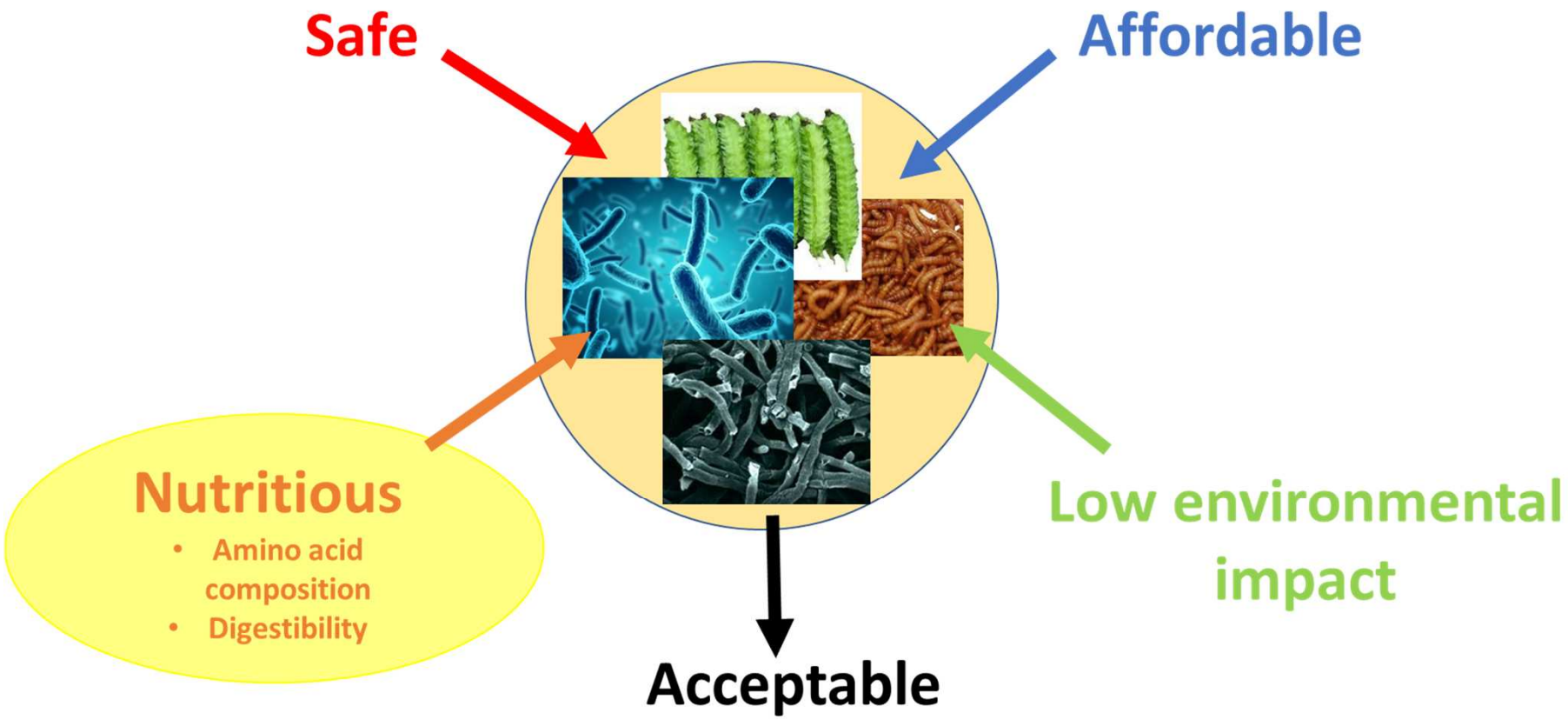




Changes in the Chicken Microbiome

Hawkey et al. unpublished

Requirements of Novel Sustainable Protein Sources



Multi-/ Inter-disciplinary Research

The cluster includes academic researchers from a broad range of areas:

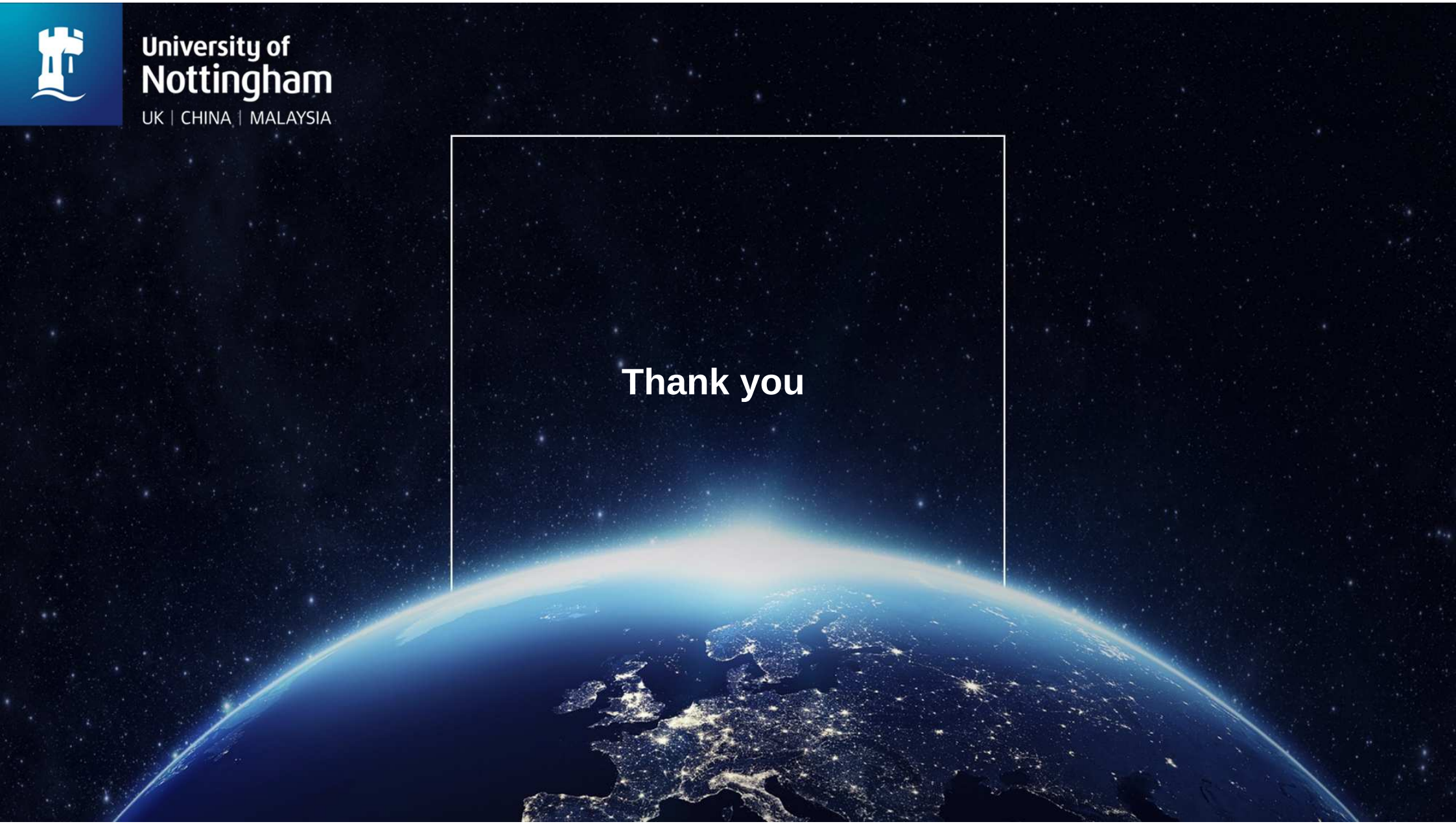
1. Primary production of alternative protein sources
   - Plants/ crops, insects, cultured meat, algae, bacteria or fungi
2. Food science and processing
3. Nutritional science and digestion
4. Flavour chemistry
5. Sensory science and consumer behaviour
6. Human appetite physiology
7. Animal nutrition

PhD applicants from any of these areas would be welcome, but must be willing to work and interact across the range of disciplines

Multi-/ Inter-disciplinary Projects (potential examples)

1. Identification of nutritionally improved varieties of foxtail millet for UK agriculture
2. Improved protein production for the mycoprotein Quorn fungus, Fusarium venenatum
3. Strain improvement for the mycoprotein Quorn fungus, Fusarium venenatum
4. Manipulation of chitin content of insects and impacts on composition, digestibility and food functionality;
5. Comparisons of protein digestibility and mineral bioavailability across different alternative protein sources using in vitro digestion methods
6. Designing functional and nutritious extruded alternative protein snacks through a consumer-centric approach
7. Comparing the effects of alternative proteins on satiety and enjoyment
8. Consumer insights on attitudes, knowledge and behaviour towards sustainable foods including plant-based, edible insect, cultured meat and food waste

Current collaborators in this area


University of
Nottingham
UK | CHINA | MALAYSIA
Thank you

Cluster presentation

Dr Federico Dajas-Bailador

RIC@N-DLA
2026

BBSRC Doctoral Landscape Awards
Bioscience for Human Health

Lead: Federico Dajas-Bailador

RNA Interdisciplinary Cluster
NOTTINGHAM

Life Sciences | Engineering | Pharmacy | Chemistry | Medicine

35 Core Labs | > 130 Scientists | > 30 Associated Groups

"To potentiate current and novel research for future knowledge and therapeutics"

