Queensland Alliance for Agriculture and Food Innovation

Honours Projects 2021

https://qaafi.uq.edu.au/honours

The Queensland Alliance for Agriculture and Food Innovation (QAAFI) is a research institute of The University of Queensland (UQ), supported by the Queensland Government

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As one of the few research-intensive universities worldwide located in a subtropical environment, UQ is a global leader in agriculture and food science research in subtropical and tropical production systems. QAAFI is comprised of four inter-related research centres, with a focus on the challenges facing tropical and sub-tropical food and agribusiness sectors in the tropical and subtropical systems. This booklet presents available research projects, which would be suitable for Honours students or Masters Project students in each of these four centres. Students are encouraged to contact the listed supervisors for further details.

Contents

For general information about undertaking Honours within QAAFI please contact QAAFI Honours Co-ordinator A/Prof Mary Fletcher (mary.fletcher@uq.edu.au).

Centre for Animal Science Projects

<table>
<tr>
<td>CAS 1 Project

<i>Prof Ala Tabor</i></td>
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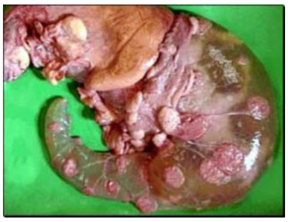
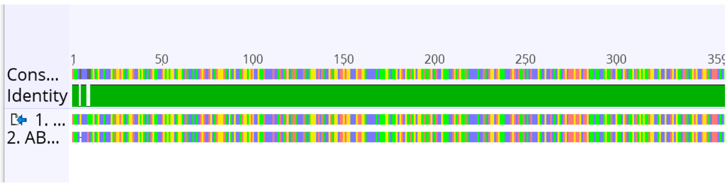
1) Bovine campylobacteriosis diagnosis and genomic analyses

Bovine venereal diseases affect cattle in northern Australia causing decreased calf output and thus a reduction in breeding efficiencies. As the causative agent of bovine campylobacteriosis, our laboratory has developing novel diagnostic methods to differentiate *Campylobacter fetus* subspecies *venerealis* from other organisms. Genomic sequencing has identified potential new diagnostic targets to separate this subspecies from the closely related species *C. fetus* subspecies *fetus.* These subspecies are currently indistiguishable using available molecular and phenotypic methods which has perplexed researchers world-wide. We have undertaken genomic sequencing as well as biolog phenotypic array analysis of several *C. fetus* subsp. *venerealis* strains, in order to identify markers for both molecular and improved culture methods. Opportunities for genomics, bioinformatics, molecular and culture method development for research are available in our laboratory – the angle of the project can be negotiated to suit the candidate.





Calf loss

Sequence alignments

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<td>Advisors contact</td>
<td>

- Prof Ala Tabor Email: a.tabor@uq.edu.au Phone: +61 3346 2176
- Associate Advisors: A/Prof Pat Blackall, Dr Conny Turni, Prof Ben Hayes

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<tr>
<td>Webpage</td>
<td>https://qaafi.uq.edu.au/profile/492/ala-tabor</td>
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<td>Useful majors</td>
<td>Microbiology / biotechnology / molecular biology / bioinformatics</td>
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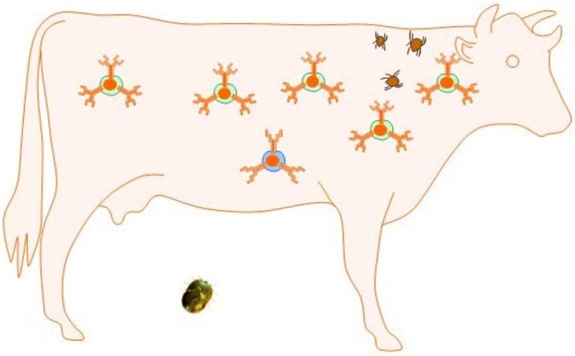
CAS 2 Project

Prof Ala Tabor

2) Biomarkers and bovine genetics to identify cattle tick resistance markers

Cattle ticks cost $22-30b worldwide in losses with 80% of the world's cattle populations at risk across tropical and sub-tropical regions. Research has focused on vaccine development which is progressing well, however the development of predictive markers would assist breeders to select cattle which may be more tick resistant. Previous studies from this group using skin immunohistochemistry have shown that certain cattle are primed with T cells in the skin before a tick challenge. New investigations using Next Generation Sequencing and proteomic methods will be used to study these phenomena further. Opportunities for molecular biology, RNA seq, proteomics, bovine genetics and bioinformatics analyses for research are available in our laboratory – the angle of the project can be negotiated to suit the candidate.



N.B. ticks and immune cells not to scale

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Webpage	https://qaafi.uq.edu.au/profile/492/ala-tabor
Useful majors	Microbiology / biotechnology / molecular biology / bioinformatics

CAS 3 Project

Prof Ala Tabor

3) Title – Optimising Oxford Nanopore sequencing for arthropod genome sequencing with large repetitive content

Ticks and the diseases they carry are second to mosquitoes as vectors of human and livestock diseases. Novel ways to control ticks can be developed from genomic data. Ticks have large repetitive genomes with up 70% repetitive content at 2-7Gb total genome size. Tick genomics is still developing and as such are relatively poorly studied at the genomic level. There are 4 published tick genomes which consist of more than 100,000 scaffolds based on the combination of long and short read technologies. Oxford nanopore sequencing of long reads has yet to be exploited for tick genome sequencing and DNA/RNA extraction method optimisations are first required. Optimising the preparation of nucleic acids for use in a Nanopore MinION and the draft assembly of a whole tick genome will be a world first. The student will have support from staff and students familiar with the equipment (in house) and will learn critical skills using modern sequencing technologies. Other sequencing project opportunities are available and can be tailored to the student's interests and skills.

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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biotechnology

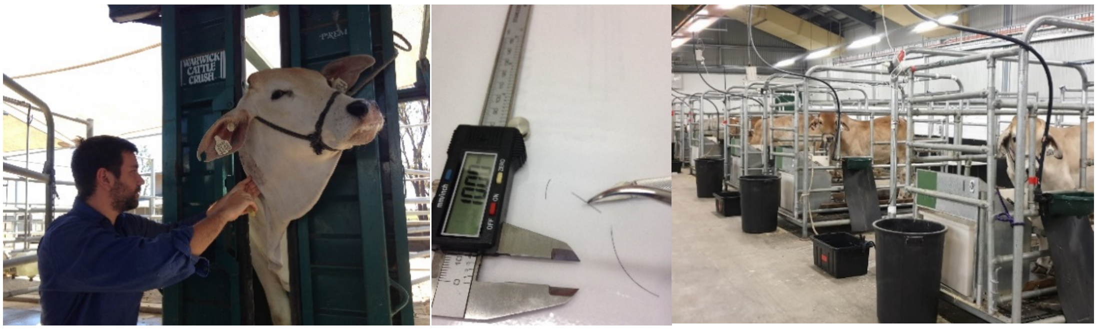
CAS 4

Project

Dr Luis Prada e Silva

4) Nitrogen recycling as determinant for feed efficiency of Bos indicus cattle

To thrive in northern Australia, cattle depend on the capacity of efficiently extract nutrients during periods of restricted availability. Therefore, the ability to recycle nitrogen (N) back to the rumen, instead of eliminating in the urine, is crucial. This project is testing four relevant hypotheses: 1) feed efficiency in low-protein diets is associated with N recycling and not correlated with feed efficiency in nutrient abundant diets; 2) rumen efficiency can be practically measured and incorporated into genetic selection; 3) N utilization efficiency (NUE) can be measured by isotopic analysis in animal tissues; and 4) differences in rumen efficiency reflect differences in rumen microbial populations. Ninety *Bos indicus* steers are being evaluated over 60 days receiving a diet supplying only 70% of the rumen degradable protein (RDP) requirements, followed by 60 days on a diet providing 100% of the RDP. After each period, efficiency of microbial protein production is measured in metabolism crates, using purine derivatives in urine and N recycling is quantified with infusion of 15N-enriched urea. Rumen contents are collected for rumen microbiome and transcriptome analysis. Tail hair has been used to evaluate a less-invasive approach to estimate NUE.



Advisors contact

- Dr Luis Prada e Silva, Email: l.pradaesilva@uq.edu.au Phone: +61 334 62166
- Associate Advisors: Dr Diogo Costa, Dr Sarah Meale

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Webpage

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Useful majors

Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Genetics / Microbiology

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CAS 5

Project

Dr Luis Prada e Silva

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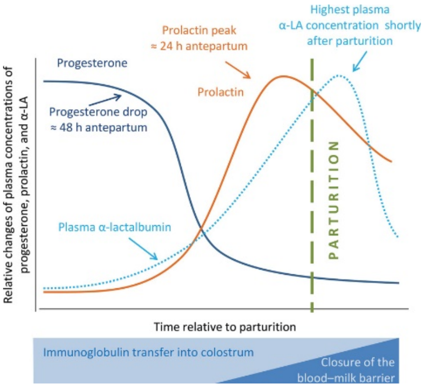
5) Nutritional modulation of the transfer of passive immunity in tropically adapted cattle

This experiment aims to clarify factors associated with the nutritional modulation of colostrum secretion and transfer of passive immunity from cows to calves. Proper colostrogenesis and transfer of passive immunity is certainly a major factor for calf survival, it is our overall hypothesis that protein metabolism during late gestation with its consequent effects on hormonal and metabolic profile are important factors modulating colostrum secretion and quality. The project aims is to determine the effect of protein and prebiotic feeding during the transition period on the transfer of passive immunity. Factors measured will include metabolite and hormonal changes in the cow around calving, colostrum quality, and calf vigour, health, and growth in the first two weeks. The practical objective is the development of efficient supplementation strategies to minimize stress and calf loss in commercial herds. The results obtained in the present study could be used to improve adoption of more efficient supplementation strategies alleviating the nutritional stress around parturition, preventing the substantial loss of calves currently occurring in parts of Queensland, and reducing the use of antibiotics in cattle.



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Advisors contact

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- Associate Advisors: Dr Geoffry Fordyce, Dr Diogo Costa

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Useful majors

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Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Genetics / Microbiology

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CAS
6 to 13

Project

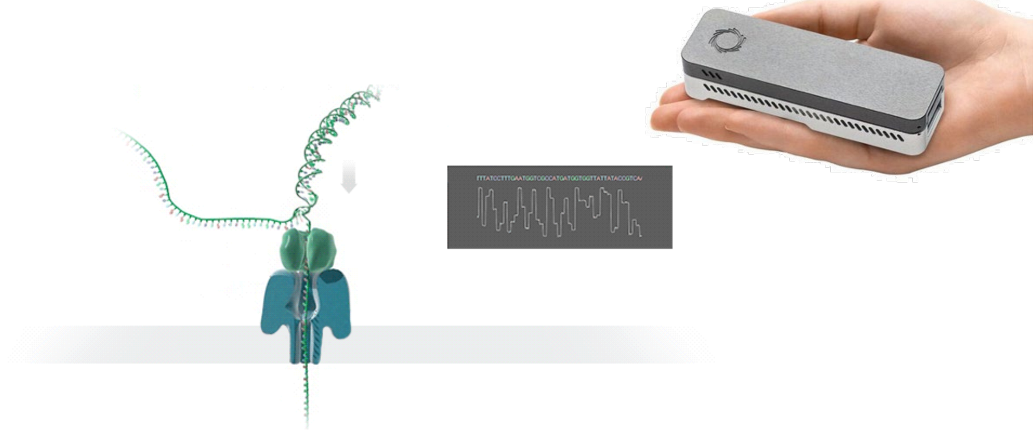
Prof Ben Hayes

6) Structural Issues: Identification of large structural variants in the bovine genome using real time long read sequencing

Structural variation is the term used to describe larger insertions, deletions, duplications and translocations in the genome. These structural variants are a largely untapped genomic resource despite the fact that they account for over 10 million base pairs.

This project will use long read sequence to identify structural variation in the bovine genome. Once structural variants are identified their abundance and distribution in the Australian Brahman population will be quantified. Finally the relationship between the identified structural variants and protein coding genes will be examined.

This project will provide students with a deep understanding of cutting edge sequencing methods, bioinformatics skills, project design, scientific communication and industry relevance. Bioinformatics, statistics, mathematics, molecular genetics and agricultural skills would all be considered favourability for this project, however they are not mandatory.



CAS
6 to 17

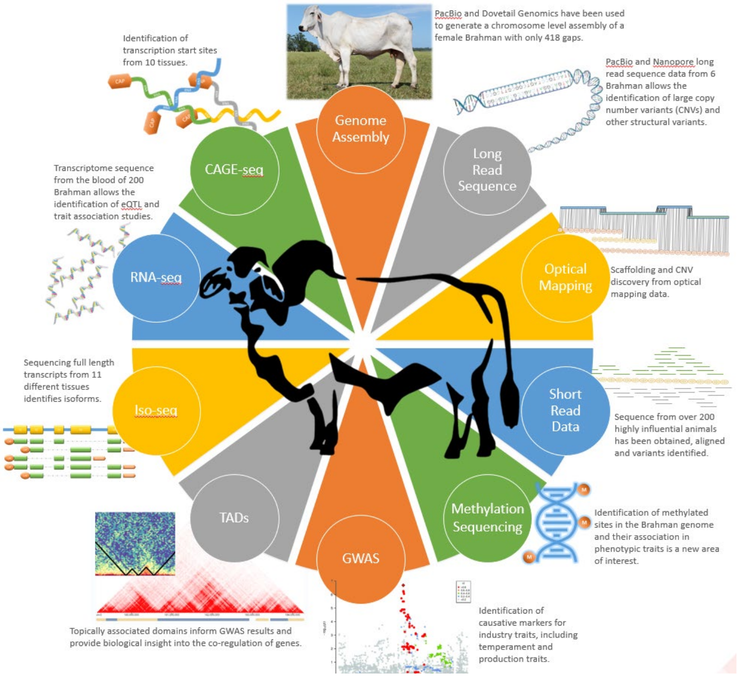
Project

Prof Ben Hayes

7) Combining omics: Examining genome structure and function for health and welfare

Students will use literature review skills to select genes that are relevant to traits important to the beef industry, including those related to health and welfare, adaptation, fertility and production. Using a broad range of data the student will then examine the selected genes for structural variations, expression level changes, epigenetic signals, and population wide variation. Data types included short and long DNA sequence, short and long expression data, as well as methylation epigenetic data. The goal of the project is to better understand important genes related to northern beef cattle production by bringing together data from various cutting edge technologies.

In this project students will develop a broad range of data analysis and bioinformatics skills as well as gain experience with project design, scientific communication and industry relevance.



PacBio and Dovetail Genomics have been used to generate a chromosome level assembly of a female Brahman with only 418 gaps.

PacBio and Nanopore long read sequence data from 6 Brahman allows the identification of large copy number variants (CNVs) and other structural variants.

Scaffolding and CNV discovery from optical mapping data.

Sequence from over 200 highly influential animals has been obtained, aligned and variants identified.

Identification of methylated sites in the Brahman genome and their association in phenotypic traits is a new area of interest.

Identification of causative markers for industry traits, including temperament and production traits.

Topically associated domains inform GWAS results and provide biological insight into the co-regulation of genes.

Sequencing full length transcripts from 11 different tissues identifies isoforms.

Transcriptome sequence from the blood of 200 Brahman allows the identification of eQTL and trait association studies.

Identification of transcription start sites from 10 tissues.

CAS
6 to 17

Project

Prof Ben Hayes

8) Filling the gap: completing the Brahman reference assembly

Students will use cutting edge long range sequencing to complete and validate regions of the Brahman reference genome assembly. They will apply bioinformatics methods to identify and validate the correct sequence with which to fill genome gaps and discover and validate structural variants both within the Brahman breed and between Brahman and *Bos taurus* cattle. The goal of the project is to increase the accuracy of the reference assembly and characterise genomic diversity within and between cattle.

In this project students will develop molecular genetics and bioinformatics skills to provide a value tool for the Northern Beef industry.

