The University of Queensland
AUSTRALIA

QAAFI
Queensland Alliance for
Agriculture and Food Innovation

The Queensland Alliance for Agriculture and Food Innovation

HONOURS PROGRAM

Queensland Government

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Participate in an honours program at UQ with QAAFI

The Queensland Alliance for Agriculture and Food Innovation (QAAFI) is a world-leading research institute, and among only a handful of similar scientific organisations anywhere in the world.

Students enrolled through a UQ Faculty may undertake an Honours project supervised by a QAAFI researcher. Participation allows students to engage with and experience the rich intellectual resources and facilities available to the Institute.

QAAFI is spread among various sites across Queensland and is comprised of four research centres, the Centre for Animal Science, Centre for Crop Science, Centre for Horticultural Science and Centre for Nutrition and Food Sciences.

You are encouraged to contact a researcher directly about which projects are available, and If you are not sure which Centre suits your research interest, you can viisit our website through the QR code.

Duration: 1 year full-time

For more information about Honours at QAAFI and available projects, visit: **qaafi.uq.edu.au/honours**

Honours Co-ordinator

Dr Vijaya Singh
v.singh@uq.edu.au

To register your interest, scan here:

Join the QAAFI Student Association

The QSA is a student organization that collectively aims to enrich the academic and social skills of graduate and undergraduate students enrolled through the Queensland Alliance for Agriculture and Food Innovation at The University of Queensland.

QSA aims to:

- To foster a sense of community on students across all four QAAFI research centres
- To enrich the academic and social experience of undergraduate and postgraduate students
- To support QAAFI's mission of research excellence through career development opportunities for its students

For more information about Honours at QAAFI and available projects, visit: **qaafi.uq.edu.au/honours**

QAAFI Student Association:

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qsa@uq.edu.au

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Version 1 | Published July 2022 | CRICOS Provider 00025B

"I had an extraordinary experience as an honours student in QAAFI as it gave me an opportunity to learn cutting edge technologies first-hand, network with people, and also be a part of the QAAFI Student Association to build my leadership skills."

Yastika Banerjee – QAAFI Honours Student

Project: Cloning and expression of conserved Mycoplasma bovis antigenic sequences into the BoHV-1 vaccine vector - Development of a BHV – M. bovis bivalent vaccine.
Supervisors: Dr. Karl Robinson and Prof. Timothy Mahony

"Being an Honours student in QAAFI was an enriching experience which made me feel well prepared for any challenges working in the food industry."

Da Wei (David) Chia – QAAFI Honours Student

Project Title: Impact of individual human variations on the sensory experience of burger patties. | **Supervisor:** A/Prof Heather Smyth

"Research is not just for the academic elite; if you have a passion for science and a strong work ethic, you have a place in research."

Tatiana Briody – QAAFI Honours Student

Project: The role of microRNAs in the replication of bovine alphaherpesvirus 1. | **Supervisor:** Prof. Timothy Mahony

Queensland Alliance for Agriculture and Food Innovation

Honours Projects 2022

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

CRICOS code 00025B

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

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.

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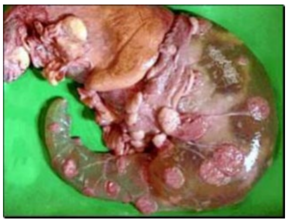
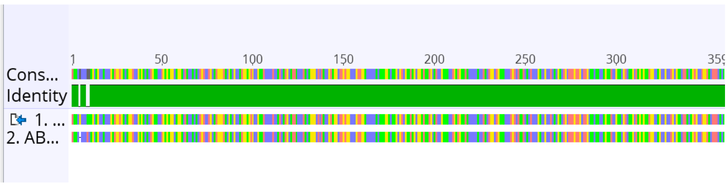
For general information about undertaking Honours within QAAFI please contact QAAFI Honours Co-ordinator Dr Vijaya Singh (v.singh@uq.edu.au).

Centre for Animal Science Projects

CAS 1 Project *Prof Ala Tabor*	**1) <u>Bovine campylobacteriosis diagnosis and genomic analyses</u>** 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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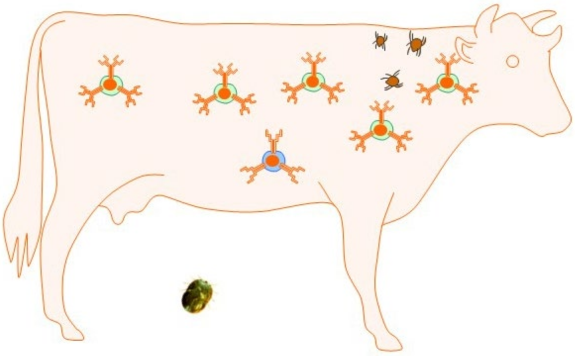
Useful majors	Microbiology / biotechnology / molecular biology / bioinformatics

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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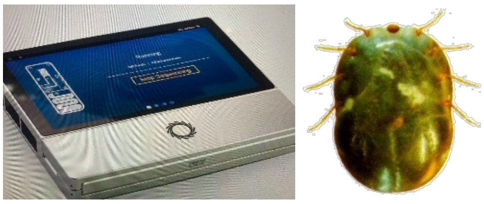
Useful majors	Microbiology / biotechnology / molecular biology / bioinformatics

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.