RNA Interdisciplinary Cluster
NOTTINGHAM

Research Themes

Cell & Developmental Biology

Molecular Biology

Structural Biology

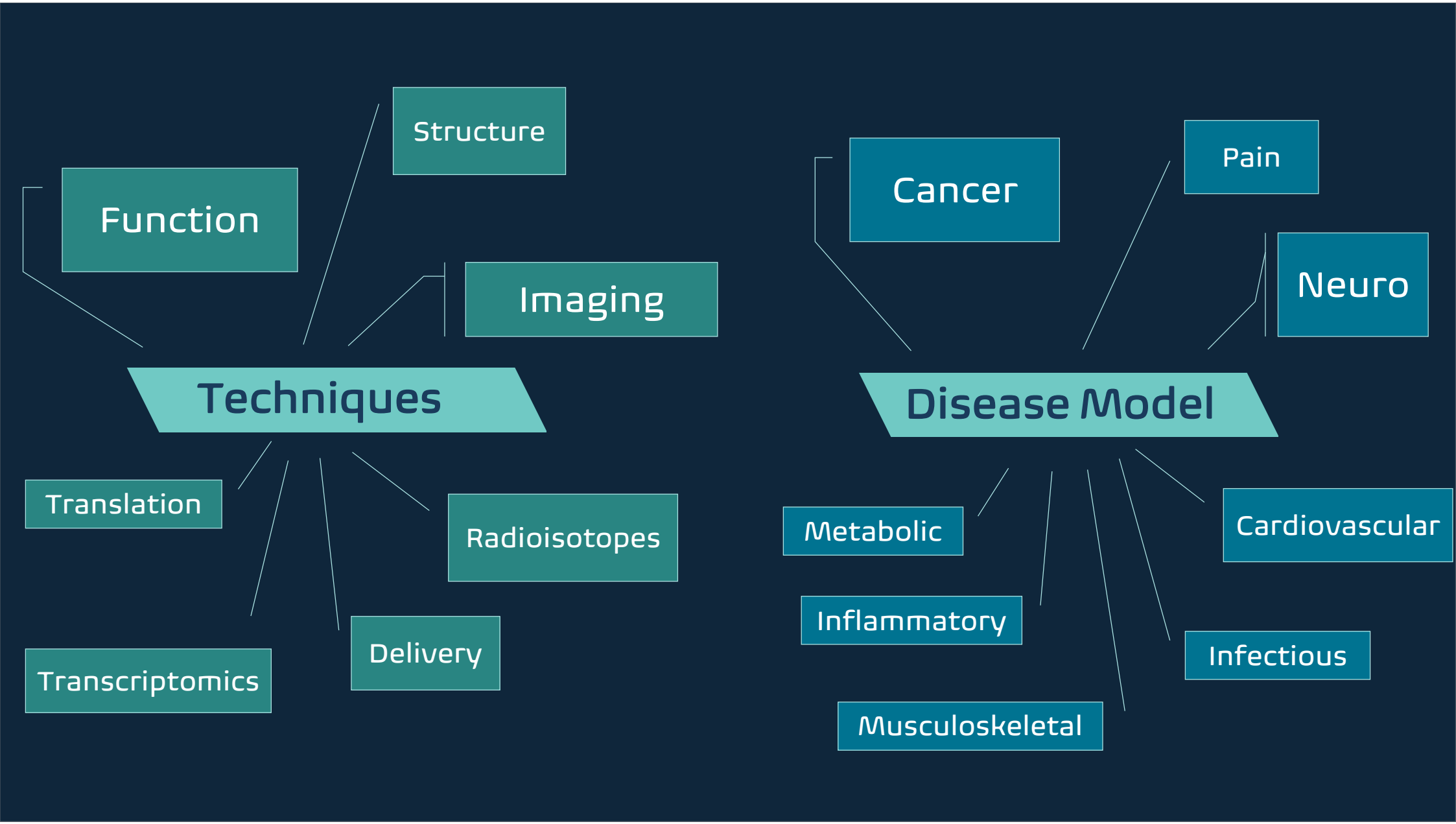
Biochemistry

Biophysics

Genetics/Epigenetics

Biotechnology

Bioinformatics


Function
Structure
Imaging
Techniques
Translation
Radioisotopes
Delivery
Transcriptomics
Cancer
Pain
Neuro
Disease Model
Metabolic
Cardiovascular
Inflammatory
Infectious
Musculoskeletal

Scope and Focus

RIC@N-DLA

Multiscale RNA Biology from Mechanisms to Applications

RIC@N

RNA biology is transforming our understanding of life and enabling powerful new technologies, from mRNA vaccines to RNA-based diagnostics and therapeutics.

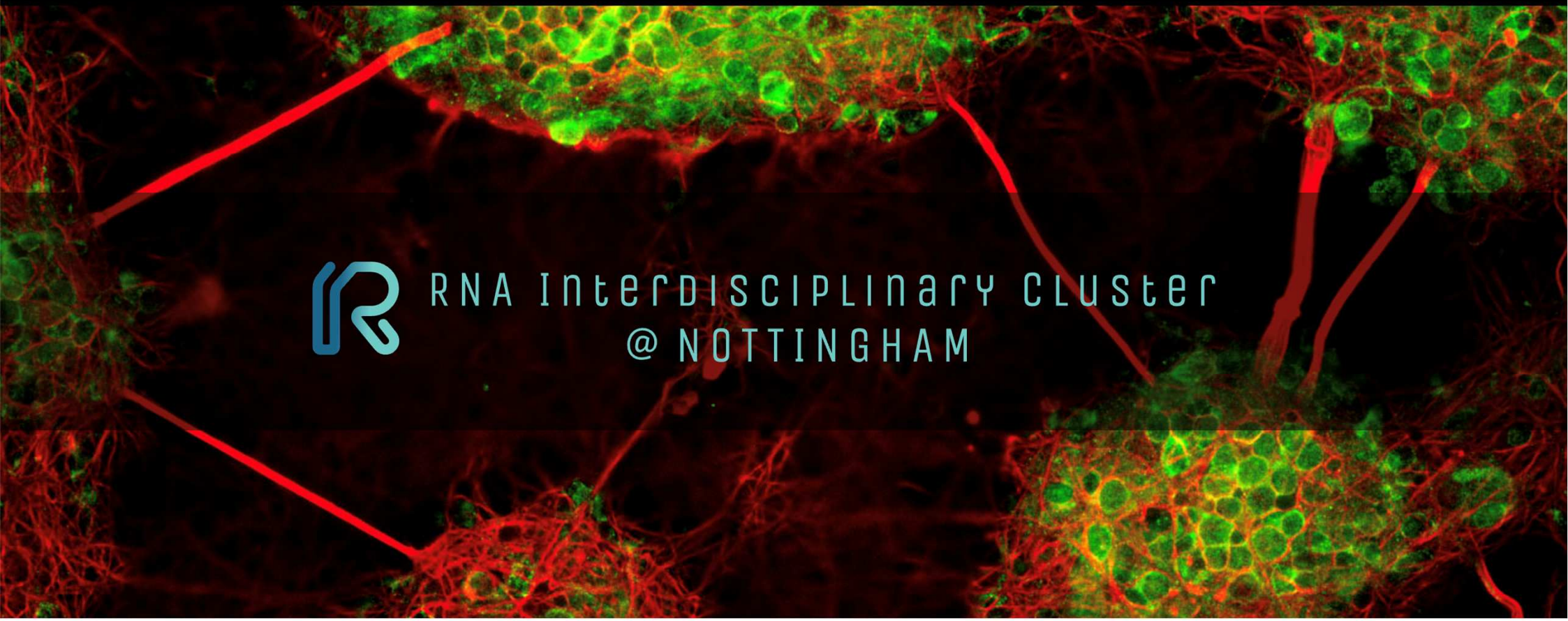
Deliver interdisciplinary doctoral training in RNA biology, spanning molecular mechanisms, systems-level regulation, and real-world application, and integrating approaches across molecular, cellular, and organismal scales.

Train PhD researchers in cutting-edge RNA science within a collaborative, cross-disciplinary research environment.

