THE UNIVERSITY OF
NEWCASTLE
AUSTRALIA

DISCIPLINE OF BIOLOGICAL SCIENCES

HONOURS AND UNDERGRADUATE RESEARCH PROJECTS

2024

Undergraduate Research in the Discipline of Biological Sciences

School of Environmental and Life Sciences

There are three main research areas in the Discipline of Biological Sciences:

- Microbiology
- Reproductive Science
- Plant Science

We encourage undergraduates to get involved in research throughout their degree. By doing so you will learn and develop skills in searching, selecting and retrieving information from scientific sources, skills in project management, experimental research skills as well as skills in presenting scientific information in a clear and concise manner, both orally and in writing. These will provide you with a strong foundation for your future career, whether it be in the industrial, commercial or academic sector.

There are three main ways to get involved in research:

a) ***Summer research project:*** Short paid undergraduate research projects over summer. Scholarships are advertised each year

b) ***SCIE3500:*** A 10-unit undergraduate course consisting of a research project under the supervision of an academic staff member. Assessment is based on a progress report, a research notebook, a final project report and an oral presentation. The course is open to third year students who have successfully completed at least 140 units and have a cumulative GPA of at least 5.0 and is offered in both semesters. Course outline link here.

c) ***Honours research project:*** A full-year research project after completion of the Bachelor of Science or Bachelor of Biotechnology. A minimum GPA of 5.0 is required for entry into honours. Program handbook link here.

This booklet contains a list of undergraduate research projects currently available in the discipline. Academics are listed in alphabetical order. In all cases you should discuss potential projects with prospective supervisors before trying to enrol or apply.

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Dr Geoffry De Iuliis

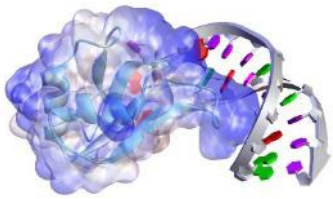
Male infertility and Protein Structure

Website: https://www.newcastle.edu.au/profile/geoffry-deiuliis
Contact email: geoffry.deiuliis@newcastle.edu.au

My research is aligned with investigating the underlying causes of male infertility, through understanding sperm cell biology and biochemistry. The potential impacts of environmental factors on these cells and in turn, human fertility, is a current focus. This research is more important than ever, especially as increasing numbers of Australians turn to assisted reproductive technologies like IVF for support. Another key focus of research is understanding the structure of proteins both in the reproduction and cancer fields. I also have a keen interest in promoting and fostering multidisciplinary science, myself having background in synthetic chemistry and an amature keen interest in quantum mechanics and cosmology

Sperm RNA binding proteins and measuring RNA damage:

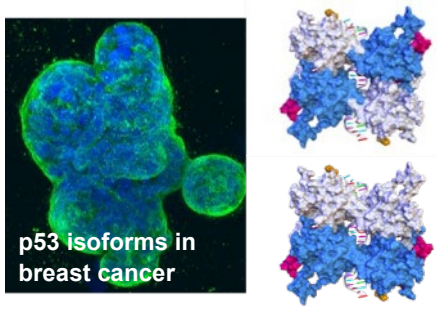
MicroRNA species are a key epigenetic factor that contributes not only to fertility but also to normal embryo development. While the importance of these epigenetic factors in reproduction is now established, how these microRNA species are packaged in the male reproductive tract and therefore their vulnerabilities to damage, particularly oxidative damage, is poorly characterised. This project will use a combination of a bioinformatics and protein/RNA isolation techniques to identify RNA binding protein candidates and to assess RNA oxidative damage.



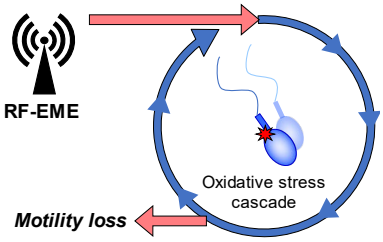
RNA Binding Protein

The quaternary structure of p53 and isoforms in drug resistant breast cancer:

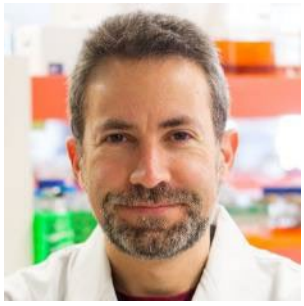
p53, known as the guardian of the genome, is a very high-profile target of investigation towards advancing cancer therapies. Surprisingly, the complete structure of this protein and its isoforms, as well as how they interact in complexes, is not fully understood. This project will predominately use molecular modelling, the newly available 'Alphafold' structures from Google Deepmind and other bioinformatics platforms towards developing our understanding how p53 variants may account for drug resistance in some breast cancer cell lines.