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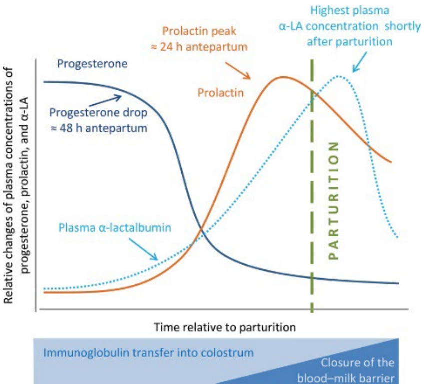
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Genetics / Microbiology

CAS 5 Project

Dr Luis Prada e Silva

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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CAS
6 to 17
Project

Prof Ben Hayes

Dr Elizabeth Ross

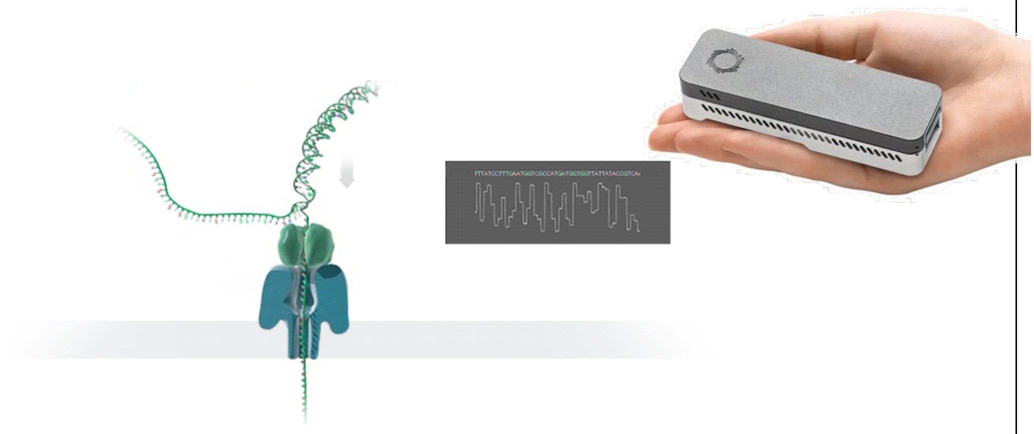
Dr Loan Nguyen

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
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Project

Prof Ben Hayes

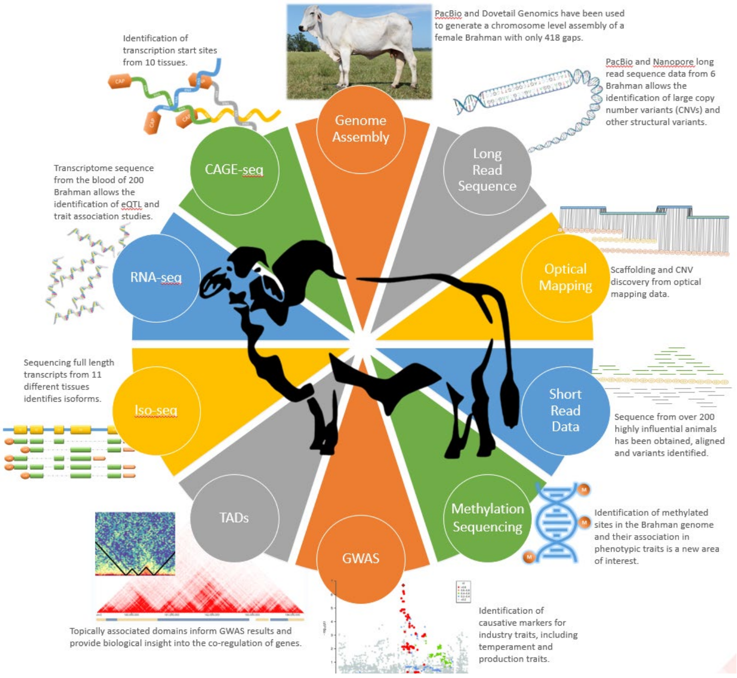
Dr Elizabeth Ross

Dr Loan Nguyen

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.



CAS
6 to 17
Project

Prof Ben Hayes

Dr Elizabeth Ross

Dr Loan Nguyen

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.

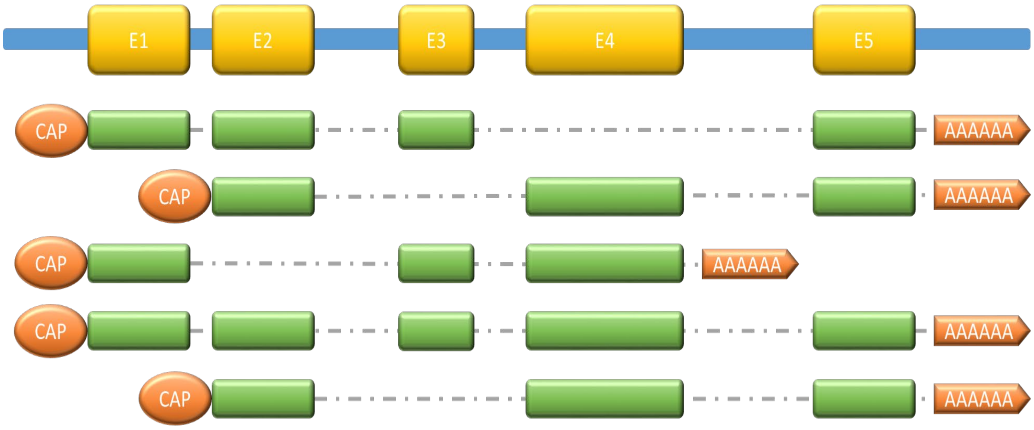
In this project students will develop molecular genetics and bioinformatics skills to provide a value tool for the Northern Beef industry.