Structured around **RIC@N** | RNA Interdisciplinary Cluster at Nottingham | https://rnanottingham.com/

RIC@N

Network Research Labs Studentships News Contact & Structure



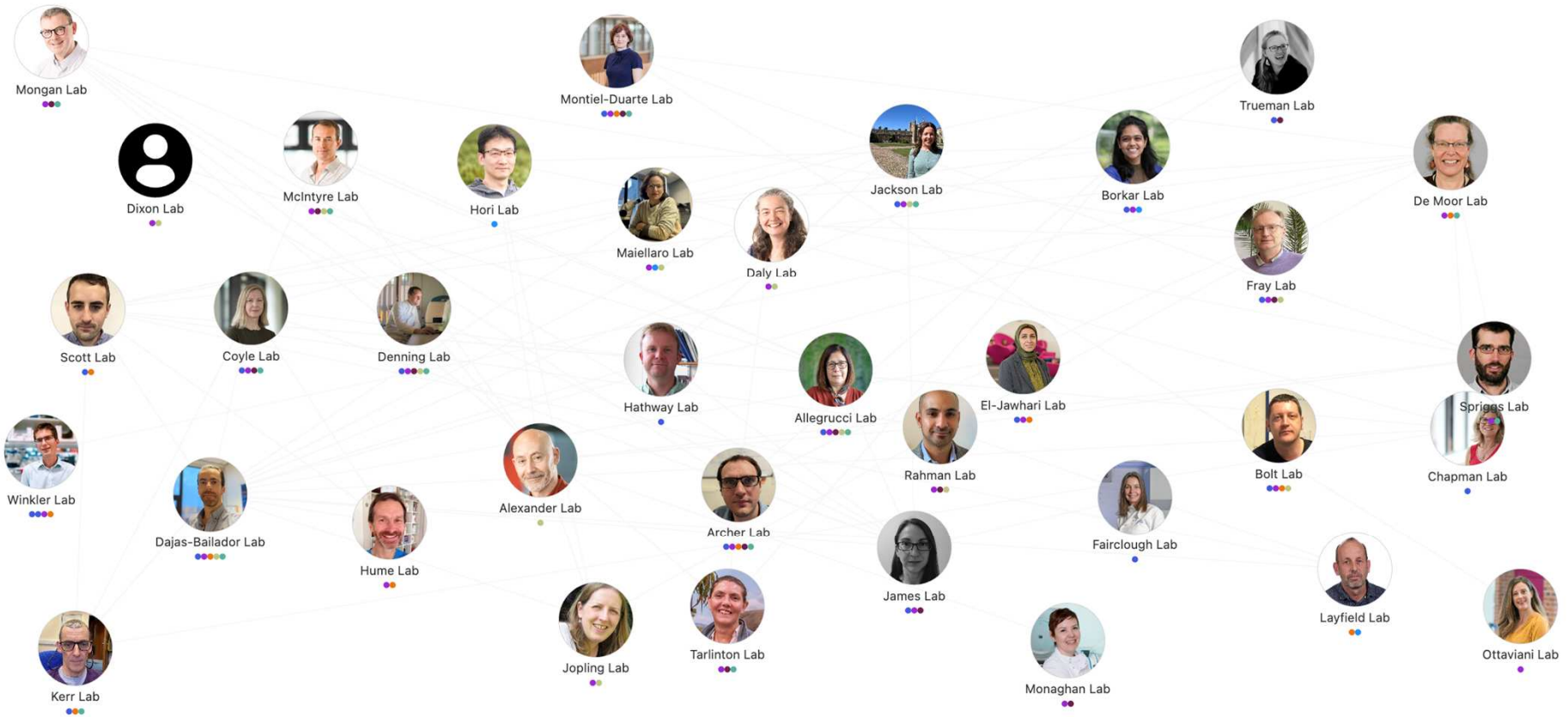
Explore the network

The RNA Interdisciplinary Cluster @ Nottingham is a new centre designed to promote collaboration and foster research insight at fundamental and applied science

RIC@N

Network | Research | Labs | Studentships | News | Contact & Structure

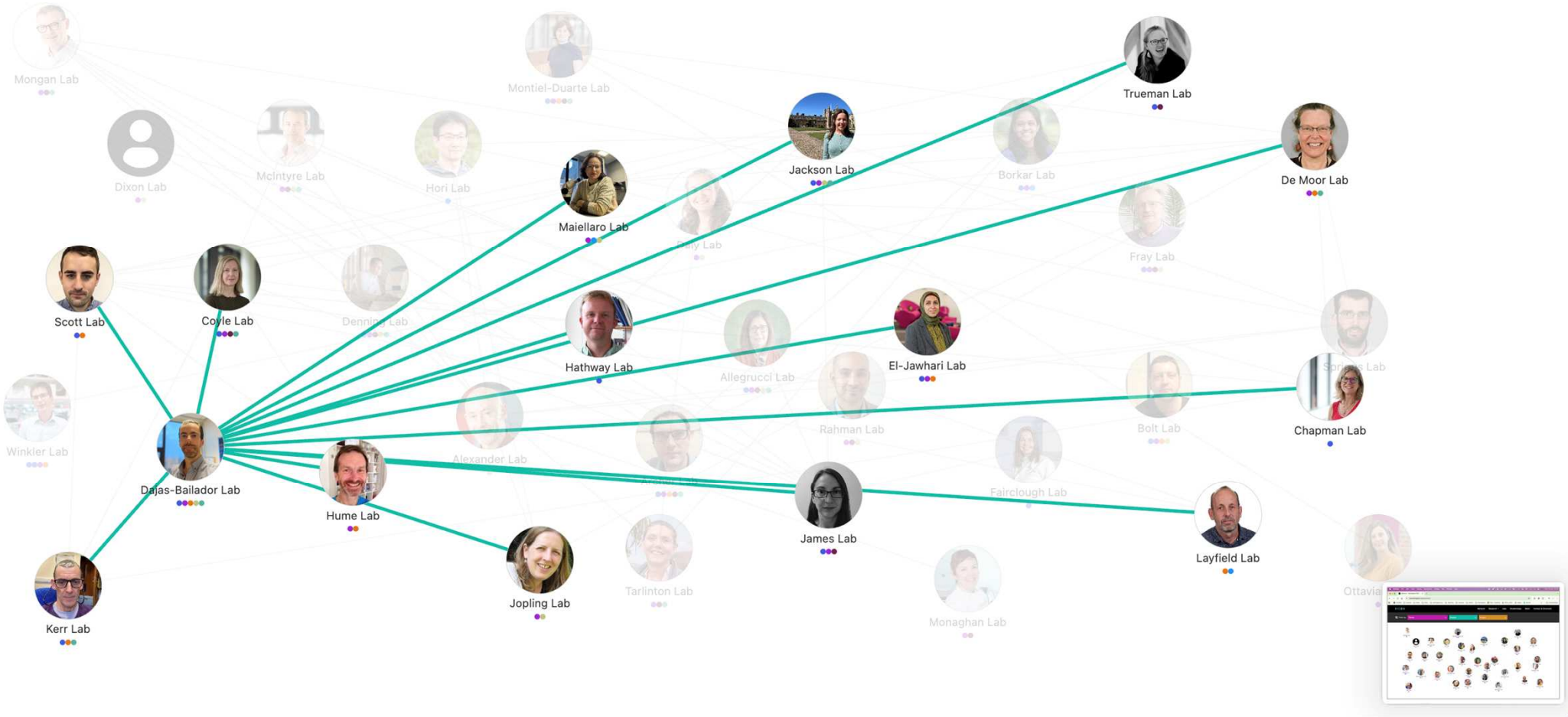
Filter by: Theme | Disease | Project



RIC@N

Network | Research | Labs | Studentships | News | Contact & Structure

Filter by: Theme | Disease | Project



RIC@N

Network | Research | Labs | Studentships | News | Contact & Structure

Filter by: Cell & Developmen... | Disease | Project

- Biotechnology
- Molecular Biology
- Genetics/Epigenetics
- Bioinformatics
- Biochemistry
- Structural Biology
- Biophysics


Fray Lab


El-Jawhari Lab


Trueman Lab


Coyle Lab


Jackson Lab


Montiel-Duarte Lab


Allegrucci Lab

Dajas-Bailador Lab


Fairclough Lab


Chapman Lab


James Lab


Winkler Lab


Scott Lab


Denning Lab


Archer Lab

Jackson Lab

Hannah Jackson

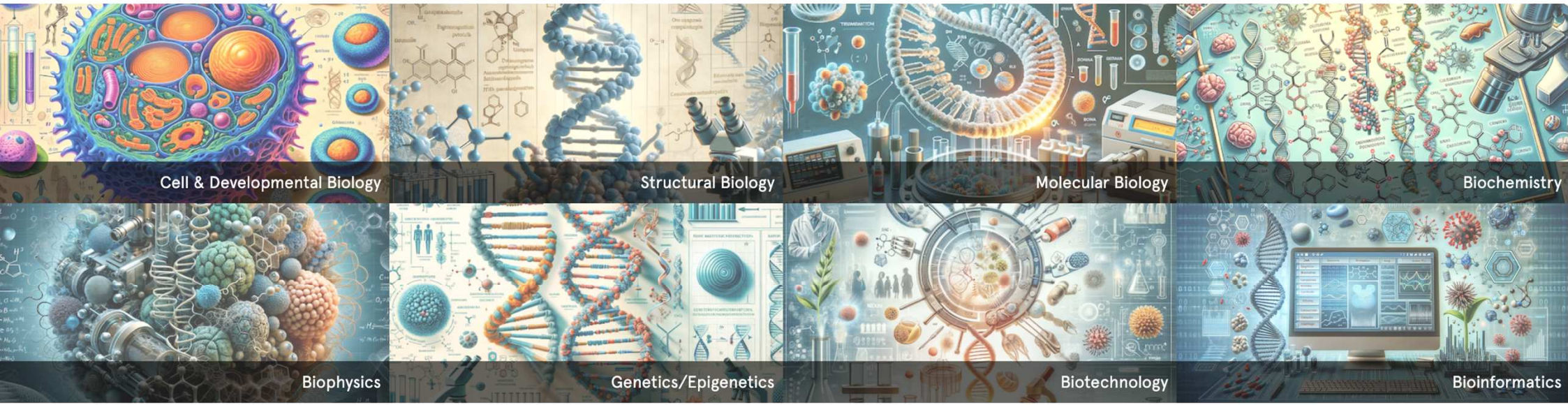
My research focuses on leveraging extracellular vesicles for early cancer diagnosis, vaccine development, and understanding neurobiological impacts of cancer and its treatments

Cell & Developmental Biology | Molecular Biology | Biotechnology | Bioinformatics

Research Brief

My research has mainly been dominated by an interest in extracellular vesicles (EVs). I began my research career investigating the role of EVs in the most prevalent malignant pediatric brain tumor, medulloblastoma, aiming to understand their role in metastasis and how they could be exploited as biomarkers to characterize disease and inform clinical phenotypes. At the University of Cambridge, I worked on bioengineering small extracellular vesicles as a novel platform for effective SARS-CoV-2 vaccine development—this work was in partnership with Exosis Inc, Florida (https://www.exosis.com/). My current work is now focusing on understanding how cancer and cancer chemotherapeutics impact sensitisation and pain, particularly the ability of extracellular vesicles to

Research Themes



We are a dynamic, multidisciplinary cluster of researchers dedicated to advancing the field of RNA biology, exploring its complexities across various cellular processes and applications.