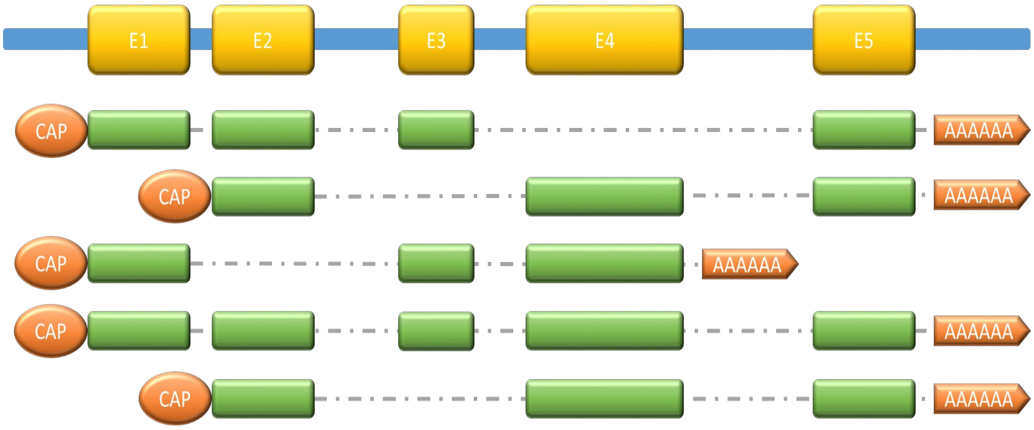
CAS
6 to 17

Project

Prof Ben Hayes

9) Form and Function: Novel isoform discovery

New technology now allows the sequencing to hundreds of thousands of full length transcripts (expressed genes) from a single sample. A dataset of 10 tissues has been generated using isoseq - a method that can sequence the full length expressed isoforms in a sample. This project will analyse that isoseq data and identify novel isoforms including those for genes at are known to of industry importance. This information will provide a deeper understanding of the genetic variation in the Australian northern beef industry and be used to inform large genome wide association studies and discovery of

	mutations controlling gene expression studies. The project focuses on bioinformatics and analysis skills in a fast developing area of research. 
CAS **6 to 17** **Project** *Prof Ben Hayes*	**10) Predicting age using methylated sites** In humans, the methylation state of CpG sites changes with age and can therefore be utilized as an accurate biomarker for aging. In cattle, biological age prediction based on methylation status could provide key information for genetic improvement programs. Additionally, comparing chronological age with biological age (based on methylation status) can provide important information about the stress an animal has been under during its lifetime. However, relatively little is known about DNA methylation patterns in cattle. Students will use cutting edge data sources including reduce representation bisulphite sequencing data, whole genome bisulphite sequencing, long read sequencing and human methylation data to identify differentially methylated regions between old and young animals and validate those regions with modern molecular technologies. This project will require skills in bioinformatics as well as molecular biology. Students will learn how to manage very large sequence data sets. 
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Webpage	https://qaafi.uq.edu.au/centre-for-animal-science
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Agriculture / Veterinary Medicine

CAS
6 to 17

Project

Prof Ben Hayes

11) FastStack - evolutionary computing to stack desirable alleles in wheat

A major emerging challenge in wheat breeding is how to stack desirable alleles for disease resistance, drought, and end-use quality into new varieties with high yielding backgrounds in the shortest time. As the number of known desirable alleles for these traits increases, the number of possible crossing combinations that need to be considered increases exponentially.

An approach using artificial intelligence (AI) platform FastStack – designed to solve highly combinatorial problems, and coupled with genomic prediction could address this challenge. The computing power of AI designed according to the patterns of data that are predictive of wheat performance will allow to estimate the best crossing strategy for breeding an improved wheat variety more quickly. To test the AI-derived wheat crosses, a speed-breeding technique employing controlled glasshouse conditions will be used to develop the populations fast, where it is possible to grow wheat up to 6 generations per year compared to only 1 in the field.

The 'gene-stacking' process through FastStack is expected to reduce the length of a wheat breeding cycle and increased genetic gain, thus will lead to more profitable wheat varieties for Australian growers, and expanded exports to high value markets that require quality grain.

Students will gain and strengthen their skills on Plant Breeding technique (i.e. crossing, population development in the speed-breeding facility, other glasshouse activities), Quantitative and Computational Genetics (i.e. basic computational analysis on simulations, genomic predictions).

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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics / Agriculture

CAS
6 to 17

Project

Prof Ben Hayes

12) Reducing methane emissions through improved understanding of the rumen microbiome

Ruminants such as cattle are host to a vast array of microbial species which reside in a specialised chamber of their stomach called the rumen. Microbes in the rumen digest the feed which the animals eat. Cutting edge sequencing technologies now allow for accurate profiling of microbiome communities. This study will analyse the microbes that live inside the rumen of cattle fed a methane mitigating diet. Methane is a potent greenhouse gas that is produced as a by-product of ruminant digestion. The goal of this study is to identify the species of microbe that have a changed abundance in response to the diet and therefore increase our understanding of how the rumen microbiome can be manipulated to reduce methane emissions from ruminants.

In this project students will develop molecular genetics, bioinformatics, quantitative genetics, and analysis skills in a fast developing area of research.

Advisors contact

Advisors:

- Prof Ben Hayes
- Dr Elizabeth Ross, Email: e.ross@uq.edu.au, Phone: +61 7 334 62162

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Webpage https://qaafi.uq.edu.au/centre-for-animal-science

Useful majors Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Microbiology / Agriculture / Veterinary Medicine

CAS
6 to 17

Project

Prof Ben Hayes

13) Cow fertility through the ages

In Brahman cattle, a heifer's age at puberty is often a general indicator of her overall fertility and how fertile she may be during her lifetime. There is a high genetic correlation between puberty and lifetime fertility, indicating that these traits share some level of genetic control. This means, that if we can better understand heifer puberty, potentially we can select for more fertile cows.

In this study, students will determine if genes associated with puberty may be used to increase our understanding of lifetime fertility, and use this information to predict a cow's potential for fertility over her lifetime. This project will combine data analysis of very large genomic and phenotypic data sets (up to 30,000 cattle), quantitative genetics, and industry relevance to help improve cow fertility in the north Australian beef industry.

	In this project students will develop data analysis and quantitative genetics skills, and will learn techniques to handle extremely large biological data sets. Students will have the opportunity to learn genomic selection techniques. 
Advisors contact	Advisors: • Prof Ben Hayes • Dr Bailey Engle, Email: b.engle@uq.edu.au , Phone: +61 7 334 66506
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics / Agriculture / Veterinary Medicine
CAS **6 to 17** **Project** *Prof Ben Hayes*	**14) Genes impacting female fertility** Fertility is an important, but complex genetic trait influenced by a large number of genes and other genetic factors. Additionally, whether or not a female will become pregnant is dependent upon a large number of environmental factors such as stress and nutrition. This makes it incredibly difficult to determine the primary genetic determinants of pregnancy, and this is true not only in human medicine, but livestock as well. In beef cattle, this combination of variables affects the breeding potential of a cow. The goal of this project is to assess genetic variation leading to different pregnancy outcomes in Brahman cows. Students will use RNA-seq data for differential gene expression analyses to identify genes and genomic regions influencing pregnancy status in female cattle. This project will develop skills in bioinformatics and data analysis, in order to better understand female fertility in Australian beef cattle. Students will gain valuable experience working with a large RNA-seq data set.

	
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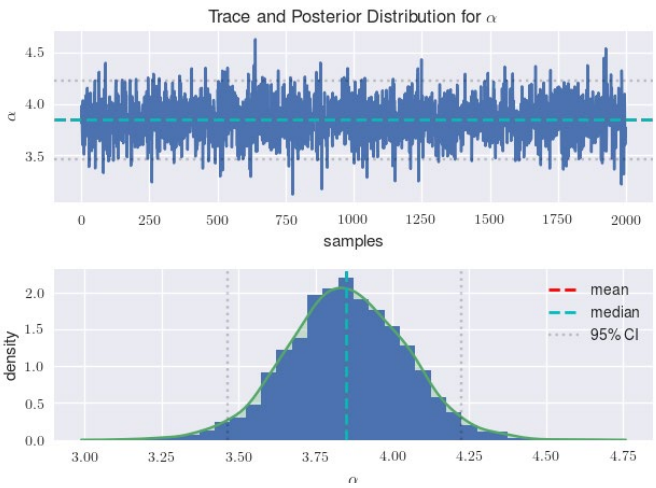
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Agriculture / Veterinary Medicine
CAS **6 to 17** **Project** *Prof Ben Hayes*	**15) The need for speed in Genomic research: Comparing algorithms to estimate polygenic effects in tropically adapted beef cattle** With the advent of new genomic technologies comes the need to develop new statistical and computational algorithms that can handle large amounts of data in Animal Science. Within the Bayesian paradigm, current methods to estimate polygenic effects for complex traits rely mostly on Gibbs sampling. These approaches are not necessarily scalable to big datasets as the computation time grows more than linearly with sample size. This means that huge computational resources, in terms of RAM memory and/or computing time, need to be used to fit such models.

The aim of this project is to compare the performance of alternative Markov chain Monte Carlo (MCMC) algorithms when estimating polygenic effects for complex traits in tropically adapted beef cattle. In addition to Gibbs sampling, at least two MCMC algorithms will be compared: Hamiltonian Monte Carlo and Variational Inference. The student will also learn the basics of Bayesian Statistics and High Performance Computing at UQ.



CAS
6 to 17

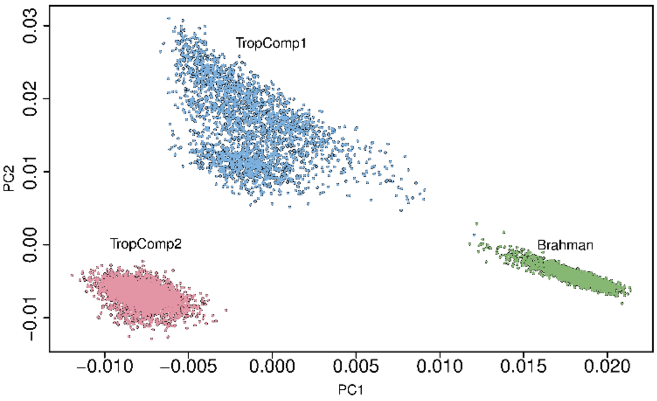
Project

Prof Ben Hayes

16) Improving genotype imputation in the tropics: using *Bos indicus* reference populations for tropically adapted beef cattle

Accurate imputation of genotypes is key in animal genetics because it increases the statistical power to detect causal variants and improves genomic selection. Genotype imputation accuracy depends crucially not only on sample size but also in the genetic similarity of the reference and target samples. Due to the lack of appropriate reference populations, genotype imputation in tropical beef cattle is often done with *Bos taurus* animals which a different sub-species.

The aim of this project is to use newly sequenced animals from a large reference population for a sample of tropically adapted Zebu animals genotyped with a low-density chip. Both reference and target (Zebu) samples are from *Bos indicus* breeds and thus are highly related genetically. To measure the impact of using *Bos indicus* animals as reference population, imputation using publicly available sequenced data from *Bos taurus* animals will also be done. The student will learn methods for genotype imputation, high performance computing and visualization in R.



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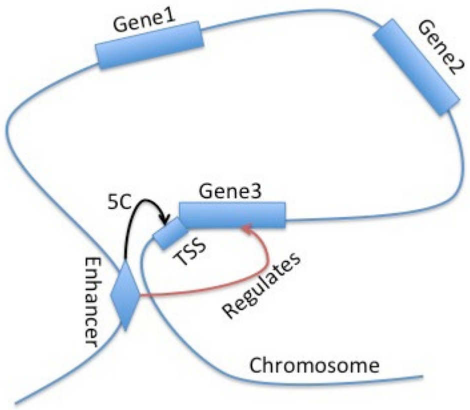
Location	• QAAFI CAS; Blg 80, St Lucia, UQ Campus
Webpage	https://qaafi.uq.edu.au/centre-for-animal-science
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics
CAS **6 to 17** **Project** *Prof Ben Hayes*	**17) Exploring TSS-enhancer correlations and identification of novel mutations in TSS-enhancer regions in *Bos indicus* species** Next generation sequencing technologies including Cap-Analysis of Gene Expression (CAGE) have made it possible to accurately identify and quantify transcriptional start sites (TSSs) and enhancer throughout the genome. Having access to both TSSs and enhancers in a single experiment makes CAGE well suited for studying many aspects of transcriptional regulation, for example TSS-enhancer correlations, super enhancer identification, mutation discovery in TSS-enhancer regions, etc. This study will analyse the CAGE-tags mapped to the *Bos taurus* reference genome to identify CAGE-enhancer and explore the TSS-enhancer correlation and discovery of novel mutation in TSS and enhancer. In this project students will develop molecular genetics, bioinformatics, quantitative genetics, and analysis skills in a fast developing area of research. 
Advisors contact	Advisors: • Prof Ben Hayes • Dr Mehrnush Forutan, m.forutan@uq.edu.au
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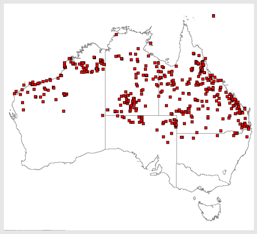
Webpage	https://qaafi.uq.edu.au/centre-for-animal-science
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics

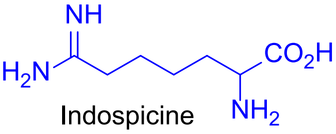
CAS 18 Project

Assoc Prof Mary Fletcher

18) Investigating the impact of the native legume *Indigofera linnaei* (Birdsville Indigo) on cattle reproduction in northern Australia

Indospicine is a toxic amino acid found only in *Indigofera* plant species, legumes which have widespread prevalence in grazing pastures across tropical Africa, Asia, Australia, and the Americas. Indospicine is an unusual in that it is non-proteinogenic and is cumulatively absorbed as the free amino acid into tissues of livestock grazing *Indigofera* plant species. It is a competitive inhibitor of arginine metabolic processes and in experimental studies causes both liver disease and abortion in cattle and sheep. The abortive effect has also been reported in pregnant rabbit does where feeding as little as 5% *Indigofera* in daily rations resulted in 100% stillborn when fed in the last 15 days of pregnancy.





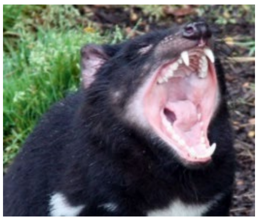
Indospicine

Indigofera linnaei (Birdsville Indigo) has a widespread distribution in north Australia rangelands of northern Australia, and given the extensive nature of cattle production systems in these regions, foetal losses due to maternal consumption of indospicine may well occur and contribute to observed reproduction losses in these regions without any specific attribution. This project is laboratory based and is designed to measure indospicine concentration in serum samples collected from pregnant cows and investigate the relationship between the measured indospicine levels and pregnancy outcomes.

This project will be located in laboratories at Food and Health Sciences Precinct, Coopers Plains (Brisbane) and utilise Liquid Chromatography Mass Spectrometry (LC-MS).