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

Dr Elizabeth Ross *Dr Loan Nguyen*	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* *Dr Elizabeth Ross* *Dr Loan Nguyen*	**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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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Agriculture / Veterinary Medicine

CAS
6 to 17
Project

Prof Ben Hayes

Dr Kai Voss-Fels

Dr Eric Dinglasan

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

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

Prof Ben Hayes *Dr Elizabeth Ross*	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.
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Microbiology / Agriculture / Veterinary Medicine
CAS 6 to 17 Project *Prof Ben Hayes* *Dr Bailey Engle*	**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. 
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics / Agriculture / Veterinary Medicine

CAS
6 to 17
Project

Prof Ben Hayes

Dr Elizabeth Ross

Dr Loan Nguyen

Dr Bailey Engle

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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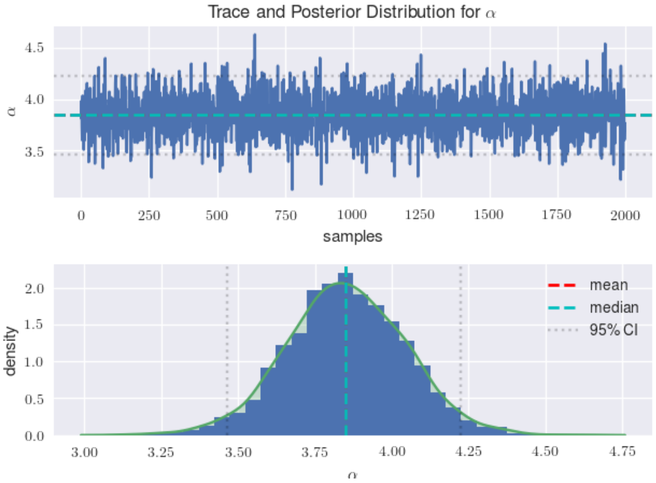
CAS **6 to 17** **Project** *Prof Ben Hayes* *Dr Roy Costilla*	**15) The need for speed in Genomic research: Comparing algorithms to estimate polygenic effects in tropically adapted beef cattle** With the advent of new genomic technologies comes the need to develop new statistical and computational algorithms 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

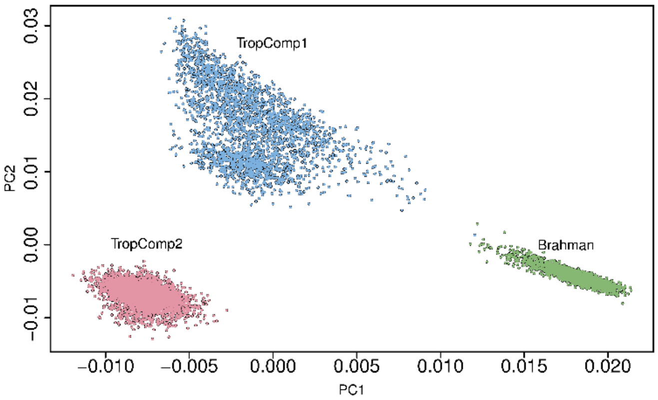
Prof Ben Hayes

Dr Roy Costilla

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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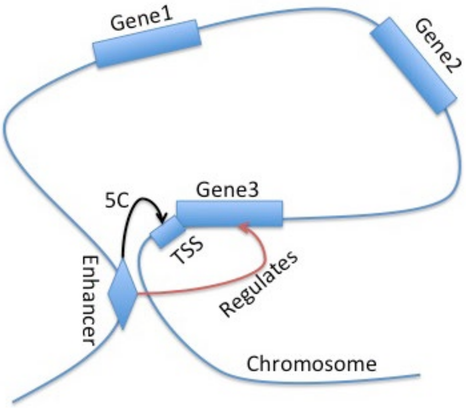
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics
CAS 6 to 17 Project *Prof Ben Hayes* *Dr Mehrnush Forutan*	**17) Exploring TSS-enhancer correlations and identification of novel mutations in TSS-enhancer regions in Bos indicus species** Next generation 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.
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics

CAS 18 Project

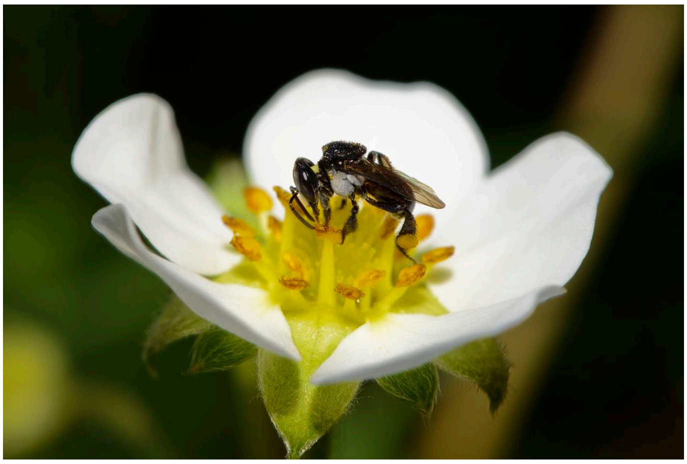
Prof Mary Fletcher

Dr Natasha Hungerford

Dr Tobias Smith (School of Biological Sciences)