Cell & Developmental Biology

In Cell and Developmental Biology we study the function, and behaviour of cells, as well as how they organise and differentiate during the development of an organism. RNA plays a crucial role in these processes, from the mRNA that directs the synthesis of proteins, to non-coding RNAs, such as microRNAs and long non-coding RNAs, which are involved in regulating gene expression, influencing cell fate, and controlling developmental processes. RNA's involvement in gene expression, splicing, and post-transcriptional regulation is essential for proper cell differentiation, tissue formation, and the overall development of multicellular organisms.

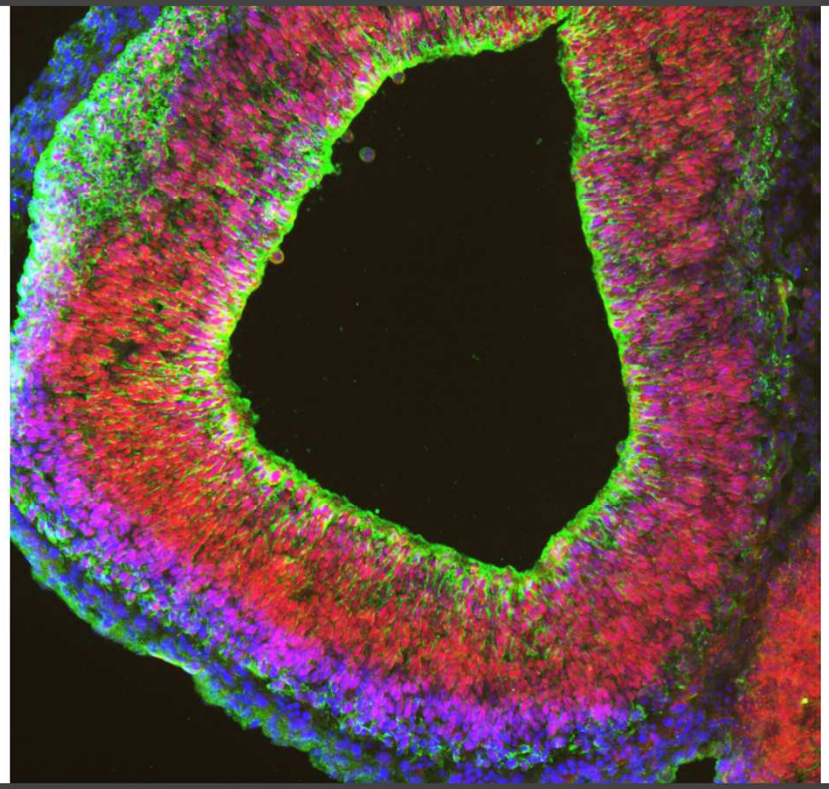
Coyle Lab | Hathway Lab | Jackson Lab | Denning Lab | Trueman Lab | Winkler Lab

El-Jawhari Lab | Scott Lab | Montiel-Duarte Lab | Fray Lab | Fairclough Lab | James Lab

Archer Lab | Dajas-Bailador Lab | Chapman Lab | Allegrucci Lab

Structural Biology

As structural biologist we investigate the three-dimensional structures of biological macromolecules, including proteins, nucleic acids, and their complexes, to understand their function and interactions. In this context, RNA plays a pivotal role, as its diverse structural conformations are key to its various biological functions. Unlike DNA, RNA is highly flexible and can adopt complex secondary and tertiary structures, which are critical for its roles in gene regulation, catalysis, and protein synthesis. The structure of RNA molecules, such as ribosomal RNA (rRNA), transfer RNA (tRNA), and small RNA species, directly influences their ability to interact with proteins and other nucleic acids. Understanding the



Neurological (developmental/degenerative)

Neurological disorders involve dysfunctions of the nervous system, often linked to genetic mutations or environmental factors. RNA biology plays a key role in these conditions, as altered RNA splicing, expression, or RNA processing can disrupt neuronal function. Non-coding RNAs also regulate gene expression, influencing disease mechanisms in disorders like ALS, Alzheimer's, and Parkinson's.

Labs studying this disease:

Hathway Lab | Jackson Lab | Denning Lab | Layfield Lab

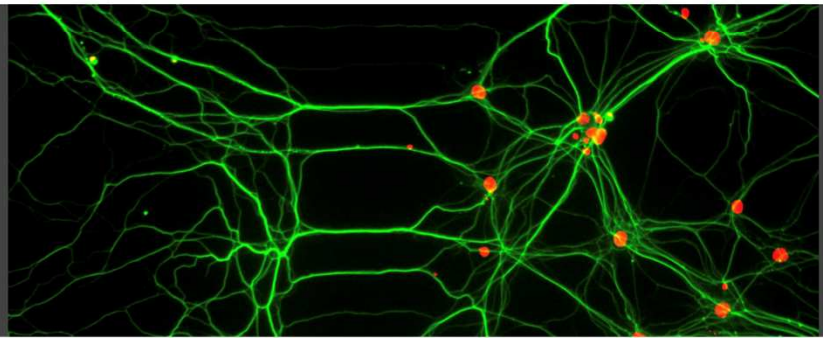
Hori Lab | Trueman Lab | McIntyre Lab | Alexander Lab

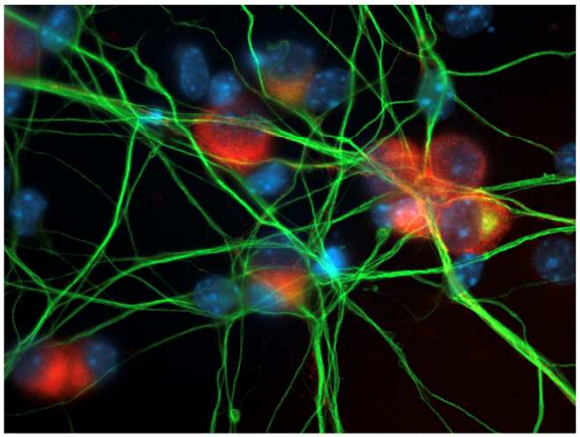
Jopling Lab | Archer Lab | Dajas-Bailador Lab | Dixon Lab

Chapman Lab | Monaghan Lab | Hume Lab

Pain

Pain is a complex sensory and emotional experience, often resulting from nerve injury or inflammation. RNA biology is linked to pain through the regulation of pain-related genes, including those encoding receptors and ion channels. RNA molecules, such as microRNAs, also modulate pain pathways and inflammatory responses, influencing chronic pain nt.



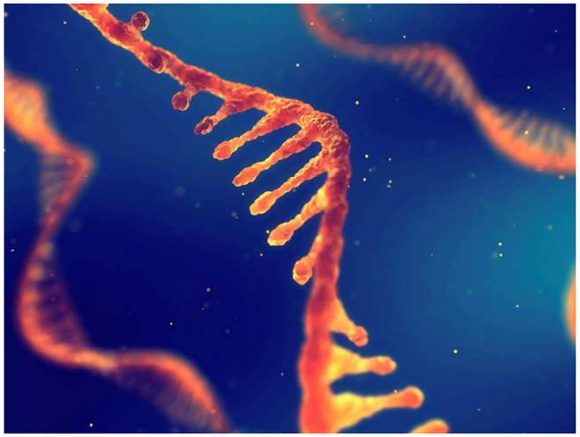


TReND: non-coding RNA network dynamics in ALS

An Eli Lilly funded project to investigate non-coding RNA network dynamics in the context of motor neuron disease. A collaboration between the labs of *Federico Dajas-Bailador* and *Dan Scott* supported by Achim Kless and the Eli Lilly bioinformatics team.

Dajas-Bailador Lab

Scott Lab



How do mRNA Cap-adjacent Modifications Shape Translation in Human Cells?

A Royal Society funded project to investigate how mRNA modifications on the starting nucleotides of mRNA affect gene expression.

Archer Lab

RIC@N-DLA: Research Hub Structure

Hub 1: RNA Modifications, Structure & Regulation
How RNA folding, chemical modification, and RNA–protein interactions shape the RNA lifecycle.

Hub 2: RNA Tools & Technologies
Development and application of RNA-based tools, including antisense oligos, CRISPR systems, and delivery platforms.