How do the electromagnetic fields used by mobile devices stop sperm motility?:



Electromagnetic energy in the radio and microwave spectrum (non-ionising radiation) are currently used for communications between mobile devices and access points (transmission towers and WiFi points). The ubiquitous nature of mobile device use in today's society has called into question the safety of such devices via the chronic exposure to low level, non-ionising radiation. We have found that experimental simulation of these fields are able to stop human sperm motility. This project will involve the exposure of spermatozoa to electromagnetic energy and the subsequent assessment of perturbed biochemical pathways that may lead to the observed motility loss. Understanding the origins of these effects in biology are critical for informing safety standards, while contributing to an area of science in the public spotlight.



A/Prof Ian Grainge

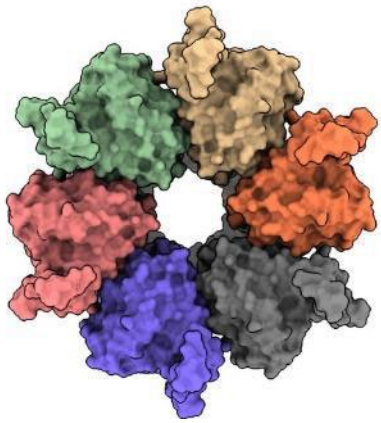
Molecular microbiology

Website: https://www.newcastle.edu.au/profile/ian-grainge
Contact email: ian.grainge@newcastle.edu.au

My lab focuses on 3 key areas:
i) genomic stability in bacteria- how bacteria copy their DNA (replication), overcome barriers in this process (DNA repair) and then ensure accurate chromosome segregation.
ii) the spread of antibiotic resistance genes in human pathogens
iii) the use of bacteriophage as novel therapeutics against antibiotic resistant bacteria.

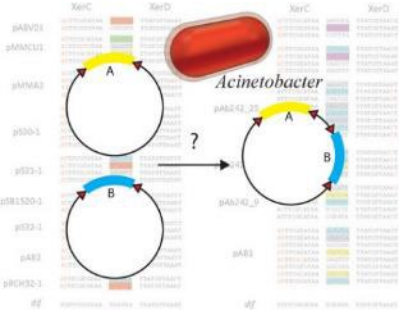
i) Genomic stability in bacteria:

This project covers three main aspects: how cells replicate their DNA, how the replication fork is processed if it stalls or collapses, and how bacteria ensure efficient chromosome segregation and cell division. We use single-molecule fluorescence microscopy to be able to count the number of proteins present in a replisome and how sub-complexes interact and exchange with each other. We then use genetics and biochemistry to establish the pathways cells use when the replisome runs into a protein block on the DNA. Finally, we are investigating a DNA translocase that co-ordinates chromosome segregation with cell division.



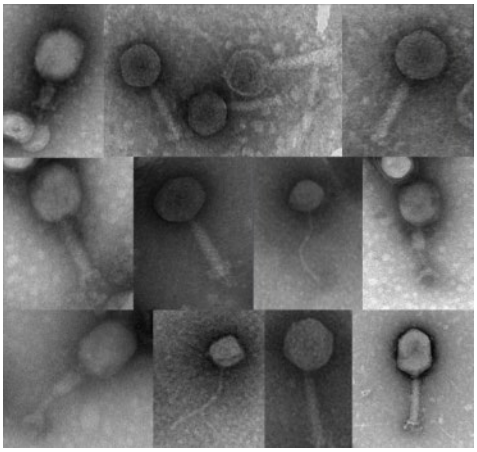
ii) A novel mechanism of antibiotic resistance gene spread in the pathogen *Acinetobacter baumannii*:

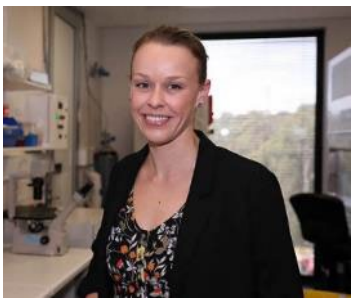
Carbapenem resistant *Acinetobacter baumannii* is ranked as the top priority pathogen for which novel treatments are required by the CDC and WHO. We have discovered a novel mobile genetic element, utilised by plasmids in this pathogen, that exchanges antibiotic resistance genes. This project will aim to uncover the molecular mechanism underlying this novel element. This will help understand the spread of antibiotic resistance genes and hopefully provide a method to combat this in the future.



iii) Discovery of novel bacteriophage:

Antibiotic resistant bacteria are predicted to become the leading cause of human death by the middle of the century unless novel treatments can be found. One alternative to using antibiotics is the use of bacteriophages - viruses that infect and kill bacteria. This project will isolate novel phages from waste-water treatment plant samples against a range of pathogens. The phage will be purified and amplified, then characterised by whole genome sequencing and electron microscopy. The purified phage can then be included in a BioBank being set up at Westmead hospital (Sydney) for use in patients.





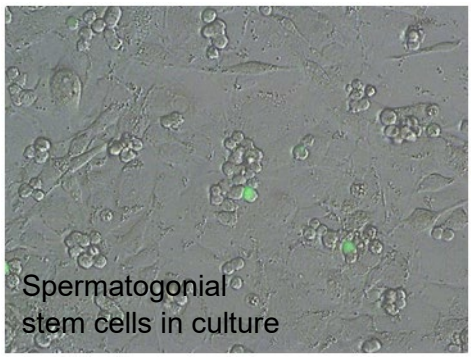
Dr Tessa Lord

Fertility and stem cell biology

Website: https://www.newcastle.edu.au/profile/tessa-lord
Contact email: tessa.lord@newcastle.edu.au

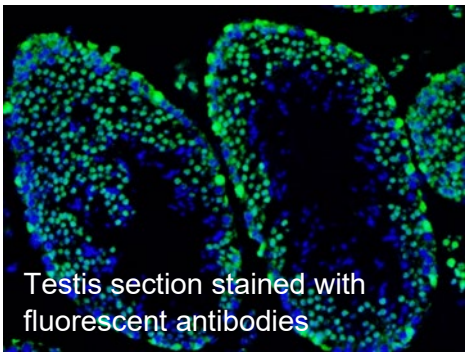
My research is primarily focused on understanding how the stem cells in the testis function to drive sperm production, and on harnessing this knowledge to support stem cell maintenance in an *in vitro* environment. Potential applications of such *in vitro* techniques include treatment of infertility in childhood cancer patients, and developing novel biobanking strategies for endangered wildlife.

Adapting oxygen concentration to better maintain stem cells in culture:


Spermatogonial stem cells in culture

Childhood cancer effects 700 Australian children each year, and while advancements in cancer research have ensured that survival rates are now over 80%, half of all male childhood cancer survivors are rendered infertile in adulthood. Because male paediatric cancer patients are not yet producing sperm, techniques for protecting their future fertility must instead utilise spermatogonial stem cells (SSCs) that are specified in the testes shortly after birth. My research looks at improving our capacity to expand and maintain these cells in *in vitro* culture, such that they could be collected prior to cancer treatments, then microinjected back into the testis in adulthood to restore fertility. My preliminary research has shown that SSCs prefer hypoxic (low oxygen) environments. As such, this project will investigate the response of SSCs to decreased concentrations of oxygen in culture.

Characterising transcription factors important for fertility:


Testis section stained with fluorescent antibodies

Because different oxygen concentrations can modulate stem cell behaviour, it is likely that oxygen-responsive transcription factors are involved in regulating SSC function and fertility. My research group has developed a novel transgenic mouse line in which a hypoxia-responsive transcription factor has been 'deleted' (i.e. a 'knockout' mouse line). We are currently performing breeding studies using these mice to establish any effects on either male or female fertility. This project will assess the outcomes of these breeding studies, and compare histology of reproductive tissues from male and female knckout mice with control mice that have not had their genome edited.