Advisors contact Location	• **A/Professor Mary Fletcher** mary.fletcher@uq.edu.au Phone: +61 7 344 32479 • **Professor Michael McGowan** (m.mcgowan@uq.edu.au) **Location: Health and Food Sciences Precinct, Coopers Plains**
Webpage	http://researchers.uq.edu.au/researcher/235 https://researchers.uq.edu.au/researcher/49
Useful Majors	Chemistry/ Chemical sciences/ Biochemistry & Molecular Biology

CAS 19 Project *Dr Conny Turni*	**19) Characterisation of antimicrobial resistance and virulence genes associated with avian *Pasteurella multocida*** *Pasteurella multocida* is the cause of fowl cholera, an economically important disease that has re-emerged in both meat chickens and layer chickens as these industries have shifted to organic and free range based systems. While now a major disease, there is little known about genes driving both virulence and antimicrobial resistance in Australian avian isolates of *P. multocida.* This project seeks to address the gaps in our knowledge. Our laboratory is the national reference centre for this pathogen and holds an extensive culture collection from around Australia, including a set of over 200 isolates that have been subjected to whole genome sequencing. A representative set of isolates will be screened by bioinformatic analysis for the presence of antibiotic resistance genes and for the genes that have been associated in overseas studies with virulence.   Fowl cholera outbreak in meat chickens Whole genome analysis
Advisor(s) contact	- Dr Conny Turni (**c.turni1@uq.edu.au**) - Associate Advisors: Dr Pat Blackall - **Dr Lida Omaleki** **Location: EcoSciences Precinct, Dutton Park**
Webpage	https://researchers.uq.edu.au/researcher/2477
Useful majors	**Biochemistry & Molecular Biology / Bioinformatics / Microbiology**

CAS 20 Project *Dr Conny Turni*	**20) Oral cavity bacteria of marsupials – a One Health Approach** Recent work at UQ has confirmed that bacteria of the *Pasteurellaceae* family are common inhabitants of the oral cavity of marsupials. In some case, these organisms have been associated with koala bite wound infections of humans. Other researchers have linked the level of the members of this family with overall koala health. In our most recent work, we have focussed on isolates the koala oral cavity and have data that suggests at least new species of the genus *Lonepinella* and possibly 2 entirely new genera within the family *Pasteurellaceae*. We now would like to start a similar study looking at isolates from other marsupials. We have a collection of isolates that includes hosts such as Tasmanian Devils, Quolls, Possums and Platypus. Understanding these organisms is important from an wildlife health view point as well as from the viewpoint of the health of wildlife carers. Our culture collection will form the basis of this study. Specific hosts will be selected and the isolates from that host screened by basic phenotypic tests. The isolates will then be subjected to molecular characterisation (sequencing) based on key "evolutionary chronometers" as well as the whole genome. Bioinformatic analysis will then be undertaken to assign the isolates to either existing genera and species or confirm the exiastience of further novel genera and species. Tasmanian devil   Spotted tailed quoll
Advisor(s) contact	- Dr Conny Turni (c.turni1@uq.edu.au) - Associate Advisors: Dr Pat Blackall; Dr Lida Omaleki Location: EcoSciences Precinct, Dutton Park
Webpage	https://researchers.uq.edu.au/researcher/2477
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CAS 21 Project *Dr Conny Turni*	**21) Phenotypic and genotypic aspects of antimicrobial resistance in porcine *Pasteurella multocida*** *Pasteurella multocida* is associated with porcine respiratory disease complex, a disease complex that is associated with high morbidity and mortality. In Australia *P. multocida* has been regarded a secondary pathogen, however, research has shown that it can also be a primary pathogen. Not much is known about the antimicrobial resistance, especially the resistance genes. The last survey of antimicrobial resistance in *P. multocida* was done in 2014. A further study was done in that year to look at the antimicrobial resistance genes of 20 isolates of *P. multocida* via PCR and the whole genome of one isolate was explored. This project seeks to address the gaps in our knowledge. Our laboratory is the national reference center for this pathogen and holds an extensive culture collection from around Australia. A representative set of isolates will be screened by a standardized phenotypic method for antimicrobial resistance. Isolates that show resistance will then be screened for resistance genes, principally by PCR but also by whole genome sequencing. The knowledge gained from this project will be an important support tool for the Australian pig industry.  
Advisor(s) contact	- Dr Conny Turni (**c.turni1@uq.edu.au**) - Associate Advisors: Dr Pat Blackall - **Dr Lida Omaleki** **Location: EcoSciences Precinct, Dutton Park**
Webpage	https://researchers.uq.edu.au/researcher/2477
Useful majors	**Biochemistry & Molecular Biology / Bioinformatics / Microbiology**

CAS
22 to 24
Projects

Prof Tim
Mahoney

22) The application of gene editing to improve animal resistance to infections

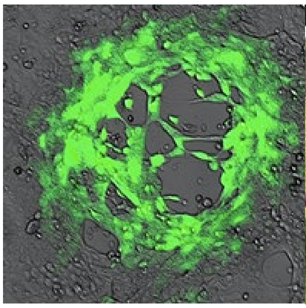
Gene editing technologies have enabled the rapid and specific modification of the genomes of complex organisms. Projects are available that will focus on the application of gene editing to increase the resilience of livestock cells to pathogens which reduce productivity. These projects will enable the candidate to gain experience in mammalian cell culture, transfection, growth and titration of viruses, molecular cloning, Western blotting, quantitative real-time PCR, genomic analyses, and fluorescence microscopy. These studies will improve our understanding of host/pathogen interactions towards the development of more resilient livestock.

23) Construction of bovine herpesvirus 5 infectious clone

Bovine herpesvirus 1 (BoHV-5) is a neurotrophic which is associated with severe and fatal disease in younger cattle. Unlike BoHV-1, BoHV-5 occurs sporadically in the world's cattle population, except in South America. In this project, you will utilise genome edit tools, such as CRISPR/Cas9, to manipulate the BoHV-5 genome to construct an infectious clone of the virus. The results of this project will provide a better understanding of gene function in BoHV-5, particularly in respect to virulence. This information will improve our understand of how BoHV-5 interacts with its host at the molecular level and lead to the development of improved control strategies.

24) Characterisation of bovine herpesvirus 2 genome

Bovine herpesvirus 2 (BoHV-2) is associated with mastitis in cattle. Of all of the herpesviruses which infect cattle, BoHV-2 is by far the most poorly characterised. This project will address this knowledge gap by using next generation sequencing and conventional PCR and sequencing technologies to completely sequence the BoHV-2 genome. The results of this project will enable the genome-wide comparisons of the BoHV-2 genome to other bovine and mammalian herpesviruses. These comparisons will improve our understanding of host/virus interactions at the molecular level for important viral properties such as tissue tropism and virulence.



	Candidates with their own project ideas that fit within the research activities described on Prof Mahony's profile page are encouraged to contact him.
Contact Advisor/s	• Prof Tim Mahony – QAAFI, Email: t.mahony@uq.edu.au Location: Blg 80, St Lucia UQ Campus
Webpage	https://qaafi.uq.edu.au/profile/486/timothy-mahony

Centre for Nutrition and Food Sciences Projects

CNAFS 1 Project *Dr Heather Smyth*	**1) Food applications of native plant foods and ingredients** Australia has a rich source of native plants that provide spices, fruits and nuts which have been part of indigenous communities' diets for generations. In the broader community native plants are becoming increasingly popular which calls for development of food applications of these unique ingredients. The aim of this study is to explore food applications of Australian native foods such as wattle seeds, seed weed, bunya nut, kakadu plum, saltbush among others. Basic chemistry, product development and sensory and consumer techniques will be used to explore food applications of Australian native foods and ingredients. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods. 
Advisor(s) contact Location	• Dr Heather Smyth, h.smyth@uq.edu.au • Associate Advisors: Dr Sandra Olarte s.olartemantilla@uq.edu.au • Associate Advisors: Dr Daniel Cozzolino d.cozzolino@uq.edu.au Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
Webpage	https://qaafi.uq.edu.au/profile/33/heather-smyth
Useful majors	The project can be tailored depending on the applicant's interest and background. A major in at least one of the following is highly desirable: Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Microbiology / Agriculture / Food Science

CNAFS 2 Project

A/Prof Daniel Cozzolino

2) Exploring the biological potential of *Terminalia carpentariae*, an Australian native plant

Plants of the genus *Terminalia* (family Combretaceae) have been used as traditional medicine, for centuries around the world. A number of studies have reported the biological potential of a number of individual *Terminalia* spp., including their antioxidative potential, antimicrobial, anti-inflammatory and anti-cancer potential. Australia is home to approximately 29 *Terminalia* species or subspecies. *Terminalia carpentariae*, commonly known as wild peach, is one of these native Australian *Terminalia* plants. Not much information is currently available on its biological potential and bioactive components. This project aims to explore the bioactive components and biological potential of *T. carpentariae*. Outcomes will help bridge the current knowledge gaps.

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Useful majors	Biochemistry & Molecular Biology / Chemistry / Microbiology

CNAFS 3 Project

A/Prof Daniel Cozzolino

3) Effect of storage conditions on sensory and bioactive qualities of Tasmanian pepper berry, an Australian native plant

Australian endemic plants have gained significant attention over recent years due to their increased use in pharmacy, medicine, food, beverages, cosmetics, perfumery, and aromatherapy. Tasmanian pepper (*Tasmannia lanceolata*, Winteraceae) is a native plant of Australia. The berries, leaves and bark of this native plant, have been used as food and medicine, for centuries. Leaves are used as a herb, whereas its berries are used as a spice. Both leaf and berry have a strong heat and pungent flavour on the palate. The spicy character of Tasmanian pepper has been associated with the sesquiterpene polygodial. For retaining premium marketability and bioactivity, the retention of characteristic volatile profile is essential. This study will focus on understating the effect of storage parameters on the sensory and bioactive qualities of the Tasmanian pepper berries.

Advisor(s) contact	**Dr Daniel Cozzolino** Email: d.cozzolino@uq.edu.au **Associate Advisors:** Dr Anh Phan and A/Prof Yasmina Sultanbawa
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Webpage	www.qaafi.uq.edu.au
Useful majors	Biochemistry & Molecular Biology / Chemistry / Microbiology

CNAFS 4 Project *A/Prof Daniel Cozzolino*	**4) Effect of maturity on biological activity and bioactive compounds in Kakadu Plum (*Terminalia ferdinandiana*) fruit** The Australian native plant, Kakadu plum *(Terminalia ferdinandiana)* has been traditionally a part of the diet of the Australian Aboriginal community. The Indigenous communities have also used this fruit for its medicinal properties. A number of studies have reported that KP contains a number of bioactive phytochemicals with health promoting properties. Research have also revealed its promising antimicrobial, antioxidative and anti-inflammatory potentials. However, effect of maturity on the bioactive potential, and chemical make-up of the fruit, is not known. This project will investigate the effect of different maturity stages, on the biological activity and bioactive compounds in Kakadu Plum fruit. 
Advisor(s) contact Location	**Dr Daniel Cozzolino** Email: d.cozzolino@uq.edu.au **Associate Advisors:** Dr Anh Phan and A/Prof Yasmina Sultanbawa Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
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Useful majors	Biochemistry & Molecular Biology / Chemistry / Microbiology

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CNAFS 5 Project

Dr Heather Smyth

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5) Edible insects for human nutrition

Edible insects have been a staple of the human diet in Asian, Central & South American countries and in Australian indigenous communities. In Australia, consumer awareness and interest in edible insects as an alternative source of protein for human consumption is growing rapidly, however, they are not readily available in conventional product forms and are largely considered a novelty. Many western consumers find the idea of insect as human food unpalatable, and the growth of this market in western culture is limited by the reluctance of food companies to incorporate insect meal as an ingredient in formulated foods (e.g. bread, pasta, protein drinks, etc.). Certainly research studies that provide evidence of the nutritional properties of insects, information about the differences between different edible insect species, as well techniques for overcoming any product formulation technical challenges, would assist with streamlining insects into the modern Australian diet.

The aim of this study is to carry out a preliminary evaluation of edible insects found in Australia such as green ants and honey pot ant. Laboratory techniques will be used to determine proximates (moisture, carbohydrates, proteins, fat, dietary fibre), minerals and trace elements, total phenolic content, antimicrobial and antioxidant activity as an initial measure of their nutritional/bioactive potential. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods.

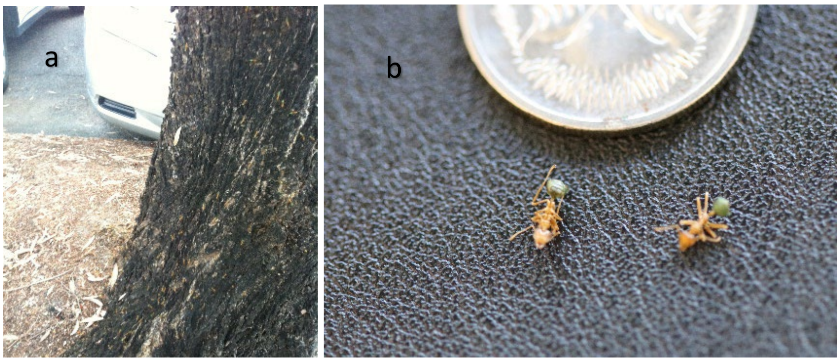

Figure 1 a) Green ants climbing a tree in Darwin CBD, b) dried green ants.

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Advisor(s) contact

Location

</td><td>

- Dr Heather Smyth, h.smyth@uq.edu.au
- Associate Advisors: Dr Sandra Olarte s.olartemantilla@uq.edu.au

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<tr><td>Webpage</td><td>https://qaafi.uq.edu.au/profile/33/heather-smyth</td></tr>
<tr><td>Useful majors</td><td>Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Microbiology</td></tr>
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CNAF 6 Project

Dr Heather Smyth

6) Flavour of native stingless bee honey

Worldwide honey and bee products such as wax and propolis are valued for their potent bioactive properties and use in traditional medicine. In Australian there are some 1500 species of native bees, many of which produce honey and associated products which have had little or no formal research in terms of composition, flavour or bioactive properties. An understanding of the value of Australian stingless bee honey and products, and defining new applications in food, medicine or cosmetics, may have the potential to support the development of a new industry for Australian native stingless bees, outside hobby native been keeping.

This project will explore, using a combination of sensory science, analytical chemistry and microbiology techniques, the flavour profile and bioactivity of native stingless bee honey and propolis. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods as well as a commercial partner who is producing commercial stingless bee honey in Queensland.

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Useful majors

The project can be tailored depending on the applicant's interest and background.
A major in at least one of the following is highly desirable:

Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Microbiology / Agriculture / Food Science / Entomology

CNAF 7 Project

Dr Heather Smyth

7) A laboratory model for evaluating the impact of honey processing

Honey quality is optimal when cured and sealed in the comb by the honey bee. Once the honey is harvested and processed for commercial consumption, the quality begins to degrade. The extent to which the delicate botanical flavours and sensory properties are modified during processing depends on a number of variables. These variables include: processing method and efficiency, temperature, exposure to oxygen, duration of processing, exposure to light or vibration and storage conditions prior to consumption. In addition, the original pre-processed honey physicochemical composition and botanical source almost certainly plays a role as to the extent of flavour modification post-process. For scientists to better understand the impact of processing, it would be advantageous to have a laboratory scale model, which mimics commercial practices, for use in controlled honey experiments. This Masters project will examine the conditions of processing used for commercial honey production in Australia, develop a lab-scale-model of commercial processing and execute a proof-of principle experiment to evaluate processing-induced changes to honey quality. The lab-scale-model will be a valuable tool for industry and researchers to develop optimised systems to harvest and extract honey and deliver higher quality product to consumers.

Advisor(s) contact	• Dr Heather Smyth, h.smyth@uq.edu.au
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Useful majors	The project can be tailored depending on the applicant's interest and background. A major in at least one of the following is highly desirable: Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Microbiology / Agriculture / Food Science / Entomology

CNAFS 8 Project

Dr Heather Smyth

8) Consumers acceptance of novel fruits and vegetables

Consumers acknowledge that fruits and vegetable are part of a healthy diet due to their high fibre content and nutritional value. What we don't know, however, is whether or not consumers would value new horticultural products that are particularly high in specific nutrients. These products might include black strawberries or purple sweetcorn that are high in anthocyanin content which supports heart health, or capsicum high in zeaxanthin which may reduce the risk of macular degeneration. Importantly, given that it is possible to breed these new cultivars through traditional (non-GMO) methods, then would these products have good consumer uptake in the market and add value, not only to human health, but for the producer.

This project will explore, using consumer and sensory science methodologies and analytical chemistry techniques, the consumer value, chemical composition and nutritional value of novel fruits and vegetable concepts. The student will work as part of a larger team working on a Hort Innovation-funded Naturally Nutritious project.

Advisor(s) contact	• Dr Heather Smyth, h.smyth@uq.edu.au
Location	Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
Webpage	https://qaafi.uq.edu.au/profile/33/heather-smyth
Useful majors	The project can be tailored depending on the applicant's interest and background. A major in at least one of the following is highly desirable: Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Food Science / Psychology

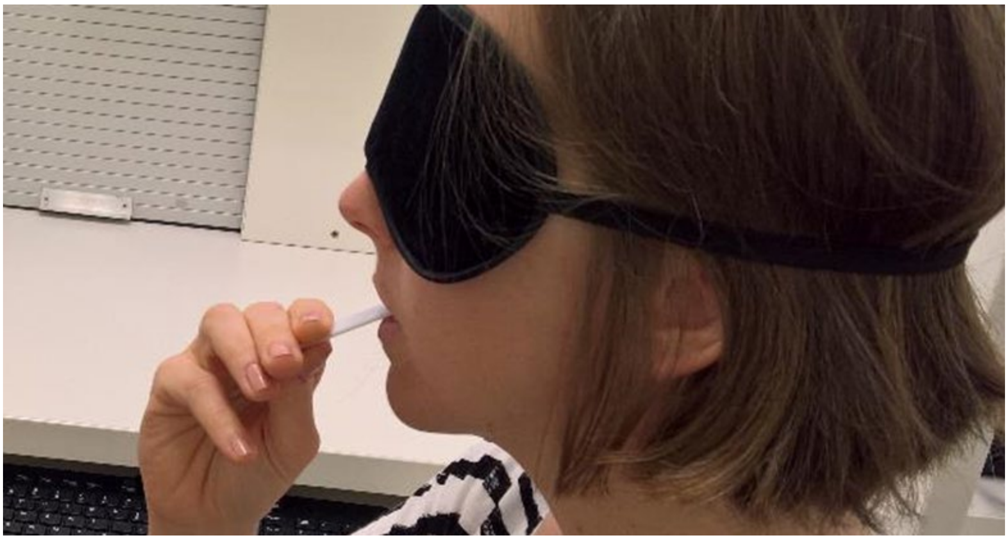
CNAFS 9 Project

Dr Heather Smyth

9) Impact of individual human variation on the sensory experience of mouthfeel and texture

Texture and mouthfeel attributes (crunchiness, smoothness, drying, sliminess, etc.) are very important factors that impact consumers every day food choice and behaviour. In recent years, food companies have moved toward producing healthier products with reduced sugar, fat and salt. The consequence, however, has been an impact of texture and mouthfeel resulting in reduced consumer enjoyment. To address this challenge, food manufactures, sensory and consumer researchers have come together to understand the fundamentals of how individual human variation relates to texture and mouthfeel sensory experiences. Such knowledge would be very powerful in new product development and product design.