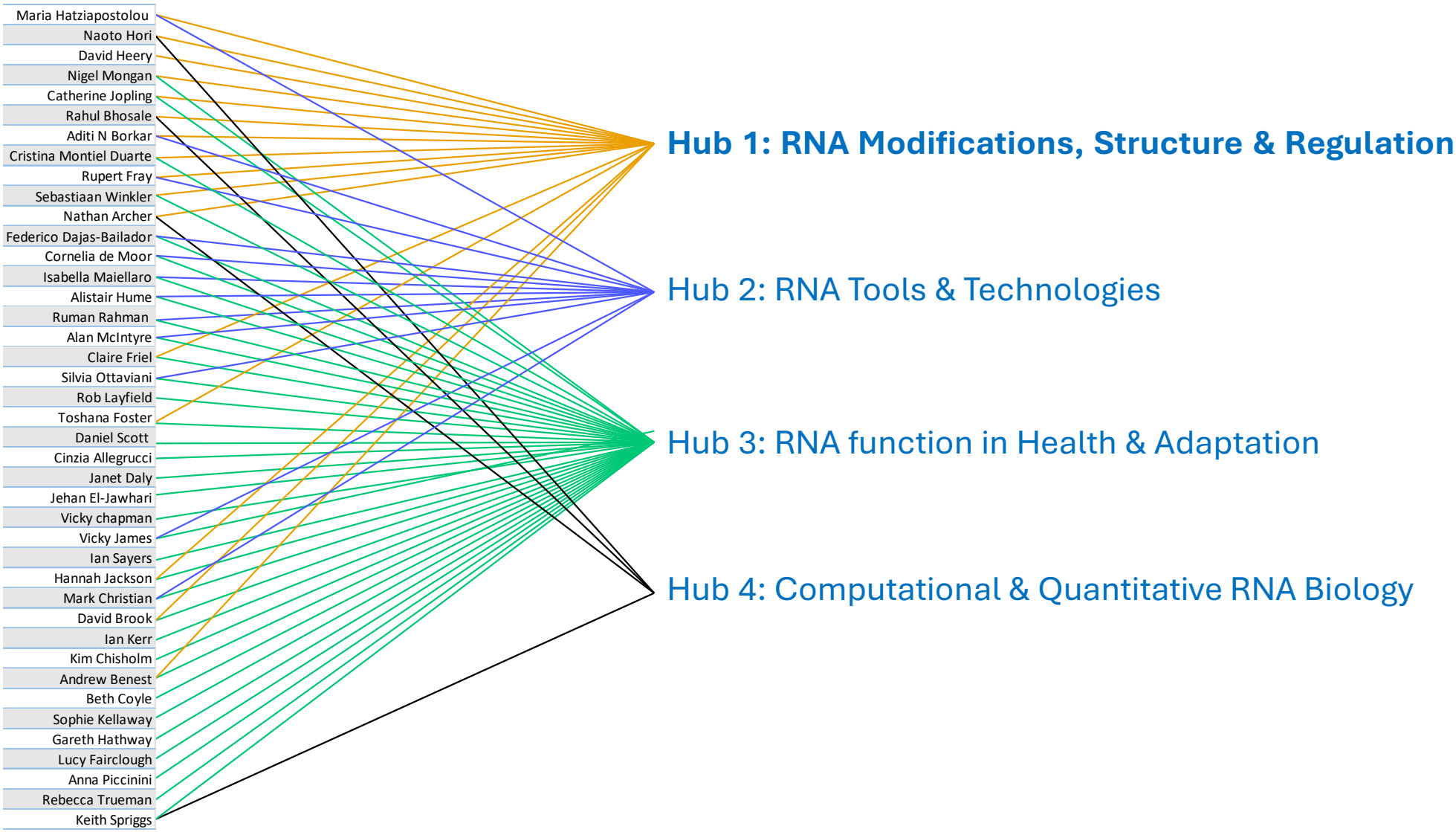
Hub 3: RNA Function in Health & Adaptation
How RNA mechanisms regulate gene expression in development, stress, ageing, and immunity, using cellular and in vivo models.

Hub 4: Computational & Quantitative RNA Biology
Integration of transcriptomic, translational, and multi-omics data to model RNA regulatory networks and function.

Interdisciplinary supervision
Connecting molecular mechanisms, RNA structure, and systems-level regulation
Advancing both fundamental understanding and applications in health and biotechnology.

Please tell us your name	Affiliation (Institution, Department)	Research Hub (up to two). Selecting those that best reflect the core expertise in your group
David Heery	Pharmacy BDI	Hub 1: RNA Modifications, Structure & Regulation
Nigel Mongan	Biodiscovery Institute	Hub 1: RNA Modifications, Structure & Regulation;Hub 3: RNA function in Health & Adaptation;
Sebastiaan Winkler	Biodiscovery Institute School of Pharmacy	Hub 1: RNA Modifications, Structure & Regulation;Hub 3: RNA function in Health & Adaptation
Cristina Montiel Duarte	NTU Biosciences Department	Hub 1: RNA Modifications, Structure & Regulation;Hub 3: RNA function in Health & Adaptation
Catherine Jopling	Pharmacy (BDI1&2)	Hub 1: RNA Modifications, Structure & Regulation;Hub 3: RNA function in Health & Adaptation;
Naoto Hori	School of Pharmacy	Hub 1: RNA Modifications, Structure & Regulation;Hub 4: Computational & Quantitative RNA Biology;
Nathan Archer	School of Veterinary Medicine and Sciences	Hub 1: RNA Modifications, Structure & Regulation;Hub 4: Computational & Quantitative RNA Biology
Isabella Maiellaro	SoLS PPN	Hub 2: RNA Tools & Technologies;Hub 3: RNA function in Health & Adaptation;
Ruman Rahman	Biodiscovery Institute School of Medicine	Hub 2: RNA Tools & Technologies;
Federico Dajas-Bailador	Life Sciences	Hub 2: RNA Tools & Technologies;Hub 3: RNA function in Health & Adaptation;
Alistair Hume	Life Sciences	Hub 2: RNA Tools & Technologies;Hub 3: RNA function in Health & Adaptation;
Lucy Fairclough	IIM SoLS	Hub 3: RNA function in Health & Adaptation
Ian Kerr	Life Sciences	Hub 3: RNA function in Health & Adaptation;
Gareth Hathway	Life Sciences	Hub 3: RNA function in Health & Adaptation;
Vicky Chapman	Life Sciences	Hub 3: RNA function in Health & Adaptation;
Sophie Kellaway	Medicine Translational Medical Sciences	Hub 3: RNA function in Health & Adaptation
Kim Chisholm	School of Life Sciences	Hub 3: RNA function in Health & Adaptation;
Rob Layfield	School of Life Sciences	Hub 3: RNA function in Health & Adaptation;
Cinzia Allegrucci	School of Veterinary Medicine and Biodiscovery Institute	Hub 3: RNA function in Health & Adaptation
Dr Toshana Foster	School of Veterinary Medicine and Science	Hub 3: RNA function in Health & Adaptation;Hub 1: RNA Modifications, Structure & Regulation;
David Brook	School of Life Sciences	Hub 3: RNA function in Health & Adaptation;Hub 1: RNA Modifications, Structure & Regulation;
Daniel Scott	School of Life Sciences	Hub 3: RNA function in Health & Adaptation;
Janet Daly	School of Veterinary Medicine and Science	Hub 3: RNA function in Health & Adaptation;
Beth Coyle	Medicine	Hub 3: RNA function in Health & Adaptation;
Hannah Jackson	Medicine	Hub 3: RNA function in Health & Adaptation;Hub 1: RNA Modifications, Structure & Regulation
Andrew Benest	Nottingham	Hub 3: RNA function in Health & Adaptation;Hub 1: RNA Modifications, Structure & Regulation;
Silvia Ottaviani	Nottingham Trent University Department of Bioscience	Hub 3: RNA function in Health & Adaptation;Hub 2: RNA Tools & Technologies
Vicky James	School of Veterinary Medicine and Science	Hub 3: RNA function in Health & Adaptation;Hub 2: RNA Tools & Technologies;
Keith Spriggs	School of Pharmacy	Hub 4: Computational & Quantitative RNA Biology;Hub 3: RNA function in Health & Adaptation;