Prof Brett Neilan

Microbial and Molecular Diversity

Website: http://uonblogs.newcastle.edu.au/bluegreen
Contact email: brett.neilan@newcastle.edu.au

My work is focused on the genetics, biochemistry and ecology of microbial natural products. These compounds, which include toxins and antibiotics, are often sourced from microbes residing in novel environments, such as hypersaline lakes, thermal springs, hot and polar deserts, or in symbiotic relationships with plants. While natural products provide producing microorganisms with an ecological advantage (e.g., through the deterrence or inhibition of other organisms), they also have a range of therapeutic and industrial uses (e.g., as drugs, insecticides and research tools).

Exploring cyanobacterial specialised metabolism using heterologous expression:

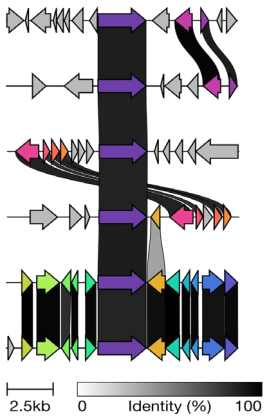
Microbial natural products have served as a major inspiration for the development of novel pharmaceuticals. The search for new natural products is a continuing endeavour, with new niches and microorganisms being probed to determine their ability to produce useful bioactive molecules. Cyanobacteria ('blue-green algae') are a largely untapped phyla that produce a multitude of natural products eliciting a range of pharmaceutically relevant activities, including antibiotic, anaesthetic, cytotoxic, and UV absorbing activities.

A large limitation for the exploitation of these molecules is the lack of accessibility in the natural host due to slow growth rates, relatively low production levels, and an inability to genetically manipulate the cyanobacteria. Therefore, this project will involve the isolation of cyanobacterial natural product biosynthesis genes, engineering them for heterologous expression in an industrial microorganism (*Escherichia coli*), and gene knockouts to characterise the enzymology of biosynthesis. The project has the potential to discover and sustainably produce novel compounds of ecological, industrial and biomedical significance.

Microbial endophytes as a source of novel medicines and pesticides:

Bacteria and fungi living within the tissues of plants offer their hosts a variety of ecological advantages. These so called 'endophytes' often produce specialised metabolites that deter pests and diseases, improve resilience to drought and salinity, or promote plant growth. Endophytes and their metabolites therefore have applications in agriculture and regenerative planting, as well as animal and human health. This project will explore endophytes from Australian plants for novel metabolites of ecological and industrial significance. Bacteria and fungi will be isolated from pant tissues, and their metabolites extracted and characterised (structurally and functionally). In parallel, endophyte genomes will be mined for specialised metabolite biosynthesis pathways, which will be expressed in an industrial microorganism (*Escherichia coli*). The project has the potential to discover novel medicines and natural alternatives to environmentally damaging agrochemicals.

The environmental antimicrobial resistome:



Antimicrobial resistance (AMR) is predicted to cause a staggering 10 million deaths worldwide by 2050. This looming public health threat is thought to be a result of antibiotic over-use and the flux of antibiotic pollution from human activity. For example, 80% of antibiotics used in aquaculture end up in the environment. This is thought to maintain environmental AMR gene prevalence that is potentially passed to pathogens of concern.
The importance of the environmental resistome in maintaining and disseminating AMR genes is little understood. The genes involved in AMR of the environment will be mined from the large datasets we have curated. AMR profiles will be compared, gene resistant families and genetic transfer elements will be identified. The data generated will be used to design novel solutions such as diagnostic tests for AMR management in a range environments.

Harnessing insect microbiomes to control mosquitoe-bourne disease:

The saltmarsh mosquito, *Aedes vigilax,* is one of Australia's most prolific mosquito species and is the primary vector of Ross River virus; a disease affecting more than 4,000 Australians annually. By characterising the mosquito holobiome (host, bacterial, fungal, archaeal, and viral community), this project will provide unique insights into the symbiotic, commensal, and transiting microbiota and their capacity to influence mosquito health and development, as well as the transmission of disease. The data generated will be used to design novel solutions for mosquito management in the Hunter region and beyond.