This project will explore, using sensory science methodologies and physical measures, the how human variation in oral physiology can impact sensory experience of texture and mouthfeel. The student will work as part of a larger multi-disciplinary team from QAAFI and the School of Chemical Engineering working on an ARC-funded Linkage project.



Advisor(s) contact	- Dr Heather Smyth, h.smyth@uq.edu.au - Dr Daniel Cozzolino, s.olartemantilla@uq.edu.au
Location	Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
Webpage	https://qaafi.uq.edu.au/profile/33/heather-smyth
Useful majors	The project can be tailored depending on the applicant's interest and background. A major in at least one of the following is highly desirable: Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Chemical Engineering / Agriculture / Food Science / Psychology

CNAFS 10 Project

Dr Heather Smyth

10) Mechanical and physical behaviour of animal fat and the relationship with sensorily perceived mouthfeel and texture

Texture and mouthfeel attributes (crunchiness, smoothness, drying, mouth coating, etc.) are very important consumer factors that impact every day food choice and behaviour. While animal fat has received negative attention for its link to cardiovascular disease, the fact remains that fat plays an incredibly important role in meat quality. Indeed for products like Wagu, a higher fat content attracts a premium due to its superior melt-in-mouth characteristics. Understanding the mechanisms involved in mouthfeel perception of meat fat could shed new insights on how to mimic fat sensations in-mouth using alternative (non-fat) ingredients. Such knowledge would be very powerful in new product development and product design where reduction of fat is the target.

This project will explore and attempt to define the mechanism of sensorily perceived mouthfeel and texture from animal fat. Sensory science methodologies and physical measures will be user to define structure-function relationships. The student will work as part of a larger multi-disciplinary team from QAAFI and the School of Chemical Engineering.

Advisor(s) contact

- Dr Heather Smyth, h.smyth@uq.edu.au
- Prof Jason Stokes, j.stokes@uq.edu.au
- Prof Louw Hoffman Louwrens.hoffman@uq.edu.au

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Useful majors

The project can be tailored depending on the applicant's interest and background.
A major in at least one of the following is highly desirable:

Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Chemical Engineering / Agriculture / Food Science / Psychology

CNAFS 11 Project

Dr Heather Smyth

11) Native Australian ingredients to replace chemical preservatives in meat products

Fresh meat in Australian is commonly preserved with nitrates, nitrites or other chemical preservatives. In low doses these chemical preservatives are thought to be harmless, but when accumulated in high concentration, they are known to be harmful to human health. There is a strong consumer movement away from chemical additives in food which has given rise to new opportunities to natural plant-based alternatives for food preservation and extension of shelf life. Native Australian plant foods show strong promise for food applications as they exhibit powerful antimicrobial, antioxidant and antifungal properties.

The objective of this project is to explore the potential of native Australian plant extracts and ingredients to replace chemical preservatives in fresh meat. Techniques utilised for the project may include meat science, analytical chemistry, microbiology, packaging technology and sensory evaluation. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods.

Advisor(s) contact

- Dr Heather Smyth, h.smyth@uq.edu.au
- Prof Louw Hoffman louwrens.hoffman@uq.edu.au

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Webpage

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Useful majors

The project can be tailored depending on the applicant's interest and background. A major in at least one of the following is highly desirable:

Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Microbiology / Agriculture / Meat Science / Food Science

CNAFS 12 Project

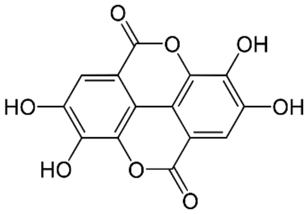
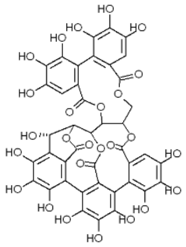
Dr Heather Smyth

12) Distinctly Australian drivers of consumer quality in chicken meat

Significant advances in production technologies for Australian poultry over the past 50 years has resulted in the availability of high quality safe chicken-meat at a very competitive price. This has led to chicken being the leading protein choice for consumers over beef, pork and lamb (since 2006). Unlike other protein choices, chicken meat is, however, at risk of becoming associated with being a commodity product by consumers with little room for product-to-product distinction and premium product placement. For this reason, it is timely that the poultry industry gain a firm understanding of premium product cues with chicken meat and to understand what quality parameters consumers are concerned about which differentiate budget chicken meat from premium chicken products.

The objective of this project is to explore consumer drivers, barriers, attitudes, credence factors and behaviour with regards to Australian chicken meat. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods.

Advisor(s) contact	• Dr Heather Smyth, h.smyth@uq.edu.au • Prof Louw Hoffman louwrens.hoffman@uq.edu.au
Location	Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
Webpage	https://qaafi.uq.edu.au/profile/33/heather-smyth
Useful majors	The project can be tailored depending on the applicant's interest and background. A major in at least one of the following is highly desirable: Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Food Science / Meat Science / Agriculture / Psychology

CNAFS 13 Project *Dr Anh Phan*	**13) Kakadu plum polyphenols and their roles in potential antimicrobial activities** Kakadu plum (*Terminalia ferdinandiana*) fruit has been used by Australian Aboriginal people as traditionally medicinal food. Evidences of potential health benefits of this native Australian fruit have been initially reported. However, there is still gap in knowledge regarding the definitive identification of main polyphenolic compounds in Kakadu plum fruits, and determination of their roles in health-related benefits, particularly antimicrobial activities. The aim of this study is to identify phenolic compounds in Kakadu plum fruits using the state of the art UHPLC-PDA-MS/MS. In addition, the potential inhibitory effects of phenolic compounds that are responsible for the antimicrobial activities of Kakadu plum fruits will be investigated. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods.   
Advisor(s) contact Location	• **Dr. Anh Phan**, a.phan1@uq.edu.au • Associate Advisors: **Dr Daniel Cozzolino, Dr Hung Hong, A/Prof. Yasmina Sultanbawa** Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
Webpage	www.qaafi.uq.edu.au
Useful majors	Biochemistry, Chemistry, Microbiology, Agriculture, Food Science

CNAFS 14 Project

Dr Anh Phan

14) Determination of Polyphenolic compounds in different Kakadu plum tissues and associated biological activities

Kakadu plum (*Terminalia ferdinandiana*) fruits have been used by Australian Aboriginal people as traditionally medicinal food. Preliminary studies have reported that different biological parts of Kakadu plum, including fruit pulp, kernel and leaves, exhibit potential health benefits. The available information on polyphenolic compounds, tissue distribution, and bioactive properties of Kakadu plum is very limited. Therefore, determination of polyphenolic compounds and the biological activities of different Kakadu plum tissues will provide better understanding of phytochemical variation and their nutritional aspects. The findings can add value to the potential use of different Kakadu plum tissues as functional ingredients for the food and nutraceutical industries.

The aim of this study is to identify phenolic compounds in diverse Kakadu plum tissues (fruit pulp, kernel, leaf) using the state of the art UHPLC-PDA-MS/MS. In addition, the bioactivities of the extracts from different Kakadu plum tissues will be investigated.

The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods.

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Useful majors	Biochemistry, Chemistry, Microbiology, Agriculture, Food Science

CNAFS 15 Project

Dr Tim O'Hare

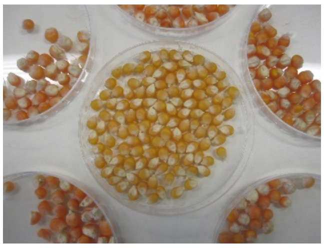
15) The effect of popping on carotenoid content in zeaxanthin-biofortified popcorn

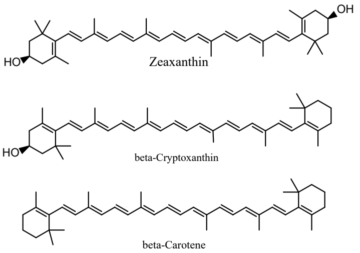
Carotenoids are lipophilic pigments responsible for the yellow, orange and red colours in plants, giving corn kernels their typical bright yellow colour. Carotenoids also play an important role in human health, including macular degeneration, the leading cause of blindness in Australia. Two carotenoids, zeaxanthin (orange) and lutein (yellow), are specifically obtained from our food, and transported to our macula, where they act as 'blue-light sunglasses' to protect our eyes' photoreceptors.

Popcorn is a good source of zeaxanthin, and we have increased its level by about 700% through biofortification. This increased zeaxanthin gives the popcorn a naturally buttery colour once it's popped (normal popcorn is white, with artificial colours added). The popping process, however, which involves high temperature and pressure, which can lead to a decline in zeaxanthin and other carotenoids immediately after popping.

The aim of this study is to explore the effect of high temperature popping on the carotenoid profile and zeaxanthin content in high-zeaxanthin popcorn accessions.

The student will work as part of a larger team in QAAFI working on the Naturally Nutritious project.





Advisor(s) contact	- Supervisor: Dr Tim O'Hare, email: t.ohare@uq.edu.au - Associate Advisor: Dr Hung Hong Trieu, email: h.trieu@uq.edu.au
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Useful majors	Biochemistry & Molecular Biology / Chemistry / Agriculture / Horticulture / Food Science

CNAFS 16 Project

Dr Tim O'Hare

16) Fresh and cooked purple sweetcorn aroma, chemical components and influence on flavour volatiles

Sweetcorn aromas are volatile compounds which can be detected in fresh and cooked sweetcorn. Aroma compounds play an important role in the taste perception of a consumer. While dimethyl sulphide (DMS) is reported to be the most implicated aroma response in cooked yellow sweetcorn, aroma compounds of purple sweetcorn are completely unknown.

The aim of this study is to determine novel volatile compounds in purple sweetcorn (a new sweetcorn established by Tim O'Hare's research group), compared to commercial yellow sweetcorn using GC-MS. The student will work as part of a larger team in QAAFI working on Naturally Nutritious project.

Advisor(s) contact

- Supervisor: Dr Tim O'Hare, email: t.ohare@uq.edu.au
- Associate Advisor: Dr Hung Hong Trieu, email: h.trieu@uq.edu.au

Location

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Centre for Nutrition and Food Sciences
Health and Food Sciences Precinct, Coopers Plains

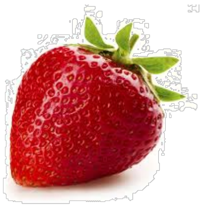
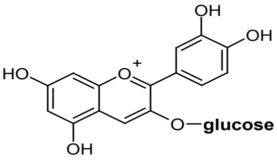
Webpage

https://qaafi.uq.edu.au/profile/459/tim-ohare

www.qaafi.uq.edu.au/Naturally_nutritious

Useful majors

Biochemistry & Molecular Biology / Chemistry / Agriculture / Horticulture / Food Science

CNAFS 17 Project *Dr Michael Netzel*	**17) Exploring the Bioactivity and Digestive Fate of Anthocyanins** Anthocyanins (Greek Anthos = flower and kyáneos = blue) belong to the flavonoid group of polyphenolic compounds, which are responsible for the red and blue colours of plant organs such as fruits, flowers, and leaves. Due to their frequent presence in plants, particularly berry fruits (including native Australian fruits), vegetables, and grapes, they are key components of the human diet. Interest in anthocyanins has increased widely during the past decade. Numerous studies have suggested that anthocyanins have a wide range of health-promoting properties. These compounds are therefore considered to be a functional food factor, which may have important implications in the prevention of chronic diseases. The aim of this study is to investigate/explore the bioactivity and digestive fate of anthocyanins using state-of-the-art analytical methods and advanced *in vitro* models mimicking the human digestive tract. Native Australian fruits will be the focus. The student will work as part of a larger team in QAAFI working on the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods.    cya-3-gluc
Advisor(s) contact	- Dr Michael Netzel, m.netzel@uq.edu.au - Associate Advisor: A/Professor Yasmina Sultanbawa, y.sultanbawa@uq.edu.au - Associate Advisor: Dr Gabi Netzel, g.netzel@uq.edu.au - Associate Advisors: Dr Olivia Wright, o.wright@uq.edu.au
Location	Queensland Alliance for Agriculture and Food Innovation Centre for Nutrition and Food Sciences Health and Food Sciences Precinct, Coopers Plains
Webpage	https://researchers.uq.edu.au/researcher/3883
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Food Science

CNAFS 18 Project

Dr Gabi Netzel

18) Bioactive Phytochemicals in Native Australian edible Plants

Aboriginal people in Australia have used indigenous edible plant species for thousands of years. Despite reports of the unique nutritious characteristics, up to date there is only limite) d information about the nutritional and bioactive properties available. The aim of this project is to characterize selected native Australian edible plants in terms of their bioactive phytochemicals (focus on polyphenols and carotenoids) and to investigate if those fruits have functional properties such as anti-diabetic and antimicrobial activities. Selected Native Australian edible plants will be assessed by state-of-the-art analytical techniques such as Stable Isotope Dilution Assays (SIDA) and UHPLC-PDA-MS as well as enzyme and antimicrobial assays.

The student will work as part of a larger team in QAAFI working in the ARC-funded Industrial Transformation Training Centre for Uniquely Australian Foods

Advisor(s) Contact

- Dr Gabriele Netzel, g.netzel@uq.eu.au, 0437721028
- Associate Advisor: A/Professor Yasmina Sultanbawa, y.sultanbawa@uq.edu.au
- Associate Advisor: Dr Michael Netzel, m.netzel@uq.edu.au
- Associate Advisors: Dr Olivia Wright, o.wright@uq.edu.au

Location

Queensland Alliance for Agriculture and Food Innovation, Centre for Nutrition and Food Sciences, Health and Food Sciences Precinct, Coopers Plains

Webpage	https://researchers.uq.edu.au/researcher/14639
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Agriculture / Food Science

CNAFS 19 Project

Dr Gabi Netzel

19) Australian grown produce as a novel dietary source of folate

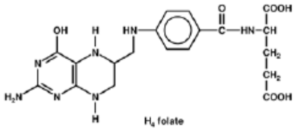
The vitamins of the folate group play a crucial role as coenzymes in the metabolism of one carbon groups, and are decisively involved in DNA synthesis, amino acid metabolism and methylations. However, intake of folate from natural sources is considered critical in many countries. Low dietary intake of folate is associated with the risk of neural tube defects in newborns and is suspected to be associated with the development of certain forms of cancer, Alzheimer’s disease and cardiovascular disease. Over 50 countries have introduced mandatory folate fortification. However, apart from fortification, the identification and consumption of fruits/food rich in natural folates are an alternative strategy to increase folate intake.

Australian grown produce will be assessed for their natural folate content, profiles (different vitamers) and nutritional value by using:

(a) state-of-the-art analytical techniques such as Stable Isotope Dilution Assays (SIDA) and UHPLC-MS

(b) *in vitro* models mimicking the human digestion process to determine the matrix release/bioaccessibility of the different folate vitamers which is crucial for their bioavailability and subsequently physiological activity.

This project presents an excellent opportunity for an Honours student to learn state-of-the-art analytical techniques and to generate novel and significant data for this critical vitamin.