RIC@N


Maria Hatziapostolou
Naoto Hori
David Heery
Nigel Mongan
Catherine Jopling
Rahul Bhosale
Aditi N Borkar
Cristina Montiel Duarte
Rupert Fray
Sebastiaan Winkler
Nathan Archer
Federico Dajas-Bailador
Cornelia de Moor
Isabella Maiellaro
Alistair Hume
Ruman Rahman
Alan McIntyre
Claire Friel
Silvia Ottaviani
Rob Layfield
Toshana Foster
Daniel Scott
Cinzia Allegrucci
Janet Daly
Jehan El-Jawhari
Vicky chapman
Vicky James
Ian Sayers
Hannah Jackson
Mark Christian
David Brook
Ian Kerr
Kim Chisholm
Andrew Benest
Beth Coyle
Sophie Kellaway
Gareth Hathway
Lucy Fairclough
Anna Piccinini
Rebecca Trueman
Keith Spriggs
Hub 1: RNA Modifications, Structure & Regulation
Hub 2: RNA Tools & Technologies
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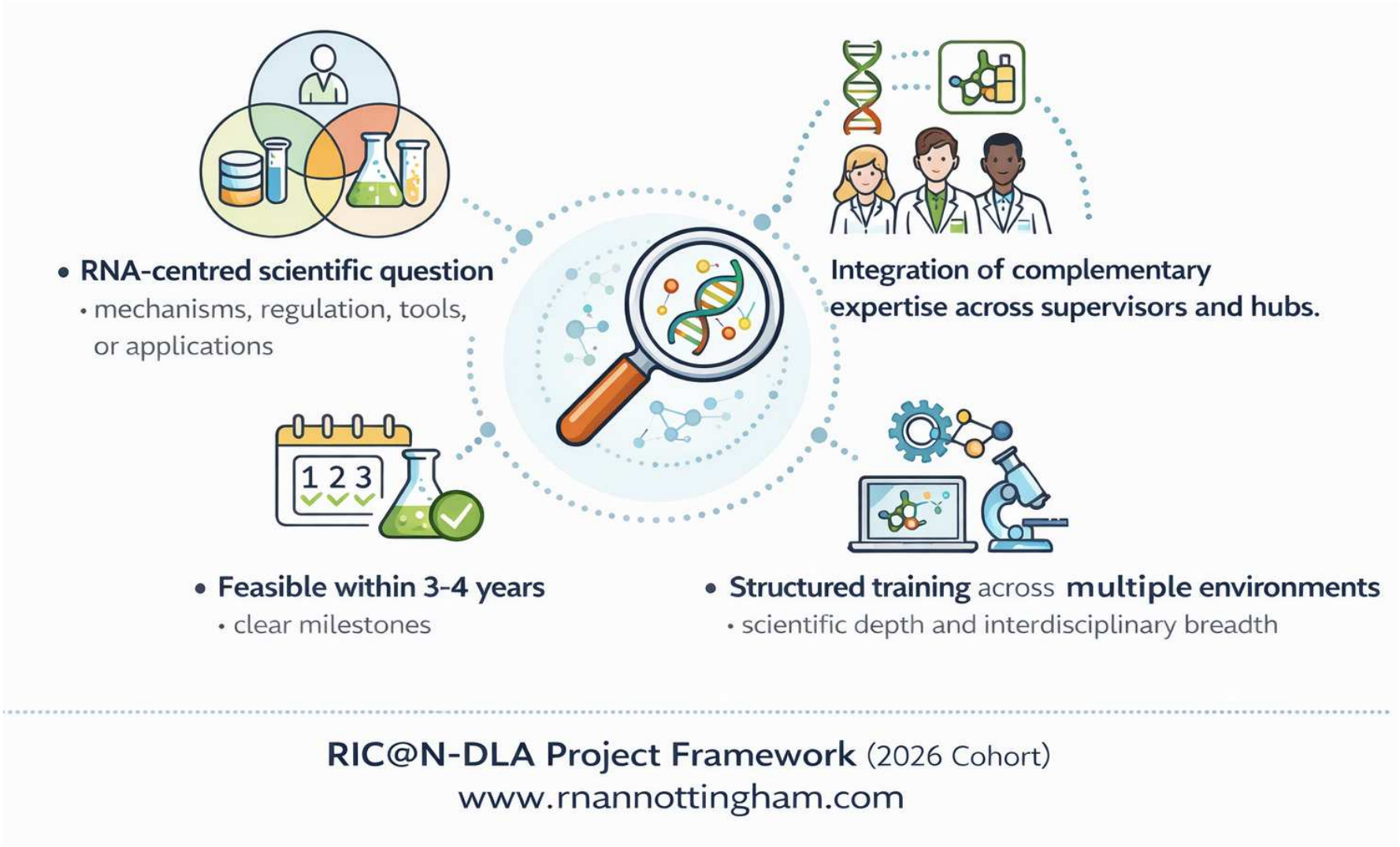
Projects at RIC@N-DLA:



Doctoral **training** at RIC@N-DLA

Training

- Span across Research Hubs
- Core competencies in RNA Research and professional training skill.
- Examples listed below:

Core Scientific Training (essential for all students)

RNA Biology Fundamentals
Structure, function, modification and lifecycle of RNA molecules.

Advanced Molecular & Cellular Techniques
RNA imaging, detection, CRISPR, RNAi, ncRNAs, RNA immunoprecipitation,
functional assays.

Quantitative & Computational Methods
Bioinformatics, statistical and structure modelling.

High-throughput & Spatial technologies
Single-cell transcriptomics, multi-omics integration

Platform & Technology Training *(Shared expertise and infrastructure)*

iPSC-Derived Systems & Organoids
Applications in modelling RNA regulation in controlled human cell contexts.

Synthetic Biology & RNA Engineering
Design, delivery, and control of synthetic RNAs for functional interrogation or therapeutic use.

Biophysical & Structural Analysis of RNA
Training in cryo-EM, NMR, and modelling of RNA-protein complexes.

Interdisciplinary and Translational Training *(cohort development)*

Ethics and RRI
Workshops on research and responsible innovation

Innovation, IP and Industry Collaboration
Scientific meetings with industry partners, workshops, etc.

Communication and Team Science
Experience working across hubs, exposure to career paths and collaborations.

RIC@N-DLA
2026

BBSRC Doctoral Landscape Awards
Bioscience for Human Health

RIC@N-DLA Studentships Application

Contact: Federico Dajas-Bailador
f.dajas-bailador@nottingham.ac.uk

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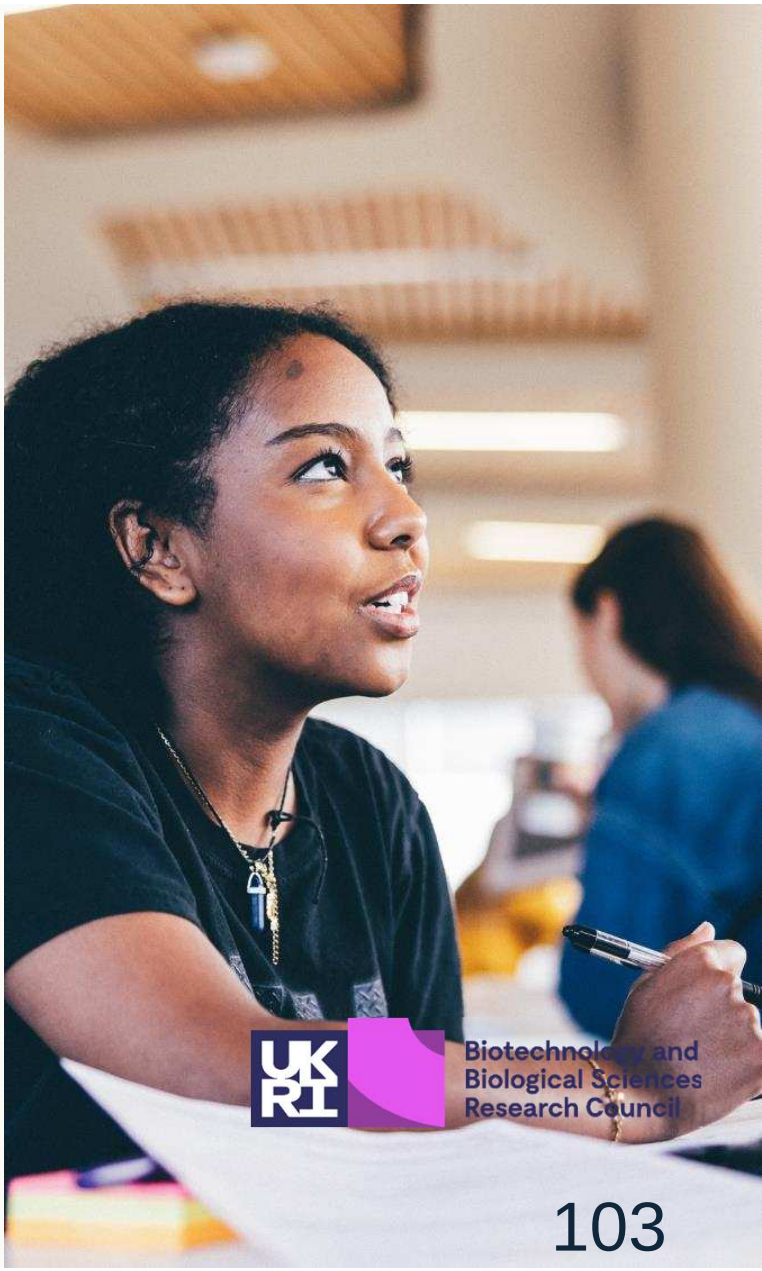
NTU Nottingham Trent University

Professional Internships for PhD Students (PIPS)

Sandra Rose, Welfare and EDI Officer
Alice Haslam, Welfare and EDI Officer

Professional Internships for PhD Students (PIPS)

- The Professional Internship for Postgraduate Students (PIPS) is a **compulsory** part of the training for a standard DTP student
- Placements are usually 12 weeks long
- Students source their own placement which they undertake between the 22nd -36th month of the programme
- Placements enable students to gain valuable and interesting experience in a different organisation and build new skills which help with future career prospects and planning



Home fee status students placements and International student placements

Home fee status students undertake a placement which is in a different field to their PhD – you have the opportunity to try out possible careers, work for a sector you are passionate about, or try something completely new

In order to meet Visa requirements **International students** undertake a placement in a field related to their degree – you have the opportunity to build additional key skills to use in your PhD, grow your professional network and build relationships with colleagues outside your supervisory team

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NTU Nottingham Trent University

UKRI Biotechnology and Biological Sciences Research Council

Support during the process

- The DTP team support you in this process and can give advice and guidance throughout – including ideas and support in finding a placement and guidance on completing the necessary paperwork

- Placements must be unpaid as your stipend payment continues during placement. In addition, you are eligible to apply for up to £1,000 to cover expenses on the placement such as relocation costs