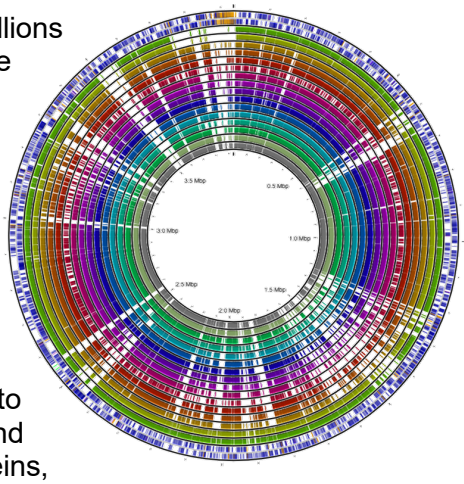
A/Prof Karl Hassan

Microbial genomics and biochemistry

Website:
Contact email: karl.hassan@newcastle.edu.au

Microorganisms impact our lives in countless ways. Some can make us sick, but many others have positive impacts on human and environmental health. Microorganisms will also play a leading role in clean energy and manufacturing futures. My lab applied comparative and functional genomics, biochemistry and synthetic biology to investigate microbial processes that have positive and negative impacts on our lives and to harness microbial activities in small molecule detection and production. Projects are available in the following research areas.

Antimicrobial drug resistance in hospital acquired bacteria

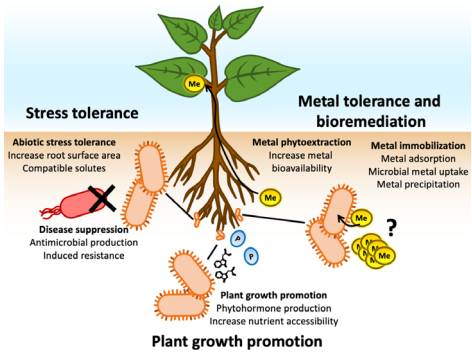


Hospital-acquired infections caused by pathogenic bacteria cost billions of dollars each year and increase patient pain and morbidity. These infections are becoming increasingly difficult to treat due to rising levels of drug resistance in the pathogens. Projects in my lab are focused on understanding the mechanisms of antimicrobial resistance and virulence in human bacterial pathogens, understand how these pathogens and their resistance genes are spreading and investigate novel approaches to controlling their growth.
We are working with colleagues in hospitals to identify reservoirs of drug resistant bacteria and examine their evolution to inform infection control strategies. We have developed new technologies to identify and functionally characterise bacterial resistance factors and used these technologies to describe new bacterial resistance proteins, including a completely new class of multidrug resistance determinants.

Synthetic Biology

The ability to design and synthetically produce biological parts has almost unimaginable potential to solve the world's challenges. One application of this technology is in the engineering of microbes to catalyse the production of industrially useful chemicals using renewable feedstocks. These chemicals could be used as alternatives to oil as fuels or in the manufacture of polymers. Our research team is investigating approaches to streamline microbial engineering to develop next-generation biocatalysts.

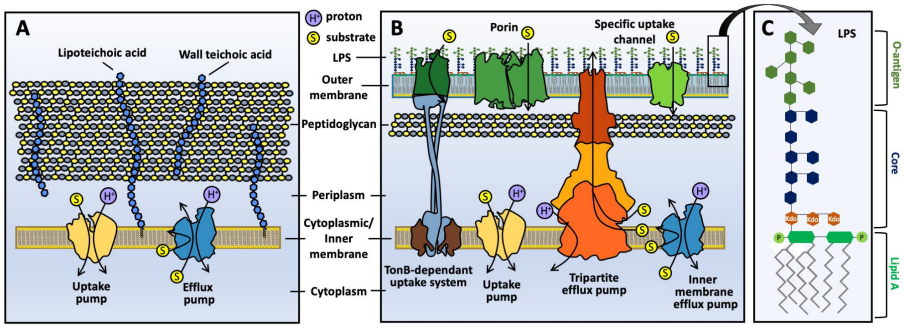
Soil bacteria in plant biocontrol and bioremediation



Soil microbes are hugely diverse and central to terrestrial ecosystems. We are investigating plant-colonising bacteria that could be used to protect crops from disease. These bacteria could alleviate the need for harmful agrochemicals. We have identified several novel gene clusters that encode plant protection factors, such as secreted specialised metabolites, and determined environmental conditions that promote their expression. We are investigating various species of soil bacteria, both plant associated and free living, that are able to degrade harmful chemical pollutants or help to prevent their spread. We have identified gene clusters that are likely to facilitate these activities.