18) Investigation of trehalulose content of different stingless bee species

Stingless bee honey has recently been shown to contain high levels of the unusual disaccharide sugar trehalulose (Fletcher et al 2020). Trehalulose is known to have beneficial properties such as having a low glycaemic index (low GI) and being acariogenic (tooth friendly). Trehalulose is an isomer of sucrose and has not previously been found as a major component in any other food, so the presence of this sugar in high proportions in Australian stingless bee honey is an exciting discovery. This project will examine the level of trehalulose in honey from related stingless bee species in Brazil.



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

Reference:
Fletcher, MT, Hungerford, NL, Webber, D, Carpinelli de Jesus, M, Zhang, J, Stone, ISJ, Blanchfield, JT, Zawawi, N (2020) Stingless bee honey, a novel source of trehalulose: a biologically active disaccharide with health benefits. *Scientific Reports* **10**, 12128. https://doi.org/10.1038/s41598-020-68940-0

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Useful Majors	Chemistry/ Chemical sciences/ Biochemistry & Molecular Biology

CAS 19 Project

Dr Lida Omaleki

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

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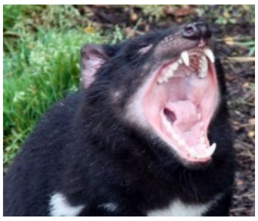
Location	EcoSciences Precinct, Dutton Park
Webpage	https://researchers.uq.edu.au/researcher/2477
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CAS 20 Project *Dr Conny Turni* *Dr Lida Omaleki*	**<u>20) Oral cavity bacteria of marsupials – a One Health Approach</u>** 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 existence of further novel genera and species. Tasmanian devil   Spotted tailed quoll
Advisor(s) contact	• **Dr Conny Turni**, c.turni1@uq.edu.au +61 7 344 32463 • **Dr Lida Omaleki**, l.omaleki@uq.edu.au +61 7 344 32576
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Webpage	https://researchers.uq.edu.au/researcher/2477
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CAS 21 Project

Dr Lida Omaleki

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.

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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CAS 22 Project

Dr Conny Turni

Dr Lida Omaleki

22) The bacteriology and the microbiome of the poultry shed environment

The poultry industries (both layer and meat chicken) have increasing pressure to demonstrate to consumers and to the regulators that the production systems have optimal hygiene including effective programs to ensure that the sheds provide a clean and hygienic environment for the introduction of a new flock. This project will be the commencement of a planned research program to look at the bacterial flora and the microbiome of the poultry shed environment. The project will involve generating culture based data on the microflora of the shed environment after a flock (multiple farms and multiple flocks will be examined). This work would include comparing the microflora before and after a hygiene intervention such as dis-infection. As well, the project will involve the initial work on establishing methods for a molecular/microbiome approach to shed microbiota characterisation. The project will examine different methods of DNA extraction for their suitability for use on dust and environmental samples. The quality of the DNA extraction methods will initially be evaluated by using the samples in standard PCR assays (and compare these results with culture based results). If time permits, the suitability of the extracts for next generation sequencing analysis will also be examined.

Barn shed for layer chickens

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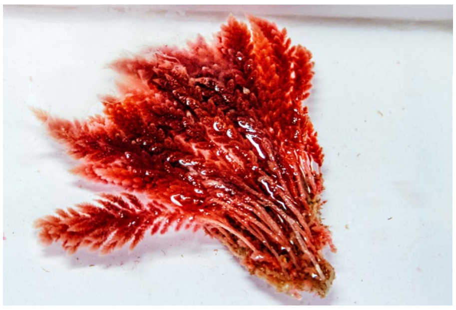
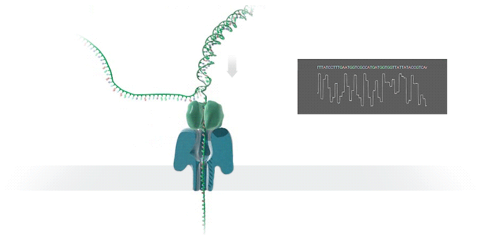
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CAS 23 Project *Prof Ben Hayes* *Dr Loan Nguyen* *Dr Elizabeth Ross*	**23) Discovering methane reducing pathways in seaweed** Cattle are a major source of methane, a potent greenhouse gas. Recently, it has been discovered that feeding some seaweeds to cattle, particularly red seaweed (Asparagopsis taxiformis) greatly reduces methane emissions. In this project, the successful candidate will sequence the red seaweed genome, and discover the gene pathways that led to the production of anti-methanogenic compounds. This knowledge could lead to new innovations to reduce methane emissions and so contribute to a large scale reduction in global warming. The student will learn skills in genome sequencing with state of the art (Nanopore) technology as well as cutting edge bioinformatics techniques.  
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Webpage	https://qaafi.uq.edu.au/profile/1059/ben-hayes
Useful majors	Please select from: Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics

<table>
<tr>
<td>**CAS 24 Project**

Dr Ali Raza

Professor Ala Tabor</td>
<td>

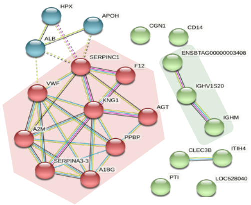
24) Title – Understanding host biology to cattle tick infestation

The cattle tick, Rhiphicephalus microplus, and the diseases it transmits lead to massive economic losses to cattle industries in tropical and subtropical countries. The widespread resistance to acaricide drugs and the absence of an effective vaccine for tick control had led to genetic selection of host resistance as a method of choice for non-chemical control of cattle tick. Previously, studies attempted to identify genetic markers for the resistance of cattle to tick burden, for example, immunological methods, genome-wide analysis studies, and quantitative trait analysis in tropically adapted genotypes. As gene expression results and actual dynamics occurring at the protein level often do not correlate due to post-transcriptional, posttranslational and degradation regulation. Host proteomics may be useful to study host response to tick exposure and thus provide reliable biomarkers to assist in selection to support traditional breeding programs.

In this project, quantitative proteomics will be used to reveal the changes in proteomes of tick-resistant and -susceptible cattle, subsequently exploring the systemic and local host response to tick infestation.

The student will gain skills in Mass Spectrometry, Data analysis with variety of software and various online database resources for functional annotation of the proteins.



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<tr>
<td>Advisor(s) contact</td>
<td>

- **Dr Ali Raza**, a.raza@uq.edu.au +61 7 334 62317
- Associate Advisor: Professor Ala Tabor, a.tabor@uq.edu.au +61 7 334 62176

</td>
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<tr>
<td>Location</td>
<td>QBP, Building 80, St Lucia campus</td>
</tr>
<tr>
<td>Webpage</td>
<td>Dr Ali Raza - UQ Researchers</td>
</tr>
<tr>
<td>Useful majors</td>
<td>Biochemistry & Molecular Biology / Bioinformatics / Biotechnology</td>
</tr>
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CAS
25 to 29
Projects

Prof Tim
Mahony

25) 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.

26) 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.

27) 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.

28) The application of synthetic biology to large DNA viral genomes

The capacity to manipulate the genomes of viruses in the laboratory remains dependent on their in vitro replication efficiency. This limitation has hindered our attempts better understand many of these viruses. This project will address this issue by applying long range PCR and DNA fragment assembly to construction copies of selected herpesviral genomes. The capacity of these genomes to facilitate rescue of infectious virus will also be determined. The availability of these infectious genome copies will aide in the development of improved diagnostics and control methods for these currently difficult to work with viruses.

29) The development of strand-specific sequencing methodologies double-stranded DNA viral genomes

	The herpesviruses are a large family of viruses that infected a broad range of hosts, such as mammals, reptiles, and molluscs. These viruses have a large double stranded DNA (dsDNA) genome. While the herpesviruses are considered to be genetically stable, variants with increased capacity to cause disease have emerged. The molecular basis underpinning the emergence of these virulent subtypes/genotypes for several herpesviruses of importance to veterinary medicine remains poorly understood. This project will utilise Oxford Nanopore sequencing technology to develop strategies to enable the strand-specific sequencing of herpesvirus genomes. The availability of strand-specific sequence data will be used to determine if the emergence of new genotypes of herpesviruses is a result of spontaneous mutation or the selection of existing genetic diversity within a viral isolate. This new knowledge will improve our understanding of this important virus family.  Candidates with their own project ideas that fit within the research activities described on Prof Mahony's profile page are encouraged to contact him.
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Centre for Nutrition and Food Sciences Projects

CNAFS 1 Project *A/Prof Yasmina Sultanbawa* *Dr Anh Phan*	**1) Nutritional and bioactive properties of Australian boab (Adansonia gregorii): an emerging functional food ingredient** Boab (Adansonia gregorii) is a big iconic tree mostly endemic in the Kimberly region of Western Australia. The multi-purpose tree is enchanted by the Australian Indigenous people with its every part being found to be useful. Different botanical tissues of boab including fruit pulp, root flesh, seeds and leaves have been traditionally used in foods and medicine as well as contributing to the livelihood of the Indigenous Australians. Several studies have reported that baobab fruits (Adansonia digitata) are good source of vitamin C (higher than other well-known fruit sources of ascorbic acid like orange and strawberry), fiber, minerals, essential fatty acids and phytochemicals. Thus, the European Commission and United States Food and Drug Administration have approved baobab fruit pulp as a novel food ingredient. Consequently, there is rise in demand of various products derived from baobab fruit pulp worldwide. However, despite the increase in cultivation of boab by the indigenous Australians, there is still limited information on the nutritional and phytochemical characterization of the different parts of the fruit. The aim of this study is to identify bioactive compounds and nutritional values in different botanical tissues of boab using the state of the art UHPLC-PDA-MS/MS. Furthermore, bioactive properties of the samples will be determined for potential application as functional food and/or nutraceutical ingredients. This study will provide valuable information about Australian boab that may be useful for the Indigenous Australians to boost local and international trade, encourage local production and enhance the livelihoods of Australian Indigenous communities. 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)	- **A/Prof Yasmina Sultanbawa,** y.sultanbawa@uq.edu.au +61 7 344 32471 - **Dr Anh Phan**, a.phan1@uq.edu.au +61 7 344 32476
Location	Elkhorn Building, Long Pocket Campus
Webpage	www.qaafi.uq.edu.au; www.uniquelyaustralianfoods.org
Useful majors	Biochemistry, Chemistry, Microbiology, Agriculture, Food Science