Wellbeing

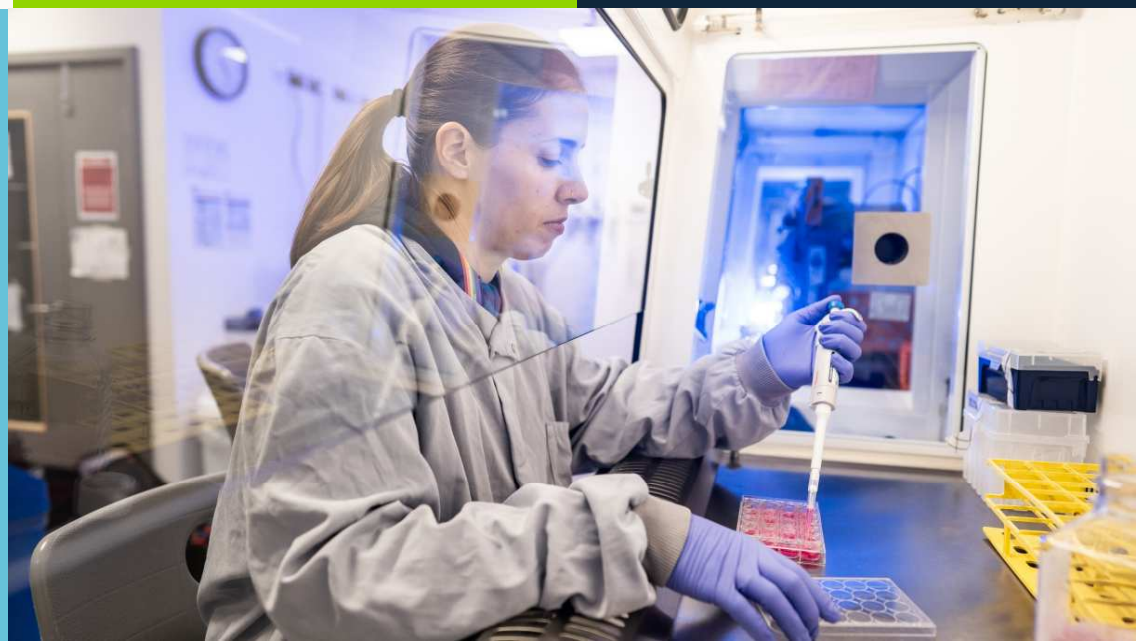
Sandra Rose, Welfare and EDI Officer
Alice Haslam, Welfare and EDI Officer

Wellbeing support on the programme

Dedicated Welfare and EDI Officers

We are here to support students through their PhD journey!

Access to wider University Support Services as needed



Wellbeing support - what we can offer

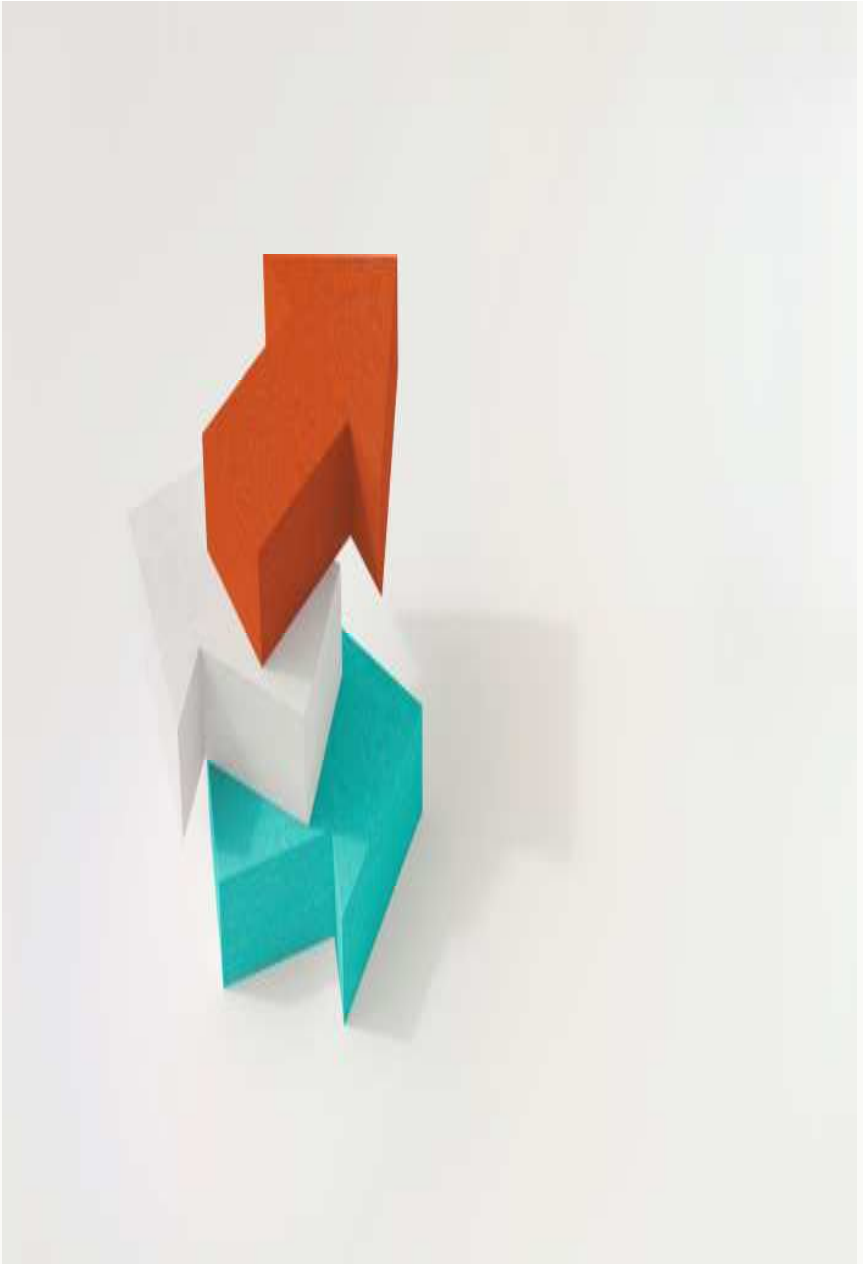
- Dedicated, tailored wellbeing support for students on the programme
- A pre arrival welcome call
- 121 support appointments available as needed and throughout your time here
- PGR focused wellbeing training programmes
- Peer mentor support
- PGR networks centred around diverse identities

Wider University support services

- There are a wide range of support services here such as a dedicated Counselling Service, Disability Support Services for anyone who has a disability or long-term health condition, Financial Support, Student's Union Advice Centre, Chaplaincy and many more!

- We can give advice and help to signpost to those services and make referrals to referral-only services as needed ensuring you are connected to the support you need as you progress along your PhD journey

- Your welfare officers can also advise on supportive processes such as paid sick leave, maternity / paternity leave and support for disabilities and long-term medical conditions, which are all supported by UKRI



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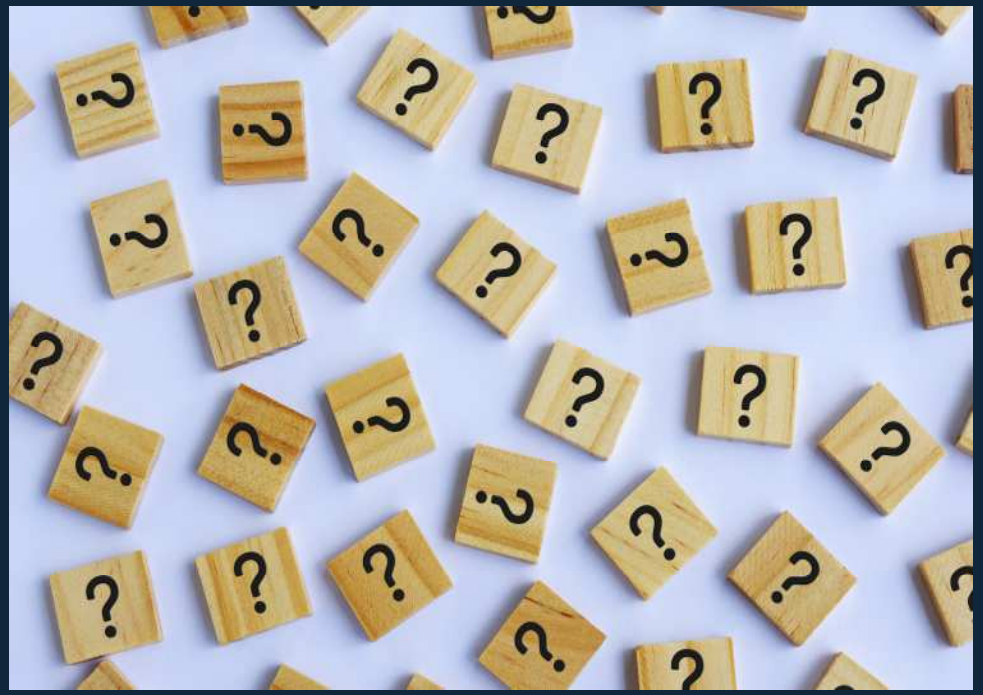
Thank you



Interview information and skills explored

Professor Mark Christian

DLA Interview Structure

- Standard DLA applicants called to interview will undertake 2 interviews online via MS Teams:
- 30 minute academic interview with panel members who are academics involved with the cluster you have selected
- 30 minutes transferable skills interview with 2 panel members

- CASE applicants will attend an additional 30 minute interview, chaired by the project supervisor. This panel will consist of other academics and where possible will have representation from the industry partner.