Membrane transport systems and bacterial cell envelopes

Biological membranes are fundamental to cellular life. These thin layers of lipids provide permeability barriers that help to prevent the entry of toxins and the exit of nutrients from cells and sub-cellular compartments. Membrane transport systems are comprised of proteins that sit in biological membranes and facilitate the movement of ions or molecules from one side to another. Our research has focused on these proteins for over a decade. We have discovered new families of transport proteins involved in antimicrobial resistance and identified novel substrates for uptake and efflux pumps that are relevant to drug resistance and biotechnology. Using protein engineering, we are working to develop new to nature pumps designed to recognise compounds of interest.



Dr Ben Long

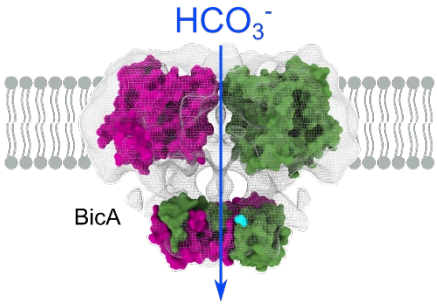
Photosynthesis research

Website: https://www.newcastle.edu.au/profile/ben-long
Contact email: mailto:ben.long@newcastle.edu.au

My research is focused on the understanding and application of CO_2 concentrating mechanisms, found in cyanobacteria (blue-green algae), for the improvement of photosynthetic CO_2 capture by plants and synthetic biological systems. This biotechnological approach to both improved crop yield and carbon sequestration is of critical importance as CO_2 emissions, climate change, and food security become more pressing global issues.

Directed evolution of bicarbonate transporters for crop improvement:

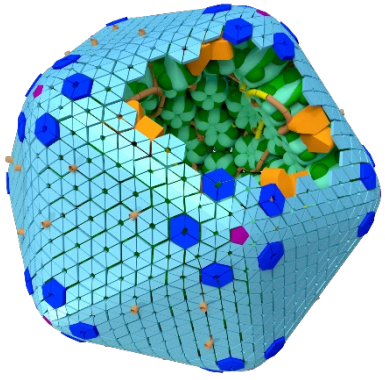
A synthetic biology aim in plant biology is the reconstruction of cyanobacterial CO_2 concentrating mechanisms (CCMs) in plants to improve carbon fixation and crop yield. Membrane bicarbonate transporters pump inorganic carbon across membranes to feed substrate to the world's most abundant enzyme, Rubisco. Engineering strategies to synthetically reconstruct CCMs in plants have been slowed by challenges to deliver functional bicarbonate transporters to plant chloroplast membranes. This project aims to evolve novel bicarbonate transporters that could be used in plant based CCMs. Using synthetic biology approaches, a library of potential membrane transporters will be screened using a directed evolution system to create new genetic parts. Sequencing of modified transporters will enable additional rational design to further modify transporter function. The project will require Loop DNA assembly to generate complex expression cassettes, protein expression analysis and DNA sequence design.



The cyanobacterial bicarbonate pump, BicA

Building carboxysomes (turbo-charged CO_2 fixation engines) in E. coli:

The central component of the cyanobacterial CO_2 concentrating mechanism (CCM) are large proteinaceous, subcellular compartments called carboxysomes. Carboxysomes are nano-metre sized protein capsules containing hundreds of copies of the CO_2 fixing enzyme Rubisco, the enzyme carbonic anhydrase. Inside carboxysomes, bicarbonate is converted into CO_2 to fuel turbo-charged carbon capture. This characteristic of cyanobacterial CCMs makes them an important target for reconstruction in crop plants to enhance carbon fixation and yield. In this project a series of component carboxysome genes will be used to test the step-by-step construction of carboxysomes in *E. coli*. Using Goldengate DNA assembly techniques and a library of genetic parts, a complex set of carboxysome genes sets will be tested. Assessment of protein expression and the purification and analysis of carboxysomes will be used to test how well different expression units perform. Successful combinations of genes will form the basis of plant transformation to generate carboxysomes in plant chloroplasts.



Carboxysomes are nanometre-sized proteinaceous 'organelles' that capture CO_2 in cyanobacteria