Advisor(s) Contact

- Dr Gabriele Netzel, g.netzel@uq.eu.au, 0437721028
- Associate Advisor: A/Professor Yasmina Sultanbawa, y.sultanbawa@uq.edu.au
- Associate Advisor: Dr Michael Netzel, m.netzel@uq.edu.au
- Associate Advisors: Dr Olivia Wright, o.wright@uq.edu.au

Location

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Webpage

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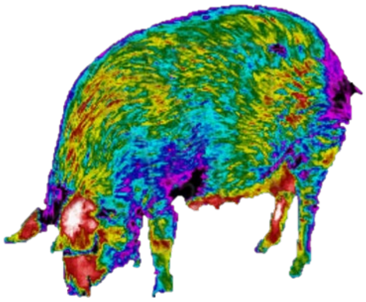
Useful majors

Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Agriculture / Food Science

CNAFS 20 Project *Dr Marta Navarro*	**20) Exploring the metabolic resilience to the heat stress in lactating sows**  Heat waves are predicted to be increase in frequency, length, and intensity as climate change conditions keep progressing. Modern pig lines have become more sensitive to hot temperatures as a result of the genetic selection to improve performance parameters (but not heat resilience). On the contrary, modern pig genetics characterised by fast and lean weight gain, is associated with a high internal heat production that jeopardizes adaptations to a challenging high ambient temperature environment. Thus, pig's hyperthermia episodes are considered one of the main welfare and economic problems in modern pig production. However, a large variation exists between individuals regarding heat tolerance. This project aims to determine metabolic biomarkers and microbiome signatures that differentiate resilient to high sensitivity to hyperthermia in sows. During lactation nutritional requirement peak to high pushing the maintenance of metabolic homeostasis to the limit particularly under heat stress. It is anticipated that the identification of metabolic biomarkers and microbiome profiles associated with heat tolerance in lactating sows will result in novel nutrition and management intervention strategies to improve sow welfare under heat stress events.
Advisor(s) contact	• Dr Marta Navarro, email: m.navarrogomez@uq.edu.au, mobile: 0458999192 • Associate Advisors: Prof Eugeni Roura, Dr Shahram Niknafs Location: 80% QASP (Gatton campus), 20% St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/26066 https://qaafi.uq.edu.au/profile/429/eugeni-roura http://researchers.uq.edu.au/researcher/24913
Useful majors	Biomedical Science / Computational Science / Microbiology

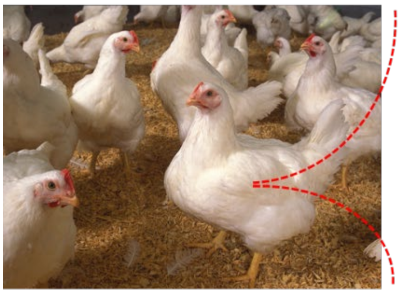
CNAFS 21 Project *Dr Marta Navarro*	**21) <u>Perinatal program to improve chicken gut health, naturally</u>** Chicken's gastrointestinal tract undergoes significant physiological changes during the first days after hatch, including the establishment of a microflora when transitioning from a clean close-to-sterile hatchery environment to the adopting "dirty" farm ecosystem. In that context, establishing a beneficial and protective microflora before to the arrival to the farm would reduce the possibility of enteric pathogens colonizing the gut. This, in turn, would decrease disease burdens later in the life of the chicken, thus, reducing the need of preventive or curative (antibiotic) treatments. The early development of a healthy gut including early microbiome development, could be facilitated during the embryonic stages. *In ovo* techniques have been developed in recent years to supplement nutrients to the chick just before hatch. However, little is known about the potential of programming the future microbiome (*ex ovo*) during the embryonic stage. This project will study use of essential oils with antioxidant and antimicrobial activities during embryonic stages, to improve gut health early in the life of chicks. The project will systematically evaluate all the parameters related with an effective inoculation of essential oils in the egg to produce healthy hatchlings. The ultimate goal of this project is to make on farm antibiotic use redundant. 
Advisor(s) contact	- Dr Marta Navarro, email: m.navarrogomez@uq.edu.au, mobile: 0458999192 - Associate Advisors: Prof Eugeni Roura, Dr Shahram Niknafs <u>Location:</u> Otto Hirschfeld Bld, St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/26066 https://qaafi.uq.edu.au/profile/429/eugeni-roura http://researchers.uq.edu.au/researcher/24913
Useful majors	Biomedical Science / Computational Science / Microbiology

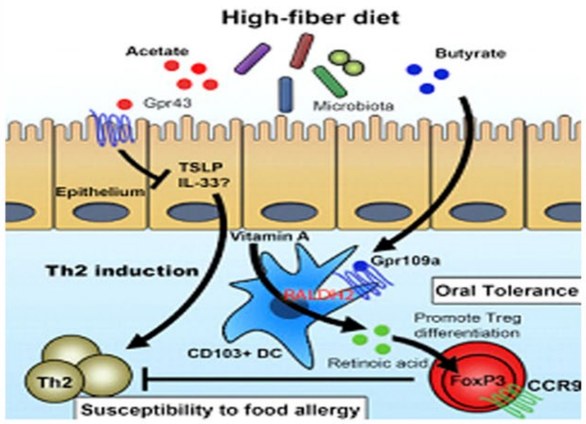
CNAFS 22 Project

Dr Shahram Niknafs

22) Dietary fibre and deciphering gut-brain communication

The fascinating complexity of edible fibres has driven a significant part of the research agenda in human and animal nutrition. Dietary Fibre (DF) has been associated with satiation (hence preventing obesity) lowering risks of colon cancer, decreasing plasma cholesterol levels (and CVD risks), and developing a healthy microbiota among other aspects. However, a lack of understanding still persists regarding how DF interacts with other essential nutrients such as amino acids and fats and their sensing in the gastrointestinal tract (GIT). The objective of this research proposal is to identify the physiological mechanisms by which common (soluble or insoluble) DF can influence the development of the GIT and the gut-brain communication relevant to food/feed intake control, energy homeostasis and gut health using the chicken as an animal model.





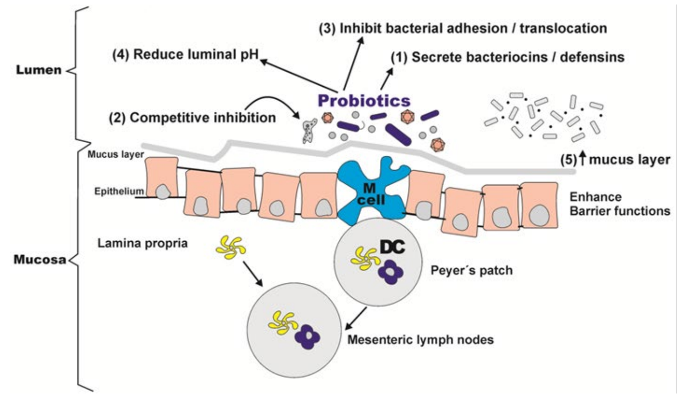
Advisor(s) contact	• Dr Shahram Niknafs, s.niknafs@uq.edu.au, 0468 691 705 • Associate Advisors: Prof Eugeni Roura, Dr Marta Navarro Location: St Lucia Campus (50%), Gatton Campus (50%)
Webpage	http://researchers.uq.edu.au/researcher/24913
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science/ Genetics / Microbiology

CNAFS 23 Project

Dr Shahram Niknafs

23) Can we replace antibiotics with probiotics in broiler chickens?

The use of antimicrobials in farm animals may account for up to 50% increase in antimicrobial resistance (AMR) in specific foodborne pathogens such as Escherichia coli affecting humans. Thus, the general consensus is that the livestock sector must stop non-essential (disease-treating) uses of antimicrobials, to help prevent sharply increasing AMR threat to human health. However, it has been anticipated that a sudden discontinuation of in-feed antimicrobials will increase animal mortality, diarrhoea incidence and reduce growth rate, potentially becoming a major welfare and cost constraints to farmers and the wider community. Therefore, to be successful, antimicrobial-free feeding strategies must guarantee animal wellness and economic viability. The aim of this project is to develop novel feed additives including new probiotic formulations using antimicrobial strains and natural ingredients to improve production performance, and carcass characteristics in broiler chickens. Through this project, we will develop in-vivo studies at The University of Queensland to screen for novel probiotic formulations that further enhance production performance, gut health and functionality, and meat quality of broiler chickens.



Advisor(s) contact

- Dr Shahram Niknafs, s.niknafs@uq.edu.au, 0468 691 705
- Associate Advisors: Prof Eugeni Roura, Dr Marta Navarro

Location: St Lucia Campus (40%), Gatton Campus (60%)

Webpage

http://researchers.uq.edu.au/researcher/24913

Useful majors

Biochemistry & Molecular Biology / Biomedical Science/ Genetics / Microbiology

CNAFS 24 **Project** *Prof Louwrens Hoffman*	**24) Title: In-vivo validation of Bioproton products: Effects on the performance and meat quality in broiler chickens** The aim of this project is to evaluate the effect of two novel probiotic formulations on the performance and meat quality of broiler chicks raised under controlled conditions that stimulate that of the commercial sector. The meat quality measurements will include physical quality determinants (pH, water binding capacity and colour) as well as the chemical composition of the chicken meat. 
Advisor(s) contact	• Prof Louwrens Hoffman, Louwrens.hoffman@uq.edu.au; +61 4 1798 4547 • Associate Advisors: Prof Eugeni Roura e.roura@uq.edu.au Location: Predominantly Blg 8150, Gatton UQ Campus
Webpage	https://researchers.uq.edu.au/researcher/22855
Useful majors	Food Sciences / Animal Sciences / Food Chemistry / Meat Science

Centre for Horticultural Science Projects

CHS 1 Project *Dr Lilia Costa Carvalhais*	**1) Sex in banana fungi** Bananas are the fourth most important food crop worldwide, surpassed only by crops such as rice, maize and wheat. The production, consumption and trade can be greatly affected by pests and mainly fungal diseases such as Sigatoka leaf spot and Fusarium wilt. The spread of the Fusarium wilt race 1 in the last century led to the replacement of Gros Michel by Cavendish variety, which is resistant to this particular race. However, new pathogens strains are constantly emerging, such as the tropical race 4 (TR4) which has been devastating banana plantations after invasion. The origins of diversity in fungal pathogens usually stem from sexual reproduction and the objective of the project you will be involved in is to gain knowledge concerning the genetic mechanisms that create diversity in *Fusarium oxysporum* f.sp. *cubense* and *Pseudocercospora musae*, the causal agents of Fusarium wilt and yellow Sigatoka, respectively. The specific aims of this study are: 1) to obtain cultures and DNA from banana fungal pathogens, 2) to screen isolates of banana fungal pathogens for the presence of mating type sequences, 3) evaluate whether mating type genes are transcribed during vegetative growth.  
Advisor(s) contact	• Dr Lilia Costa Carvalhais, l.carvalhais@uq.edu.au, Ph: 0426 197 372 • Associate Advisors: Prof Andre Drenth, Dr Alistair McTaggart, Dr Vivian Rincon-Florez Location: Ecosciences Precinct, Dutton Park
Webpage	https://qaafi.uq.edu.au/profile/3177/lilia-costa-carvalhais
Useful majors	Microbiology/Genetics

CHS 2 Project *Assoc. Prof. Andrew Geering*	**2) <u>Population genomics of *Ustilago cynodontis* causing smut disease on green couch (*Cynodon dactylon*)</u>** The basidiomycete *Ustilago cynodontis* causes smut on green couch (*Cynodon dactylon*). It is a widespread disease in Australia and has economic impacts for the turf industry. Several questions on the distribution and dispersal of smut between turf farms can be answered by studying the population of smut across Australia. Specifically we are interested in whether populations of smut are structured by turf farms, whether new infections blow-in from natural environments, and whether *U. cynodontis* is native to Australia? In order to answer these questions, a cultures of the fungal pathogen will be collected from different locations in Australia and overseas. The culture collection will then be genotyped using genotyping by sequencing (GBS). Addressing these questions will shed light on the source on inoculum, spread of the pathogen and its reproduction, which are crucial steps to develop effective management strategies.  Figure 1. Inflorescence of couch grass completely destroyed and covered with masses of spores of the smut fungus *Ustilago cynodontis*.
Advisor(s) contact	• Assoc. Prof. Andrew Geering (a.geering@uq.edu.au, 07 344 32459) • Associate Advisors: Dr Alistair McTaggart (a.mctaggart@uq.edu.au), Dr Nga Tran (n.tran3@uq.edu.au) <u>Location:</u> Ecosciences Precinct, Dutton Park 4102
Webpage	https://qaafi.uq.edu.au/profile/81/andrew-geering
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Genetics / Microbiology

CHS 3 Project

Assoc. Prof. Andrew Geering

3) Identification of mosaic viruses in buffalo grasses

Buffalo grass (*Stenotaphrum secundatum*) is of the most important turf species in Australia. Buffalo grass yellowing is an emerging problem in the country, particularly in the Sydney Basin, where severe disease outbreaks have been noticed over the summer of 2018/19. Evidence for viral infections was found on grass obtained from affected turf farms, however the actual causes of the problem is unknown. Worldwide, three different types of plant viruses, namely panicum mosaic virus (PMV), sugarcane mosaic virus (SCMV), and Johnsongrass mosaic virus (JGMV) have found in buffalo grass. In this project, the viruses associated with buffalo grass yellowing will be characterized using next generation sequencing and diagnostic assays developed to allow early and accurate identification of the causal agents for improved management of the disease.

Figure 1. Buffalo grass showing yellowing patches that are affected by mosaic viruses (Photo courtesy Mr Ken Johnston, WA)

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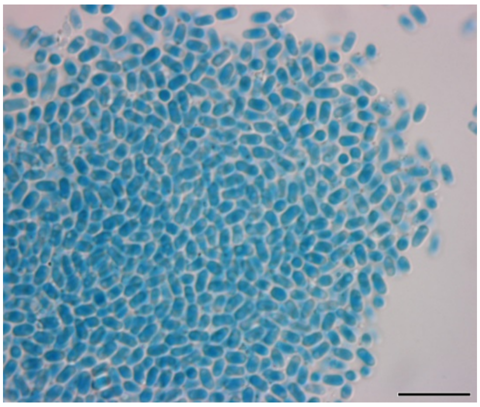
Webpage	https://qaafi.uq.edu.au/profile/81/andrew-geering
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Genetics / Microbiology

CHS 4 Project *Dr Louisa Parkinson*	**4) <u>Phylogeny and taxonomy of *Claviceps* associated with ergot of native grasses in Australia</u>** Ergot is a disease of some cultivated and wild grasses caused by species of the ascomycete *Claviceps*. In Australia, ergot is an economically important disease of some grain crops, e.g. sorghum, and is a problem in some native Australian grasses, e.g. *Paspalum*. The fungus is also known to produce alkaloids that are hallucinogenic to humans and toxic to grazing livestock. Worldwide there are approximately 60 species of *Claviceps* known, including about 14 Australian species. A collection of 31 *Claviceps* isolates from native Australian grasses held in the Queensland Plant Pathology Herbarium (BRIP) requires taxonomic identification and phylogenetic revision. Novel species of *Claviceps* may result from this study and these will require formal taxonomic description. The aim of this Honours project is to identify the *Claviceps* isolates held in BRIP to species-level with multigene phylogenetic analyses and to formally classify and describe new taxa. The project methods will develop skills in microbiology (isolation and culture of isolates); morphology (descriptions of new taxa), molecular biology (fungal DNA extractions, PCR); phylogenetics and bioinformatics (analysis of DNA sequences); and plant pathology (fungus-host interactions).  Claviceps purpurea on barley (*Hordeum vulgare*). Scale Bar = 1 cm  Conidia of *Claviceps purpurea* on perennial ryegrass (*Lolium perenne*). Scale bar = 20 µm.
Advisor(s) contact	• Dr Louisa Parkinson (QAAFI), l.parkinson@uq.edu.au, (07) 3443 2457 • Associate Advisors: Professor Roger Shivas (DAF Biosecurity; USQ) and Associate Professor Andrew Geering (QAAFI) <u>Location:</u> Ecosciences Precinct, 41 Boggo Road, Dutton Park
Webpage	https://qaafi.uq.edu.au/profile/585/louisa-parkinson
Useful majors	Molecular Biology, Bioinformatics, Microbiology, Plant Pathology

CHS 5

Project

Dr Louisa Parkinson

5) Investigation of biosecurity threats to the Australian avocado industry

Avocado is a billion-dollar industry and is threatened by exotic and emerging pests and diseases, which could hinder production and impact Australia's ability to enter global markets. Plant biosecurity and pathology diagnostics contributes towards food security and protecting agricultural crops by enabling the capacity for quickly identifying and responding to incursions.

Although a primary pathogen of potato, Potato Spindle Tuber Viroid (PSTVd) is a biosecurity threat to avocados and has been reported to infect avocados in several locations in Peru, where potatoes are grown as a staple crop. In Australia, PSTVd outbreaks have been reported in commercial tomato glasshouse facilities, and have been successfully eradicated. However the ability of Australian PSTVd isolates to cause disease in avocado has not been tested.