CNAFS 2 Project *A/Prof Yasmina Sultanbawa* *Dr Oladapo Olukomaiya*	**2) Bioprocessing of seaweed into protein-enriched food product: effect of solid-state fermentation on the physicochemical, functional properties and extraction of bioactive compounds** Seaweed is a high-yield crop, with productivity levels as high as a dense terrestrial vegetation. It is the largest aquaculture crop in the world with more than 25 million tonnes of seaweed produced per annum, which is steadily increasing at a rate of 8% per year and represents a $US7 billion-dollar aquaculture industry. Seaweed can have versatility and diversity in its use. In addition to seaweed being an important food source for a growing human population, there is also a massive scope to increase the commercial side of the industry and to create optimistic environmental change at a grand scale. Some studies have reported on the potential of seaweed, including its chemical composition, functionality, and effectiveness in reducing methane emission in cattle. However, it is still unknown how solid-state fermented seaweed can mitigate climate change's ongoing problems and support the concept of a circular economy, as well as how this relates to the development of novel value-added products. This project aims to explore the effect of solid-state fermentation on the physicochemical, functional properties and extraction of bioactive compounds. Outcomes will help bridge the current knowledge gaps. 
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Useful majors	Chemistry, Microbiology, Food Science

CNAFS 3 Project *A/Prof Heather Smyth*	**3) 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 research would be to explore potential for food applications of Australian native foods such as wattle seeds, seaweed, bunya nut, kakadu plum, saltbush, native stingless bee honey, among others. Chemical compositional analysis, product development, flavour chemistry and sensory and consumer techniques may be used to explore food applications of Australian native foods and ingredients. The project can be tailored to the skills and interest of the applicant. 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	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 4 Project

A/Prof Heather Smyth

4) Impact of processing on honey quality

Honey quality is optimal when cured and sealed in the comb by the honeybee. 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. 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 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.

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

CNAFS 5 Project *A/Prof Heather Smyth* *Dr Thoa Nguyen*	**5) Flavour chemistry of tropical fruits** Australia is home to a delicious variety of tropical and sub-tropical fruits. Among these fruits, such as papaya, passionfruit, pineapple, strawberry and mango, there are different varieties which have differing flavour profiles. Some consumers prefer certain flavour profiles over others. Fruit flavour comes from a balance between sugars and acids (taste) as well as a wide array of small molecules known as volatile aroma compounds. It's the volatile composition of fruits which gives their distinctive flavour profiles. While breeding programs are well equipped for breeding to production targets, they are less able to breed new varieties of fruits with specific flavour profiles. The main reason for this is that genetic markers for fruit flavour targets have not been established. Such targets would allow for more efficient breeding of new cultivars with desirable consumer qualities. This project will apply flavour analytical chemistry techniques and sensory science methodologies to understand fruit quality with view to identifying biochemical pathways of flavour development. The student will work as part of a larger team working on a Hort Innovation-funded Genetics of fruit quality project. 
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Food Science / Psychology

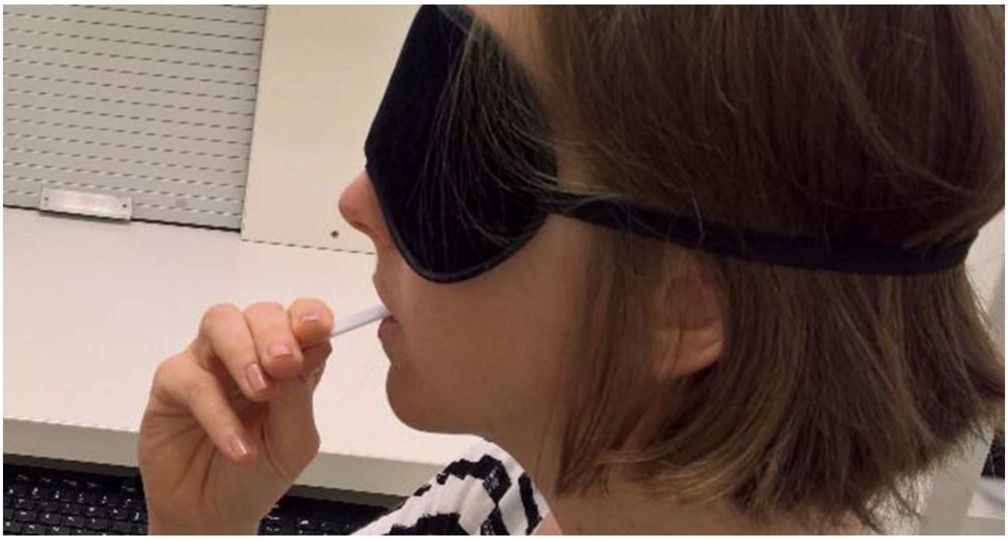
CNAFS 6 Project

A/Prof Heather Smyth

6) Individual human variation and sensory experience

Aroma, flavour, texture and mouthfeel attributes 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 sensory properties 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.