- Interview questions will be sent to all candidates at least seven days in advance of the interview.

- Interviews are expected to be held the week commencing 16 March 2026.

Interview format

Academic interview

- Candidates will be asked to make a short presentation about a recent research project – there are no standard questions for this section and you should be prepared to response to questions directly related to information you shared.

- Each cluster lead will select two papers that will be shared with candidates. You can choose to discuss both or concentrate on one in greater depth. You will be expected to discuss the strengths and weaknesses of the paper and how it relates to your experience in research.

Transferable skills interview

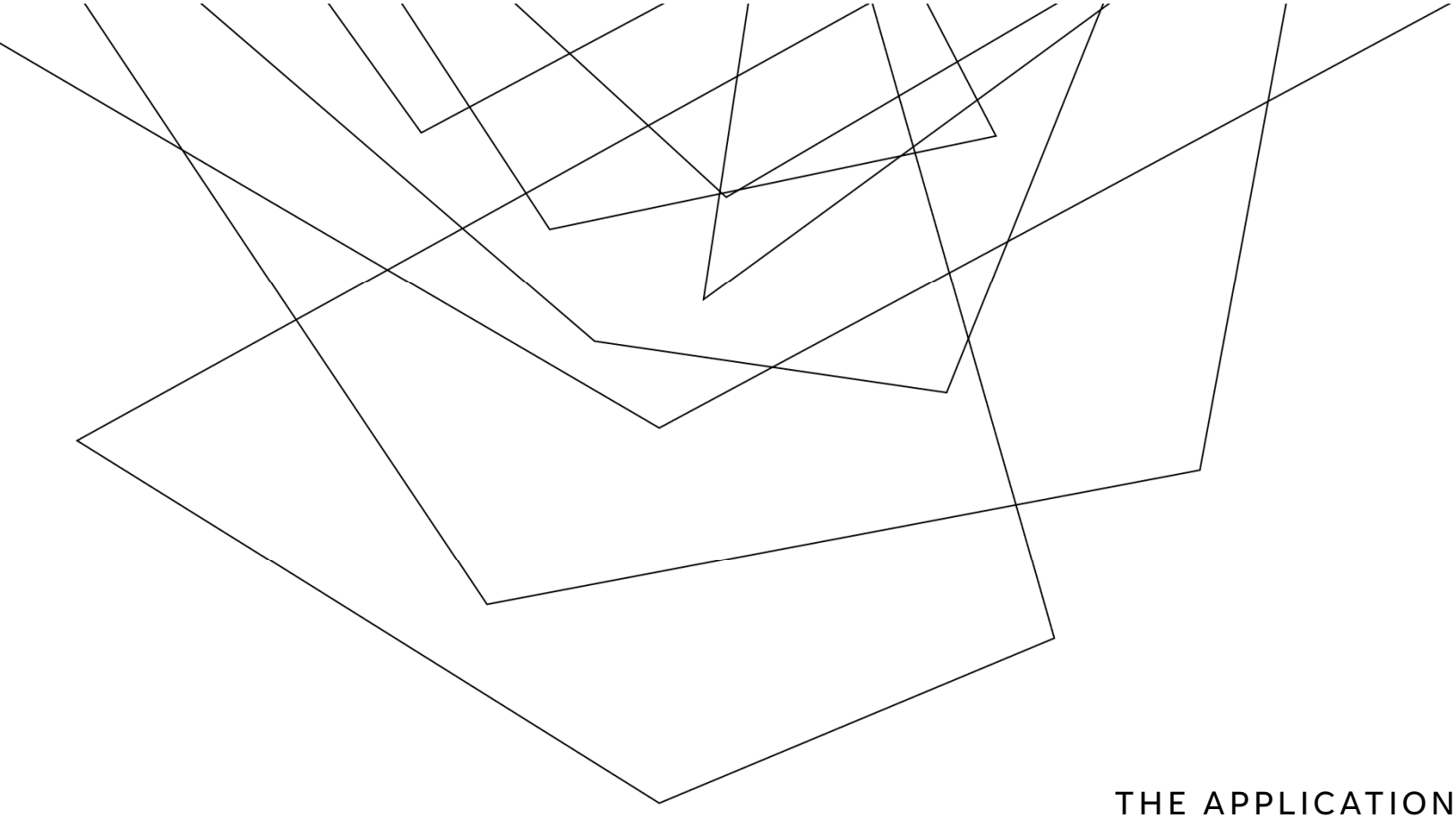
- These interviews will be conducted by members of the DLA team and academics.

- Questions will assess additional skills needed during a PhD, such as resilience, problem solving, teamwork and time management. Candidates will be expected to provide specific examples from academic life, work life or personal experience – whatever best demonstrates the skills set.

Student experience

Our current cohort

Olivia Haigh
Patrycja Lukasiewicz
Regina Galan Bataller
Ebikeseye Jeremiah



THE APPLICATION AND INTERVIEW PROCESS

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NOTTINGHAM TRENT UNIVERSITY

APPLICATION EXPERIENCE

Straightforward.

Don’t be afraid to “show off”.

Well-rounded.

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NOTTINGHAM TRENT UNIVERSITY

interview experience

Academic questions.

Transferable skills.

Don’t be afraid to say “I don’t know”!

ADVICE AND TIPS

Be aware of character count!

Do your research.

Adapt your experiences to the answers.

Experience so far!

Cohort

Lab rotations and training

Opportunities

Thank you!

If you have any further questions, please don't hesitate to contact me.

Olivia Haigh

University of Nottingham
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NOTTINGHAM TRENT UNIVERSITY

My first-year experience so far…

Patrycja Lukasiewicz

Overview of first semester

The start

- First two weeks, the whole cluster was together to complete general induction to the BBSRC DLA
  - oIntroductions to training expectations, support, and programme structure
  - o Ended with Crystal Maze

Separated into three themed clusters

- Following induction, the cohort was split into the three themed clusters
- Each cluster delivered the first semester training differently
  - Variation depended on: cluster size, number of available project options, how many labs could host rotations
- Training ended in December
- At the end, we had to submit a literature review and project choices

And now we are starting the individual projects

However, this won't be the last time the cohort will come together..

My thoughts

Being in a cluster

Benefits of first semester training

Project choices

Advice to future applicants

Be open-minded — your interests may shift once you see the labs

Engage with your cohort; they become your support network

Use rotations to ask questions and explore different research styles

Don’t stress about choosing the “perfect” project

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Thank you

University of Nottingham
UK | CHINA | MALAYSIA

Biotechnology and Biological Sciences Research Council

BBSRC Virtual Open Day

My experience as a CASE PhD student

Regina Galan-Bataller
2nd year PhD student

Applying for a CASE project

Why consider a CASE PhD?

- Gain industry-focused experience.
- Complete an internship of up to 12 months with the partner company (CV booster).
- Have an overall research direction outlined from the beginning.
- Learn how to work within a company environment and timelines.
- Build industry contacts.

My experience in applying & tips

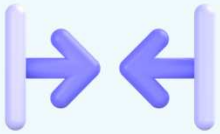
1. CASE application requires to express why you are a good fit for that specific project.

2. CASE application includes an additional interview with the main supervisor and the partner company, covering technical knowledge, relevant experience, fit for the project and overall research goals.

Top tips

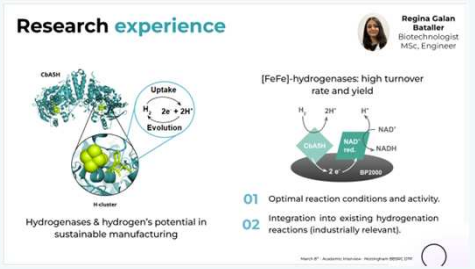
1. Research the company beforehand

2. Think how your research experience aligns to their proposed project



3. Be clear about your motivation

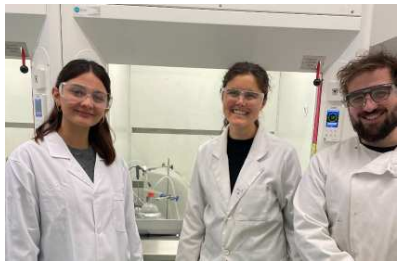
4. Prepare your presentation with good graphics and examples



Working with a CASE partner/supervisor

My CASE partner

HydRegen



Biochemistry-focused start up in Oxford

Extra considerations compared to a standard PhD

- Your research goals have to align with the project's main objective.
- You must meet with them every 1-3 months.
- The CASE supervisor may have influence in the experiments you perform.
- Tighter deadlines, clearer objectives and reports.
- Any poster or presentation you share must be approved by them (IP issues).
- Comply with some of their policies or preferences of work.
- A lot more people to communicate with and report to, not just your internal supervisors.
- First few months are intense since you start your project immediately (a lot of planning at the beginning).

But you get many benefits!

Benefits and final thoughts

But you get many benefits!

01
Exposure to work culture (good communication, reports)

02
Networking and industry contacts

03
External and business-focused input on your project

04
CV boost and many transferable skills

05
More feedback and help

06
Possibility of more collaborations and publications

07
Clearer research direction and aim

08
Quicker start on your project

University of Nottingham
UK | CHINA | MALAYSIA

Thank you