Branch dieback of avocado trees is an ermerging problem in Queensland, and is associated with tree-boring ambrosia beetles, *Euwallacea perbrevis* (formerly *E. fornicatus*), known in Australia as the Tea Shot Hole Borer (TSHB). The beetles carry *Fusarium* fungal symbionts in their mouth parts, which they deposit into the heartwood of tree branches for the beetles and larvae to feed; the fungus causes branch dieback. The *Fusarium* symbionts in Australia represent new species within the Ambrosia Fusarium Clade (AFC) of the *Fusarium* genus, and the pathogenicity of these species are yet to be demonstrated. Other ornamental and horticultural trees in Queensland, such as tuckeroo (*Cupaniopsis anacardioides*), have also been reported with branch dieback associated with TSHB. The ability of AFC species affecting tuckeroo to cause disease in avocados (and vice versa) has not been tested; an investigation of cross-pathogenicity may shed light on the potential host range of the beetles and *Fusarium* symbionts. A molecular diagnostic test for detecting *Fusarium* species within the AFC clade would be useful in confirming diagnoses of Ambrosia beetle-vectored branch dieback horticultural and ornamental trees in Australia. Moreover a test for quick molecular identification of TSHB (*Euwallacea perbrevis*) is yet to be developed. Molecular identification of beetles is often done with morphology or sequencing of the cytochrome c oxidase subunit 1 (CO1) gene. A qPCR molecular test for TSHB based on the CO1 gene would be useful in aiding quick identification of beetle specimens from symptomatic trees.

This Honours project aims to (i) test Australian PSTVd isolates for pathogenicity on avocado in glasshouse pathogenicity experiments (ii) test the ability of Fusarium AFC isolates from tuckeroo and avocado to cause disease on both hosts in glasshouse pathogenicity experiments; (iii) and develop a real time qPCR diagnostic test for identifying *Fusarium* AFC species or TSHB using available gene sequence data. The project methods will develop skills in microbiology through culturing of isolates; molecular biology through molecular diagnostic design and optimization of qPCR assays; bioinformatics through analyses of gene sequence data and primer design; and plant pathology through fungus-host interactions investigated in glasshouse pathogenicity experiments.

Advisor(s) contact	• Dr Louisa Parkinson (QAAFI), l.parkinson@uq.edu.au, (07) 3443 2457 • Associate Advisors: A/Prof Andrew Geering (QAAFI), A/Prof Elizabeth Dann Location: Ecosciences Precinct, 41 Boggo Road, Dutton Park
Webpage	https://qaafi.uq.edu.au/
Useful majors	Molecular Biology, Bioinformatics, Microbiology, Plant Pathology

CHS 6

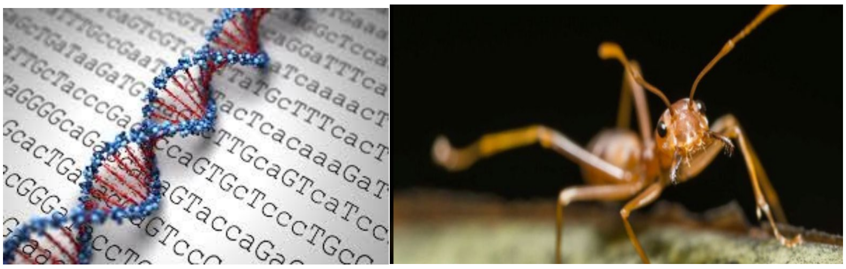
Project

Prof Neena Mitter

6) Topical application of RNAi for management of Fire Ants

Fire ants are a serious pest because they have the potential to cause major social, environmental and economic impacts in Queensland and Australia. Fire ants were first detected in Brisbane in 2001, and in September that year the National Red Imported Fire Ant Eradication Program was formed in partnership with State governments.

The current project is aimed at investigating RNA interference (RNAi) as a tool to manage fire ants. RNAi targeting neuropeptides and pheromones resulted in increased fire ant mortality (Choi et al. 2012 and Qiu et al. 2017). In this project, the RNAi platform will be further explored to develop novel targets to control fire ants.



Students in both Themes can learn valuable techniques in cloning, PCR, qRTPCR, sequencing, RNA/DNA extractions, bioinformatics and RNAi biology. The student will work closely with other members of the Mitter laboratory and industry partners to develop scientific outcomes and a highly productive research.

Advisor(s) contact

- Prof Neena Mitter, E: n.mitter@uq.edu.au, P: 07 334 66513
- Associate Advisors: Dr Karishma Mody, E: k.mody@uq.edu.au, P: 07 336 62318

Location: Queensland Bioscience Precinct (Bldg 80); 306 Carmody Rd, St Lucia, Australia 4072

Webpage

https://researchers.uq.edu.au/researcher/1427

Useful majors

Biochemistry & Molecular Biology / Bioinformatics

CHS 7

Project

Dr Karishma Mody

7) Clay innovation: sustainable alternative to pesticides for protecting Queensland's livestock

Sheep flystrike and lice-infestation are the top two diseases economically affecting the Queensland's sheep and wool industry. L. cuprina (blowfly) has developed resistance to nearly all control chemicals used in the past and resistance has now emerged to cyromazine and dicyclanil (chemicals accounting for ~90% of the current market). Control of sheep lice relies almost exclusively on chemical controls and has suffered similar resistance problems. With ongoing requirements to increase production efficiency, constraints on the availability of labour, and providing mandatory pain-relief while mulesing (to-be soon effective in NSW and Victoria), it is critical to develop an effective biological control that can protect the unmulesed flocks.

Current control measures and limitations:
- Resistance build up to the existing chemicals.
- Mulesing sheep
- Withholding periods for live exports
- Longer slaughter intervals impacting trade

RNAi delivery using Clay nanoparticles – Innovative Solution

The current project is aimed at investigating RNA interference (RNAi) as a tool to manage sheep blowfly and lice-infestation. In this project, the RNAi platform will be further explored to develop novel targets to control both blowfly and lice. Students in both Themes can learn valuable techniques in cloning, PCR, qRTPCR, sequencing, RNA/DNA extractions, bioinformatics and RNAi biology. The student will work closely with other members of the Mitter laboratory and industry partners to develop scientific outcomes and a highly productive research.

Advisor(s) contact

- Dr Karishma Mody, E: k.mody@uq.edu.au, P: 07 334 62318
- Associate Advisors: Prof Neena Mitter and Prof Tim Mahony
- Location: Queensland Bioscience Precinct (Bldg 80); 306 Carmody Rd, St Lucia, Australia 4072

Webpage

https://researchers.uq.edu.au/researcher/23229

Useful majors

Biochemistry & Molecular Biology / Bioinformatics

CHS 8 **Project** *Dr Alice Hayward*	**8) Exogenous RNAi in Plants – The Next Big Thing?!** A new field of plant biotechnology is emerging wherein genetic regulatory molecules such as double-stranded RNAs and microRNAs are applied exogenously to plants to control endogenous gene expression through the RNA interference (RNAi) pathway. The Mitter lab is working in this space applying artificial microRNAs and double-stranded RNAs to control the expression of genes involved in root induction in plants. This technology has importance for investigating gene function in crop species that are recalcitrant to genetic engineering such as avocado, one of the Australia's most important high value food crops. Students will gain key techniques in plant physiology and molecular biology such as in vitro transcription, cloning and qPCR as well as plant sterile culture. They may have opportunity to be an author on a scientific paper building on prior data. **Two Projects are available in this space!** 
Advisor(s) contact	- Dr Alice Hayward and Prof Neena Mitter Location: QAAFI, QBP (building 80) Level 3 South. St Lucia.
Webpage	https://researchers.uq.edu.au/researcher/9841
Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology

CHS 9

Project

Dr Alice Hayward

9) Novel Tissue Culture Technologies to Improve Plant Production and Conservation

The Mitter Lab has received global media coverage for developing the **world's first** system for mass-production of avocado plants in tissue culture. This is important as a sustainable, cost effective and food-secure way to produce crop plants. We have also developed cryopreservation (cryostorage at -196C) of avocado, with plants able to be revived from cryo and grown into new plants! This is a safe and de-risked way to conserve precious rainforest and food species that can not be seedbanked.

Dedicated students can be a part of our new research developing systems for other food crops or our incredible Australian Native species that are highly endangered in the wild.

Students can gain valuable experience in plant physiology and tissue culture such as aseptic culture, optimisations of culture media and hormone treatments, assessments of plant growth and health, cryopreservation, embryo rescue, somatic embryogenesis. They may have opportunity to be an author on a scientific paper building on prior data.

Advisor(s) contact	- Dr Alice Hayward, Prof Neena Mitter, Dr Jayeni Hiti-Bandaralage Location: QAAFI, QBP (building 80) Level 3 South. St Lucia.
Webpage	https://researchers.uq.edu.au/researcher/9841
Useful majors	Biochemistry & Molecular Biology / Plant Biology/ Botany / Microbiology

CHS 10

Project

A/Prof Femi Akinsanmi

10) Disease Epidemiology and Management in Tree Nuts

Plant pathogens cause severe economically damaging diseases to field and horticultural crops, which lead to massive reduction in the quantity and quality of food we consume. The effect of some environmental variables on pathogens and plants can have favourable or detrimental outcomes on plant disease development. We aim to identify the window of opportunity for the development and application of innovative practical solutions, through understanding of ecological bases of plant pathogens and their interaction with the plant.

The scholars will use an array of high level instruments in microbiology, molecular biology and plant pathology to examine a specific area of plant disease epidemiology in a tree nut crop such as macadamia:

1. Characterization of the biology of causal agents of diseases of macadamia **(pathogen biology)**
2. Examine infection processes of plant disease-threatening pathogens (**molecular epidemiology)**
3. Understanding the evolution and key processes of pesticide resistance in fungi **(practical solutions)**

Scholars will join the macadamia pathology team and have opportunity to contribute to publications arisen from the research.

Advisor(s) contact	Associate Professor Femi Akinsanmi Email: o.akinsanmi@uq.edu.au Phone: 07 34432453 Location: Ecosciences Precinct, Boggo Road, Dutton Park. (10 min. walk from St Lucia Campus)
Webpage	https://qaafi.uq.edu.au/profile/186/femi-akinsanmi
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CHS 11

Project

Dr Inigo Auzmendi

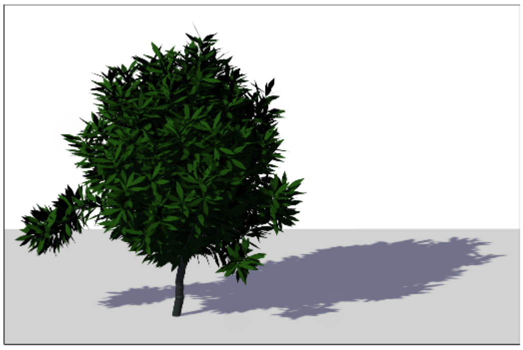
11) Simulating fruit tree growth and development

Functional-structural plant models simulate organ growth and development in complex plant canopies. They are employed to improve our understanding of physiological mechanisms and interactions between management practices, environmental factors, plant carbon balance and growth.

This project will use avocado, macadamia or mango data already collected from field trials and/or previous literature to simulate growth with different training systems, planting densities and cultivars, and interpret the results of field trials, as well as to generate new hypothesis and experiments.

The project focuses on four areas: tree architecture, light interception, vegetative vigour and crop load. Our final aim is to improve management practices, e.g. training, pruning, thinning, bending, planting density and tree size that will allow better yields in fruit and nut trees.

The student will gain experience in computer simulation and computational modelling using L-systems, as well as in plant physiology.



Advisor(s) contact	• Dr Inigo Auzmendi, i.auzmendi@uq.edu.au, Ph: 07 344 32702 • Associate Advisors: A/Prof Jim Hanan Location: St Lucia
Webpage	https://qaafi.uq.edu.au/profile/762/inigo-auzmendi
Useful majors	Biochemistry & Molecular Biology / Biophysics / Computational Science / Plant Science / Horticulture

CHS 12 **Project** *Dr Craig Hardner*	**12) Genomics of horticultural tree crops**  Horticultural tree crops produce high value and nutritious fruit and nuts. Genomic approaches, particular genomic prediction, offer opportunities for improving efficiency of genetic improvement. Projects with Dr Hardner in this area include • Robustness of Japanese genomic prediction models for mandarin fruit quality in Australian germplasm • Chromosome structural variation in citrus using nanopore technology • Global prediction of sweetness in peach • Selection for timing of fruit maturity for adaption of cherry to changing environment Student in these projects will collaborate with local and international research groups in Japan, US and Europe. Projects in citrus, peach and cherry will to use genomic prediction methods to connect data collected from across the global with results. The citrus project will explore if chromosome structural variation can account for variation among sweet-orange varieties. Student will develop skills in field assessment, big-data management, bioinformatics, molecular and quantitative genetics, and scientific writing. All projects are aimed at producing manuscripts for submission to peer-reviewed journals.
Advisor(s) contact	• Dr Craig Hardner (c.hardner@uq.edu.au, 3346 9465) • Potential Associate Advisors: Dr Liz Ross, Dr Robyn Cave, Dr Mulsuew Fikere Location: St Lucia
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Bioinformatics, (Agriculture, Horticulture, Plant breeding)

CHS 13 **Project** *Dr Craig Hardner*	**13) <u>Optimising horticultural tree crops breeding</u>** Horticultural tree crops produce high value and nutritious fruit and nuts. Nevertheless, horticultural tree crop breeding is long and expensive. The projects below will undertake research to identify opportunities to improve efficiency of horticultural tree crops breeding • Bio-economic models for trait evaluation in macadamia or coffee • Modelling apple, macadamia, mango breeding strategies Student will collaborate with local and international research groups. Student will develop skills in systems modelling, economics, plant breeding, quantitative genetics, and scientific writing. All projects are aimed at producing manuscripts for submission to peer-reviewed journals.
Advisor(s) contact	• Dr Craig Hardner (c.hardner@uq.edu.au, 3346 9465) • Potential Associate Advisors: Dr Vivi Arief, Dr Robyn Cave, Prof Bruce Topp, Shane Mulo (QDAF) <u>Location:</u> St Lucia
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Plant breeding, Agricultural economics,

CHS 14

Project

Dr Craig Hardner

14) Genomic platform for understanding the population genetics of pre-colonisation distribution of Bunya pine

Bunya pine is a special Queensland forest tree. While widespread prior to European colonisation, the only remnant large population occurs in Bunya mountains with isolated individual trees distributed throughout SEQ Queensland.

Anthropogenic dispersal by first nations people may have had a major role in the distribution of the species. This proposed aims of this project are the development and evaluation of molecular tools for studying the distribution of these species, and survey the remnant Bunya population and individuals throughout SEQ Queensland investigate the spatial relationship between the remnant population at Bunya Mountains and the isolated trees.

Advisor(s) contact	• Dr Craig Hardner (c.hardner@uq.edu.au, 3346 9465) • Potential Associate Advisors: To be advised Location: St Lucia
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Bioinformatics, Social history

CHS 15

Project

Dr Craig Hardner

15) General recursive equations for estimating relationship coefficients in auto-polyploid organisms

The aim of this project is to extend general recursive equations used to estimate relationship coefficients for genetic effects in diploids to account for the more complicated inheritance pattern in auto-polyploid organisms. This project will involve development of probabilistic models of identical-by-descent of genes in diploid and auto-polyploid genetic systems, simulation of multiple population structures under varying polyploidy to validate relationship coefficients, analysis of existing phenotypic data with alternative genetic models to evaluate differences in accuracy of predict genetic values, and preparation of a manuscript for publication in high impact journal.