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Webpage	www.qaafi.uq.edu.au
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 7 Project

A/Prof Heather Smyth

7) Plant protein – towards better tasting meatless burgers

There is a growing trend towards eating plant protein as an alternative to meat which is being led by young flexitarian consumers who are concerned about climate change and their personal impact through their own food choices. As such, there has been an explosion of new commercial products where plant protein sources are used to make meatless-analogues of otherwise well-loved meat products such as plant burgers and sausages. While much progress has being made by food companies in recent years, the flavour, texture and mouthfeel of these plant products still leave a lot to be desired. Importantly, we need to understand how plant protein differs from meat protein in a product, and then develop novel techniques to bridge the gap. The ideal commercial outcome would be a plant protein burger that is indistinguishable from a high quality meat product.

This project will apply techniques such as new product development, ingredient formulation, sensory science, flavour chemistry and physical texture analysis to improve the sensory quality of meatless protein food products. The student will work as part of a larger multi-disciplinary team from QAAFI and the School of Chemical Engineering on an ACR-funded linkage grant in collaboration with Motif Food Works.

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

CNAFS 8 Project

Dr Tim O'Hare

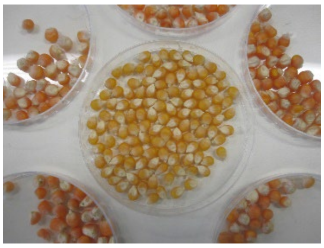
8) The effect of popping on carotenoid content in zeaxanthin-biofortified popcorn

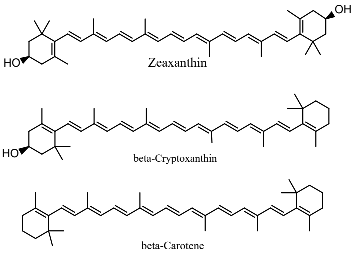
Carotenoids are lipophilic pigments responsible for the yellow, orange and red colours in plants, giving corn kernels their typical bright yellow colour. Carotenoids also play an important role in human health, including macular degeneration, the leading cause of blindness in Australia. Two carotenoids, 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.





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

CNAFS 9 Project *Dr Tim O'Hare*	**9) 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.  
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Webpage	https://qaafi.uq.edu.au/profile/459/tim-ohare
Useful majors	Biochemistry & Molecular Biology / Chemistry / Agriculture / Horticulture / Food Science

CNAFS 10 Project

Dr Michael Netzel

Dr Olivia Wright

Dr Hung Trieu Hong

Prof Yasmina Sultanbawa

10) Exploring the nutritional value of Saltbush, an Australian indigenous edible Halophyte

Salinity and shrinkage of water tables are among the major crises in the world which adversely affect food production. It has been reported that about one-fifth of total farming land is salt-affected worldwide. Currently, immense attention is granted to the domestication of halophytes (salt-tolerant plants) due to their evolved adaptive mechanisms to salinity. Halophytes are ecologically important plants, of which saltbush (Atriplex sp.) has been traditionally used as medicine, food, animal feed and as a "tool" for rehabilitation of degraded lands. This plant species has the potential to be used as a source of functional food/functional food ingredients but is under-utilised due to lack of popularity or limited knowledge. Therefore, the aim of this project is to determine the nutritional and phytochemical composition of selected Australian saltbush samples and to assess their potential bioactivity. State-of-the-art analytical techniques such as Stable Isotope Dilution Assays (SIDA) and UHPLC-PDA-MS/MS as well as enzyme and antimicrobial assays will be used. 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.

Saltbush (*Atriplex* sp.)

Advisor(s)	**Dr Michael Netzel**, m.netzel@uq.edu.au M: 0400 887 072 **Dr Olivia Wright**, o.wright@uq.edu.au +61 7 336 56116 **Dr Hung Trieu Hong**, h.trieu@uq.edu.au **Prof Yasmina Sultanbawa**, y.sultanbawa@uq.edu.au +61 7 344 32471
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Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Agriculture / Food Science

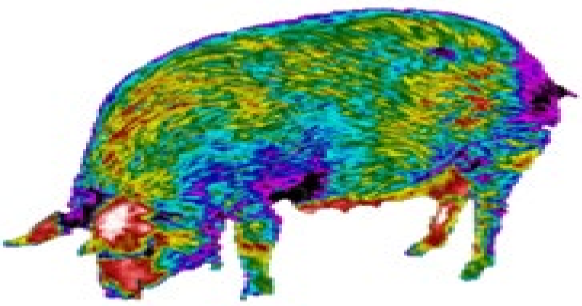
CNAFS 11 Project

Dr Marta Navarro

Prof Eugeni Roura

11) Metabolic resilience to 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.



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CNAFS 12 Project

Dr Shahram Niknafs

Prof Eugeni Roura

12) Peri-hatching programs that naturally improve chicken gut health

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.