Advisor(s) contact	• Dr Craig Hardner (c.hardner@uq.edu.au, 3346 9465) • Potential Associate Advisors: AProf Mark Dieters, Dr Vivi Arief Location: St Lucia
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Quantitative genetics, statistics, poly-ploid genetics

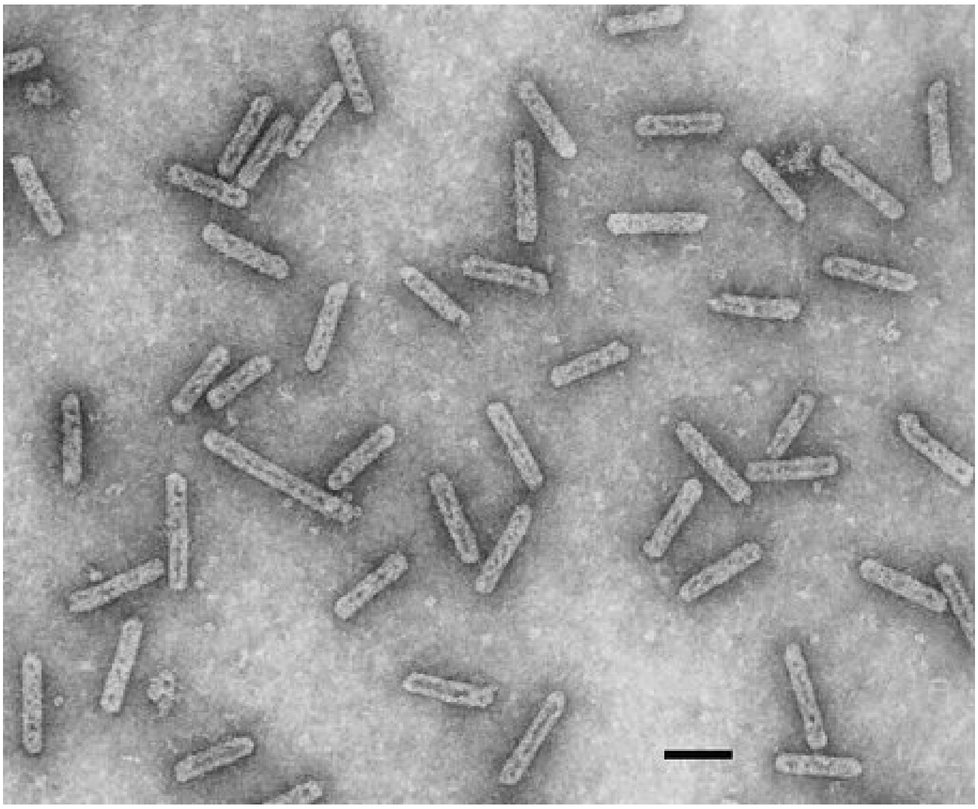
CHS 16 Project *Dr Mobashwer Alam*	**16) Inheritance of stomatal size and density in Macadamia** To cope with global climate change, one of the key focuses of the plant breeding program is to develop climate-smart varieties with efficient water use and photosynthesis. Finding out heritable and simple traits associated with less water loss and high photosynthesis can help breeders to select drought and high temperature tolerant elite cultivars. Stomatal pores on the leaf epidermis are the windows of water loss through transpiration and CO_2 uptake for photosynthesis. By altering the stomatal size and density, it can be possible to optimize the amount of CO_2 uptake and water loss. The focus of this project is to identify the variability in stomatal apparatus across a large number of breeding progeny, cultivars and wild germplasm of macadamia. The genetic and environmental effects on the variability of stomatal size and density will also be estimated. The inheritance pattern of the traits can be useful for future breeding decisions and planning. The student will develop skills in plant phenotyping, genetics, data analysis, and interpretation of results.
Advisor(s) contact	• Dr Mobashwer Alam| Email: m.alam@uq.edu.au| Phone: 0407925991 • Associate Advisors: Prof Bruce Topp Location: St Lucia and Nambour
Webpage	https://researchers.uq.edu.au/researcher/13285 https://researchers.uq.edu.au/researcher/2467
Useful majors	Genetics

CHS 17 Project

A/Prof Andrew Geering

17) Expression of the banana streak virus aspartic protease *in planta*

Banana streak virus (BSV) is a plant-infecting pararetrovirus, and is a distant relative of human immunodeficiency virus (HIV), with which it shares the same set of replication proteins, including an aspartic protease, which post-translationally processes other viral proteins to give rise to the active forms of these proteins. The aspartic protease is a critical protein in the replication cycle, and with HIV, has been a target for the design of antiviral drugs. We have successfully expressed the BSV AP in *E. coli* but there have been problems with misfolding of the protein, probably due to the fact that this is a prokaryotic protein expression system. In this project, a tobacco mosaic virus protein expression system will be trialled for the expression of the aspartic protease *in planta* with the aim of expressing an active form of the enzyme. This protein expression system will also be used for other proteins produced by the virus to determine their cell localization.



Advisor(s) contact	• Associate Professor Andrew Geering • Associate Professor John Thomas • Associate Professor Ralf Dietzgen Location: Ecosciences Precinct an Centre for Electron Microscopy and Microanalysis
Webpage	https://qaafi.uq.edu.au/profile/81/andrew-geering
Useful majors	Biochemistry & Molecular Biology / Microbiology

CHS 18 Project *A/Prof Andrew Geering*	**18) 3-D imaging of badnaviral replication structures** Badnaviruses are some of the most common viral pathogens in the tropics and infect a range of economically important plants such as banana, citrus, cacao, sugarcane and yam. Very little information is available on the replication strategies they use but an important advance has been made by our group with the discovery of replication structures (viroplasms) in the cytoplasm of infected cells. This project, a collaboration between QAAFI and the Centre for Electron Microscopy and Microanalysis, will utilize cryosectioning and transmission electron microscopy to image multiple layers of an infected cell, which will then be integrated using software to construct a 3-D image of the cell including the replication structures. Methods will then be developed to fluorescently label the replication structures, with the ultimate aim of dissecting out these structures using laser technology for analysis of protein and nucleic acid composition. 
Advisor(s) contact	• Associate Professor Andrew Geering • Associate Professor John Thomas • Mr Richard Webb Location: Ecosciences Precinct an Centre for Electron Microscopy and Microanalysis
Webpage	https://qaafi.uq.edu.au/profile/81/andrew-geering
Useful majors	Biochemistry & Molecular Biology / Microbiology

CHS 19 Project *Dr Louisa Parkinson*	**19) Developing molecular diagnostic tests for rapid detection of *Phytophthora* and *Phytopythium* spp. causing root rot of avocado** Phytophthora root rot (PRR) of avocado is the most important soilborne disease of orchard avocado trees, estimating an annual $17 million loss to the Australian avocado industry. The primary cause of PRR is oomycete, *Phytophthora cinnamomi*, a fungal-like microorganism. However numerous other species have been increasingly isolated from symptomatic roots and also demonstrated to cause PRR, including *P. multivora*, *P. niederhauserii*, *P. nicotianae*, *P. palmivora* and *Phytopythium vexans*. Testing for PRR typically involves baiting and isolating the pathogen from root and soil samples, however such methods render it difficult to distinguish between oomycete species based on oomycete morphology alone. Rapid molecular diagnostic tests such as loop-mediated isothermal amplification (LAMP) assays can enable fast, sensitive and specific detection of PRR-causing oomycetes in symptomatic roots. This research project aims to develop rapid LAMP diagnostic tests for the detection of *P. cinnamomi, P. multivora, P. niederhauserii* and *Pp. vexans* in avocado roots. Project activities will include using bioinformatics software for analysing the phylogeny of Phytophthora and Phytopythium to select candidate genes as a backbone for the LAMP assay; analysing gene sequence data for the design of species-specific LAMP primers; testing and optimising the assay in laboratory conditions followed by validation with inoculated avocado roots and lupin baits. The Honours research candidate will develop skills in bioinformatics, plant pathology, molecular biology and molecular diagnostic design and development.
Advisor(s) contact	• Dr Louisa Parkinson, l.parkinson@uq.edu.au, 3443 2457 • Associate Advisor: A/Prof Andrew Geering, a.geering@uq.edu.au Location: Ecosciences Precinct, 41 Boggo Road, Dutton Park
Webpage	www.qaafi.uq.edu.au
Useful majors	Please select from: Biochemistry & Molecular Biology / Bioinformatics / Microbiology / Plant Pathology

CHS 20 Project *A/Prof Elizabeth Dann*	**20) Investigating the role of soil health status on Phytophthora root rot and its management in avocado orchards** Phytophthora root rot, caused by the soil borne pathogen, *Phytophthora cinnamomi* (Pc), is the main disease affecting the avocado industry world-wide. Previous work has shown that tree health and decline due to Pc may be linked to soil health and microbial activity, with healthier trees growing in soils with higher microbial activity. However no study has quantified this relationship. Therefore the main aim of this Honours project will be to study the role of soil health and the activity and diversity of the soil microbial community, on Phytophthora root rot disease, and to evaluate management options. This honours project aligns with a larger avocado project titled "Improving avocado orchard productivity through disease management". There are established field trials assessing the efficacy of several soil amendments on tree health, fruit yield and quality. The honours project will utilise the soil samples from those trials and from other avocado orchards, and perform Micro Resp ™ plate assays to measure soil basal respiration and substrate induced respiration. An identification of the soil microbial community may be assessed using different molecular analyses. In-field assessments of tree health will complement laboratory analyses. The honours candidate will gain good knowledge and laboratory skills in plant pathology, soil science and molecular techniques. There will be scope for the student to undertake their own field and glasshouse-based experiments. As a part of the avocado pathology team, the student will gain experience in undertaking a project which is highly relevant to industry priorities.
Advisor(s) contact	• A/Prof Elizabeth Dann, e.dann@uq.edu.au, 07 3443 2455 • Associate Advisor: Dr Akila Prabhakaran, a.prabhakaran@uq.edu.au Queensland Alliance for Agriculture and Food Innovation Center for Horticultural science Location: Ecosciences Precinct, 41 Boggo Road, Dutton Park
Webpage	https://qaafi.uq.edu.au/profile/477/elizabeth-dann https://qaafi.uq.edu.au/profile/3104/akila-prabhakaran
Useful majors	Please select from: Agriculture/Horticulture/ Microbiology/ Plant Pathology/ Agronomy/Molecular Biology

Centre for Crop Science Projects

CCS 1

Project

Dr Erin Wilkus

1) Sorghum root growth and water availability in cold soils

Water stress and extreme heat at flowering are common abiotic stresses limiting yield in sorghum production across the Northern Grains Region. Winter sown sorghum could avoid heat and water stress at flowering. We test the theory that sorghum sown in winter, on cold soils, have deeper rooting systems that create greater access to water at depth during flowering, making them more resilient to heat stress and dry spells than crops sown at conventional times of planting.

This project compares water stress at flowering across three times of sowing (very early, early, conventional) in Cecil Plains, QLD. It spans two seasons of an on-farm field trial. One season of data collection is complete. We are currently preparing for a second season and processing above ground canopy and below ground root length and density specimens. These data are paired with soil moisture data, to reasonably estimate water stress. Early stage analysis suggests that water stress at flowering was highest under the conventional time of sowing and lowest under very early sowing.

This project gives students an opportunity to gain on-farm field experience and skills in root collection, washing and imaging to deepen their understanding of plant physiology.

Advisor(s) contact	• Dr. Erin Wilkus Email: e.wilkus@uq.edu.au Phone +61 4 68961546 • Associate Advisors: Dr Daniel Rodriguez and Dr Joseph Erye Location: Building 8115 Level 2 Room 206, UQ Gatton Campus
Webpage	https://www.qld-fsr.info/
Useful majors	Biochemistry & Molecular Biology Biophysics /Computational Science

CCS 2 **Project** *A/Prof Lee Hickey*	**2) Need for speed: growing plants fast to feed the world**  We need more robust and productive crops to feed the world, but developing new crop varieties is slow using traditional plant breeding approaches.  A technology developed at UQ called *speed breeding* enables the growth of plants up to 3x faster than normal conditions. This provides a powerful tool for plant breeders, but we don't understand plant behaviour under the rapid growth conditions.  Insight into the physiological and genetic mechanisms that drive faster plant growth will help us to improve the technology and deliver future crops capable of feeding the world.  This Honours project will involve performing experiments in the lab and glasshouse on a range of important food crops such as wheat, barley and chickpea. The student will gain hands on experience measuring key plant growth and development parameters, while learning from leading plant geneticists and plant physiologists.
Advisor(s) contact	**A/Prof Lee Hickey** l.hickey@uq.edu.au +61 408 210 286 Associate Advisors: Dr Millicent Smith, Prof Graeme Hammer **Location:** St Lucia or Gatton
Webpage	https://qaafi.uq.edu.au/profile/108/lee-hickey
Useful majors	Biochemistry & Molecular Biology / Genetics / Plant Science

CCS 3 **Project** *Dr Karine Chenu*	**3) Genotypic variability of transpiration efficiency and its impact on productivity in wheat** Water availability is a critical limiting factor for many cropping areas across the globe. Selecting germplasm that produces 'more crop per drop' (i.e. higher transpiration efficiency) could increase grain yield in water-limited environments. Greater transpiration efficiency is thought to be due to decreased stomatal conductance under high evaporative demand (e.g. hot hours in the middle of the day). This project will investigate for contrasting wheat genotypes how stomatal conductance varies in response to environmental factors, what impact this has on transpiration efficiency and how this translates to biomass production. This project aims at characterising transpiration efficiency and stomatal conductance response to evaporative demand in a phenotyping platform and assess in the field how these traits correlate to biomass production and potentially grain yield. The project will focus on contrasting genotypes recently identified including promising lines with potential to increase productivity in drought-prone conditions. The student will be in charge of an experiment in the recently built lysimeter facility at the University of Queensland Gatton Campus and will participate in field trials at Gatton and Tosari. In the lysimeter platform, whole-plant transpiration rate and environmental factors will be measured automatically. Other traits of interest such as stomatal conductance and photosynthetic activity will be measured during the experiment. In the field, the student will follow the growth and development of targeted genotypes, focusing on biomass accumulation. ***Location***: UQ Gatton Campus / Toowoomba ***Stipend***: 5000$ ***Duration***: 6-9 months
Contact Advisor/s	Dr Karine Chenu | Email: karine.chenu@uq.edu.au | Tel: 07 4529 4252 Dr Behnam Ababaei | Email: b.ababaei@uq.edu.au Dr Najeeb Ullah | Email: n.ullah@uq.edu.au
Webpage	https://qaafi.uq.edu.au/profile/18/karine-chenu https://qaafi.uq.edu.au/profile/3389/behnam-ababaei https://qaafi.uq.edu.au/profile/3335/najeeb-ullah
Useful majors	Plant Science / Agronomy / Biochemistry and Molecular Biology / Genetics

CCS 4 Project

Assoc Prof Bhagirath Chauhan

4) Effect of elevated carbon dioxide on weed growth and fecundity

The atmospheric carbon dioxide concentration is predicted to nearly double by the end of the century. Much research is ongoing to investigate the potential effect of this change on crop plants, but little work has been done on the weeds that infest these crops. Weeds are a major cause of yield loss for agricultural crops and cost close to $5 billion in Australia alone. The establishment of weeds is a crucial time for controlling their growth as they compete with crops for resources. This project will evaluate the response of various weed species to elevated concentrations of carbon dioxide during their early stage of growth.

Advisor(s) contact	• Assoc. Prof. Bhagirath Chauhan, b.chauhan@uq.edu.au, phone no. 0427923272 • Associate Advisors: Dr Michael Thompson, michael.thompson1@uq.edu.au Location: UQ Gatton campus
Webpage	https://qaafi.uq.edu.au/profile/738/bhagirath-chauhan
Useful majors	Plant Physiology, Agriculture, Biochemistry

CCS 5 Project

Assoc Prof Bhagirath Chauhan

5) Effect of environmental parameters on bioactive compounds in Amaranthus species

Leaves and seeds of *Amaranthus retroflexus* and *A. viridis* have medicinal values and could be an excellent dietary source for humans given their apparent strong antioxidant activities and nutrient contents. However, plants may vary in their antioxidant capacity and nutritive values with age when grown in different environments. Very limited is known of possible environmental effects on the medicinal value of *Amaranthus* species. The goals of this research are to study

- the effect of plant age on crude protein, soluble sugar, and total phenols content
- the effect of abiotic stress (temperature, shade, water) on crude protein, soluble sugar, and total phenol content
- the biological part (leave, stem or seed) of the plant that has more crude protein, soluble sugar, and total phenols content

Advisor(s) contact	• Assoc. Prof. Bhagirath Chauhan, b.chauhan@uq.edu.au; Ph: 0427923272 • Dr Gulshan Mahajan, g.mahajan@uq.edu.au; Ph: 0432467954 Location: QAAFI, UQ, Gatton Campus
Webpage	https://qaafi.uq.edu.au/profile/738/bhagirath-chauhan
Useful majors	Agriculture, Weed Science, Biochemistry, Plant Physiology

CCS 6 Project *Prof Daniel Rodriguez*	**6) <u>Matching adapted chickpea genotypes with soil and climate to maximise yield and profit: Field experimentation</u>** Pulses can increase profits, diversify income and increase sustainability. Megatrends in global food markets favour consumption of plant-based protein. However, significant productivity gaps remain, driven by lack of understanding of pulse physiology and agronomy. As part of a collaborative effort between UQ-QAAFI Centre for Crop Sciences, CSIRO, SARDI, NSW DPI, WA DPI and VIC DPI, this project aims to improve our understanding of the impact of different water availabilities and temperature relationships on chickpea growth, development and yield potential. This Honours project will focus on the collection of empirical data. The student will join a team of field agronomists and crop physiologist that are conducting on-farm and on-research station trials to research the impacts of water availability and temperature regimes during critical periods of biomass partitioning and yield formation for chickpeas. Field, trials will be conducted during the autumn and winter of 2021 at UQ-Gatton Campus, as well as on farm in the Darling Downs. The focus of the trials is to improve our understanding of the dynamics of yield formation under contrasting stresses. Frequent travelling to the field and working outdoors in farmers' fields will be required. This project will complement and collaborate with a second Honours project focused on the development of crop simulation model for chickpeas using the APSIM model (www.apsim.info). 
Advisor(s) contact	- Prof Daniel Rodriguez (UQ-QAAFI) - Dr Fer Dreccer (CSIRO), Dr Jeremy Whish (CSIRO), Dr Joe Eyre (UQ-QAAFI) <u>Location:</u> UQ Gatton Campus
Webpage	https://www.qld-fsr.info/ https://qaafi.uq.edu.au/profile/471/daniel-rodriguez
Useful majors	Agriculture, crop physiology, agronomy

CCS 7 Project

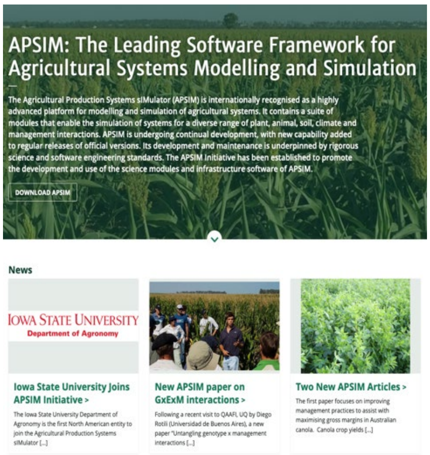
Prof Daniel Rodriguez

7) Matching adapted pulse genotypes with soil and climate to maximise yield and profit: Cropping systems modelling

Pulses can increase profits, diversify income and increase sustainability. Megatrends in global food markets favour consumption of plant-based protein. However, significant productivity gaps remain, driven by lack of understanding of pulse physiology and agronomy.

As part of a collaborative effort between UQ-QAAFI Centre for Crop Sciences, CSIRO, SARDI, NSW DPI, WA DPI and VIC DPI, this project aims to improve the crop simulation modelling capabilities of the APSIM model (www.apsim.info).

This Honours project will focus on the use of experimental data to parameterise and run crop models. The student will join a team of crop physiologist and APSIM programmers that are working to improve APSIM's modelling capabilities for chickpeas and lentil crops. Field, trials have been conducted and will continue to be run to collect the required datasets for model development. The focus of the work will be desktop at UQ's Gatton Campus. The parameterised model will then be used to assess the benefits of alternative physiological traits and crop management strategies across Australian chickpea and lentil growing environments. Frequent travelling to the field and working outdoors in farmers' fields might be required. This project will complement and collaborate with a second Honours project focused on on-farm and on-research station research. There is also opportunity to combine both types of activities (modelling and field experimentation).



APSIM: The Leading Software Framework for Agricultural Systems Modelling and Simulation

The Agricultural Production Systems sIMulator (APSIM) is internationally recognised as a highly advanced platform for modelling and simulation of agricultural systems. It contains a suite of modules that enable the simulation of systems for a diverse range of plant, animal, soil, climate and management interactions. APSIM is undergoing continual development, with new capability added to regular releases of official versions. Its development and maintenance is underpinned by rigorous science and software engineering standards. The APSIM Initiative has been established to promote the development and use of the science modules and infrastructure software of APSIM.

Iowa State University Joins APSIM Initiative >

The Iowa State University Department of Agronomy is the first North American entity to join the Agricultural Production Systems sIMulator [...]

New APSIM paper on GxExM interactions >

Following a recent visit to QAAFI, UQ by Diego Rotili (Universidad de Buenos Aires), a new paper "Untangling genotype x management interactions [...]

Two New APSIM Articles >

The first paper focuses on improving management practices to assist with maximising gross margins in Australian canola. Canola crop yields [...]

Advisor(s) contact	• Prof Daniel Rodriguez (UQ-QAAFI) • Dr Peter de Voil (UQ-QAAFI), Dr Jeremy Whish (CSIRO) Location: UQ Gatton Campus
Webpage	https://www.qld-fsr.info/ https://qaafi.uq.edu.au/profile/471/daniel-rodriguez
Useful majors	Agriculture, crop physiology, agronomy, systems modelling, IT, software engineering

CCS 8 Project

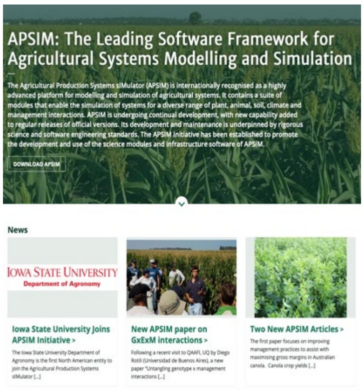
Prof Daniel Rodriguez

8) Winter sown sorghum as an adaptation to present and future climates

Water stress and extreme heat at flowering are becoming common abiotic stresses limiting sorghum production across the Northern Grains Region. These stresses can only be expected to increase in frequency and intensity as our climate changes. Winter sown sorghum has been proposed as a practice to increase sowing opportunities, avoid heat and water stress at flowering, and increase the frequency of double cropping i.e. planting a winter crop after a short summer fallow following the winter sown sorghum.

As part of a collaborative effort between UQ-QAAFI Centre for Crop Sciences, NSW DPI and QDAF, this project aims to assess the likely benefits of the practice using datasets from a network of trials run over the last two years across NSW and QLD, APSIM-Sorghum (www.apsim.info), and climate projections from a wide range of global circulation models.

This Honours project will focus on desktop activities that will analyse existing experimental data, parameterise and run simulation models. The student will join a team of crop physiologist, APSIM programmers and climate modellers, using QAAFI's facilities at UQ's Gatton Campus. Frequent travelling to the field and working outdoors in farmers' fields might be possible if interested.



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The Agricultural Production Systems sIMulator (APSIM) is internationally recognised as a highly advanced platform for modelling and simulation of agricultural systems. It contains a suite of modules that enable the simulation of systems for a diverse range of plant, animal, soil, climate and management interactions. APSIM is undergoing continual development, with new capability added to regular releases of official versions. Its development and maintenance is underpinned by rigorous science and software engineering standards. The APSIM Initiative has been established to promote the development and use of the science modules and infrastructure software of APSIM.

News

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Two New APSIM Articles >

The first paper focuses on improving management practices to assist with maximising gross margins in Australian canola. Canola crop yields [...]

Advisor(s) contact	- Prof Daniel Rodriguez (UQ-QAAFI) - Dr Peter de Voil (UQ-QAAFI), Dr Joe Eyre <u>Location:</u> UQ Gatton Campus
Webpage	https://www.qld-fsr.info/ https://qaafi.uq.edu.au/profile/471/daniel-rodriguez
Useful majors	Agriculture, crop physiology, agronomy, systems modelling, IT, software engineering, climate sciences

CCS 9 Project

Prof Ian Godwin

9) Climate Challenges in the Pacific Islands, tackling salinity and its effects on the Pacific's principle staple crop, Taro (*Colocasia*).

Islands in the Pacific are observing increased groundwater salinity that is affecting the production of Taro (Colocasia), a staple food crop. It is not known how Taro responds to salinity or whether there is diversity for this trait that could be exploited in crop improvement.

The aim of this project is to ascertain the dose-response relationship between taro and salinity in order to identify 'susceptible', 'tolerant' and 'lethal' doses. An evaluation of spectral imaging (NDVI, Green Chromatic Coordinates) vs conventional phenotyping techniques will be conducted to develop a salinity screening protocol for the Pacific Islands.

In this project, the student will conduct a glasshouse experiment on the response of Taro to salinity. The student will develop important skills in experimental design, plant physiology, phenotyping and data analysis through the lens of an international agricultural development program for emerging Pacific nations.

Advisor(s) contact

- Professor Ian Godwin, Email: i.godwin@uq.edu.au, Phone: +61 409 582 481
- Associate Advisors: Dr Bradley Campbell & Dr Millicent Smith

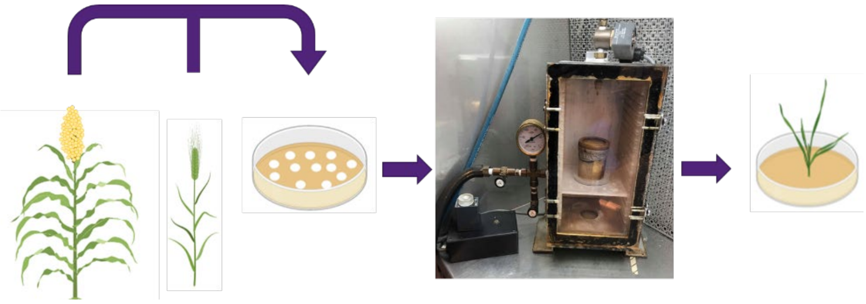
Location: John Hines Bld (62), Lab 319, St Lucia.

Webpage

https://qaafi.uq.edu.au/profile/384/ian-godwin

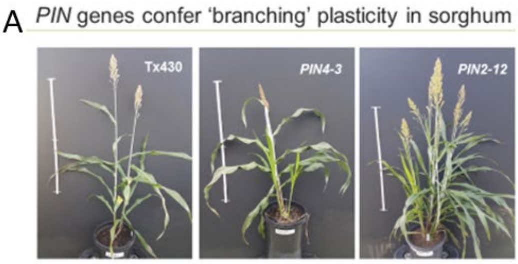
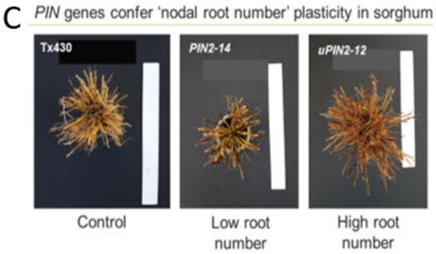
Useful majors

Plant Physiology /Computational Science / Genetics / Plant Science

CCS 10 Project *Prof Andrew Borrell*	**10) Improving drought tolerance of cereals using gene editing technologies to modify plant architecture** New breeding strategies are required to quickly adapt to the rapidly changing climate, where designing high-yielding and high-quality cereal crops that use less water is of the utmost importance. Since crop adaptation to water-limited environments is dependent on the balance between water supply and demand, it is hypothesized that uncoupling root and shoot architecture will lead to a more favourable water supply/demand balance in cereals. This project combines novel genetic editing technologies with plant physiology, providing insights into the molecular and physiological mechanisms for drought adaptation strategies. Recent breakthroughs through dissemination of developmental and stress-responsive genes have led to modifications of the plant architecture which can have enormous impacts on both yield and water-use efficiency of these crops. This honours project will include generation of stable CRISPR/Cas9 gene edited crop plants targeting specific developmental genes and analysing the outcoming progenies in hopes of disseminating the molecular mechanisms.  
Advisor(s) contact	- Prof Andrew Borrell; Dr. Karen Massel Associate Advisors: Prof Ian Godwin; A/Professor Lee Hickey Location: Rm 319, John Hines (62), St Lucia
Webpage	https://qaafi.uq.edu.au/profile/234/andrew-borrell https://qaafi.uq.edu.au/profile/384/ian-godwin http://hickeylab.com/resume-lee-hickey/ https://qaafi.uq.edu.au/profile/6037/karen-massel
Useful majors	**Biochemistry & Molecular Biology** / **Bioinformatics** / **Genetics**

CCS 11 Project *Dr Jack Christopher*	**11) Sustaining food production on the face of climate change through crop root adaptation** Access to water is the major production limitation in many important cropping regions of the world. It has been predicted that climate change will lead to increased drought frequency in many of these regions. We have demonstrated that optimizing root structure to improve access to deep stored soil moisture can substantially increase production and yield stability in the face of drought. We have developed a number of methods to measure plant root systems to identify root traits associated with improved deep soil moisture extraction. Our aim is to assist breeders to select for superior root systems for particular cropping environments by providing rapid phenotyping systems and molecular markers. We have developed a range of root observation systems to measure root systems in crop plants from early seedling stages right through to maturity.
Advisor(s) contact	• Dr Jack Christopher, 07 45291413, j.christopher@uq.edu.au • Associate Advisors: Dr Karine Chenu Location: Leslie Research Facility, Toowoomba
Webpage	https://qaafi.uq.edu.au/profile/261/jack-christopher
Useful majors	Biochemistry & Molecular Biology / Agriculture

CCS 12 Project *Dr Jack Christopher*	**12) Increased food production on constrained soils** Food demand is increasing with increasing population and increasing income but climate change is threatening production. With little potential for increasing the cropping area, it will be essential to increase production on existing land. Unfortunately, in Australia a large proportion of the wheat cropping area is subject to soil constraints limiting production. In this project, we aim to identify wheat genotypes with superior adaptation to soil constraints limiting wheat production in Queensland. Identifying superior genotypes in the field is difficult due to extreme seasonal differences in the magnitude of the effect of the soil constraints. A high level of spatial variability in the severity of soil constraints over small distances also limits selection in field trials. We would like to provide rapid phenotyping systems and molecular markers to allow breeders to pre-screen large numbers of genotypes before expensive field-testing. We are developing screening techniques in growth cabinets and in the glasshouse to this.
Advisor(s) contact	• Dr Jack Christopher, 07 45291413, j.christopher@uq.edu.au • Associate Advisors: Dr Yash Dang, SAFS Location: Leslie Research Facility, Toowoomba
Webpage	https://qaafi.uq.edu.au/profile/261/jack-christopher
Useful majors	Biochemistry & Molecular Biology / Agriculture

CCS 13 Project *Professor Andrew Borrell*	**13) <u>Enhancing drought adaptation in *sorghum* through gene editing</u>** Producing more food with less water is one of the greatest challenges facing humanity today. Two families of genes, *PIN* and *VRN*, have been found to regulate plant architecture, with *PIN* genes affecting both canopy development and root architecture in sorghum's stay-green trait and *VRN1* modulating root architecture in wheat and barley, in addition to regulating flowering behaviour. We have recently developed transgenic and gene-edited lines of sorghum containing various *PIN* and *VRN* genes. In this project, you will measure a range of drought-adaptation mechanisms in transgenic and gene-edited sorghum plants. An expected outcome of this Project is enhanced drought adaptation for cereals in a dry world. **A $10,000 scholarship will be granted to the student on this project.** A *PIN* genes confer 'branching' plasticity in sorghum  C *PIN* genes confer 'nodal root number' plasticity in sorghum  
Advisors contact	• Professor Andrew Borrell: a.borrell@uq.edu.au Phone: +61 0419 704 550 • Associate Advisors: Dr Karen Massel, A/Prof Lee Hickey, Prof Ian Godwin <u>Location:</u> John Hines Building, St Lucia UQ Campus
Webpage	https://researchers.uq.edu.au/researcher/1239

CCS 14 Project *Professor Andrew Borrell*	**14) Enhancing drought adaptation in *barley* through gene editing** Producing more food with less water is one of the greatest challenges facing humanity today. Two families of genes, *PIN* and *VRN*, have been found to regulate plant architecture, with *PIN* genes affecting both canopy development and root architecture in sorghum's stay-green trait and *VRN1* modulating root architecture in wheat and barley, in addition to regulating flowering behaviour. We have recently developed transgenic and gene-edited lines of barley containing various *PIN* and *VRN* genes. In this project, you will measure a range of drought-adaptation mechanisms in transgenic and gene-edited barley plants. An expected outcome of this Project is enhanced drought adaptation for cereals in a dry world. **A $10,000 scholarship will be granted to the student on this project.**  
Advisors contact	- Professor Andrew Borrell: a.borrell@uq.edu.au Phone: +61 0419 704 550 - Associate Advisors: Dr Karen Massel, A/Prof Lee Hickey, Prof Ian Godwin Location: John Hines Building, St Lucia UQ Campus
Webpage	https://researchers.uq.edu.au/researcher/1239