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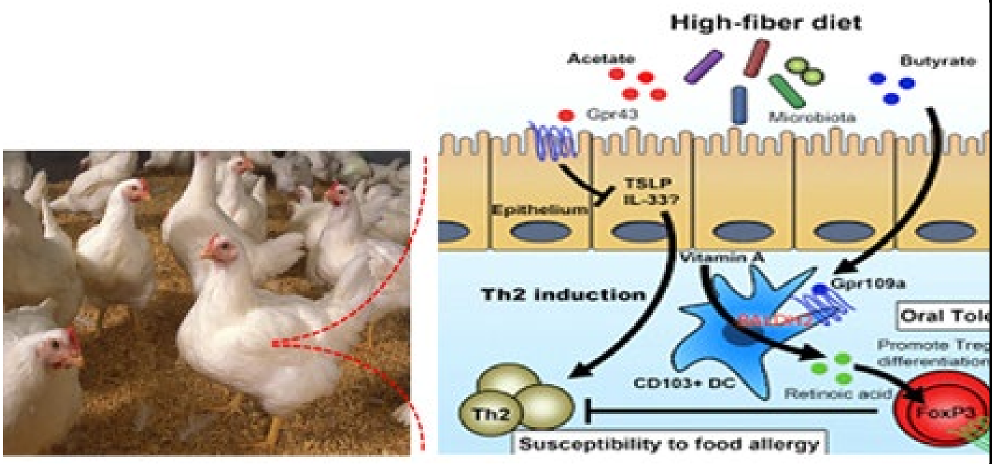
CNAFS 13 Project

Dr Shahram Niknafs

Prof Eugeni Roura

13) Dietary fibre involvement in gut-brain dialogues

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.



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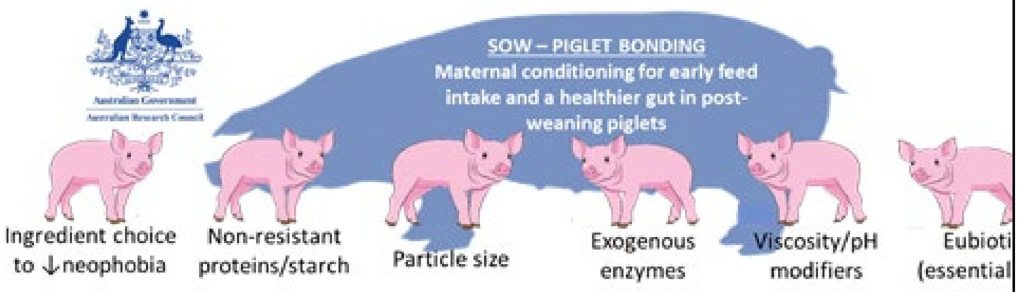
CNAFS 14 Project *Dr Marta Navarro* *Prof Eugeni Roura*	**14) <u>How to make antibiotics in pig feed redundant, naturally</u>** The maternal-progeny relationship has been a major focus of research in humans, pigs, and other species because the trans-generational communication between future mothers and developing embryos/foetus has life-changing potential. For example, the mother's diet has a profound and long-lasting impact on early food preferences in babies. In livestock animals such as the pig, this phenomenon may translate in improving feed intake and gut health early in the post-weaning phase, a critical moment in the life of a pig that often relates to enteric diseases (i.e., diarrhoea). Thus, improving post-weaning feed intake has the potential to improve the overall health and reduce the need for veterinary care (including antibiotics) in pigs. However, the complex intricacies involved in this early biochemical dialogue sow-piglet are not well understood. This project aims to develop nutritional strategies to foster sow-piglet dialogues and help piglets thrive through the critical post-weaning phase. The project has extraordinary cross-disciplinary links including nutrition, welfare, immunology, microbiology and digestive physiology. In addition, this project is part of a larger research consortium funded by the Australian Research Council (ARC) involving external leading research institutions such as The University of Melbourne and some of the main pork industry stakeholders. 
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CNAFS 15 Project *A/Prof Daniel Cozzolino* *Prof Louw Hoffman*	**15) <u>Non-invasive and non-destructive analytical methods for food evaluation</u>** The increasing market and consumer desire for quality foods has created a need for efficient and accurate analytical methods to measure different food properties (e.g. chemical composition) through the value chain. High throughput methods and techniques based in vibrational spectroscopy such as near (NIR) and mid infrared (MIR) spectroscopy own intrinsic benefits such as being non-invasive, rapid, and almost no sample preparation required. These methods have being able to determine simultaneously physical and chemical parameters in different food matrices. Data fusion and multivariate data analysis techniques are also integrated into the analysis to increase the effectiveness of these approaches. The aim of this project is to develop protocols and test analytical methods based in vibrational spectroscopy (e.g. NIR, MIR) combined with multivariate data analysis to analyse and monitor the composition of a wide range of foods of economic importance in order to ensure the integrity of the food value chain.
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CNAFS 16 Project *A/Prof Daniel Cozzolino* *Prof Louw Hoffman*	**16) Sensors and math to assure value and provenance in the food chain** The increasing market and consumer desire for quality foods has created a need for efficient and accurate analytical methods to measure different food properties (e.g. chemical composition) through the value chain. However, issues related with authentication, functionality, provenance, security and traceability, are some of the main challenges facing the modern food industry. Authentication, traceability, denomination of origin, provenance of foods are of primary importance to keep consumers demands and to maintain the sustainable nature of the modern food industry. These issues in food have different aspects, one related with authenticity with respect to production (e.g. geographical origin, organic vs. non-organic, provenance) and authenticity with respect to the description (e.g. adulteration issues, counterfeit, food security). Sensors based in vibrational spectroscopy techniques such as near (NIR) and mid infrared (MIR) spectroscopy with their intrinsic benefits such as being non-invasive, rapid, and almost no sample preparation, have being able to determine simultaneously physical and chemical parameters in different foods matrices as well as to authenticate and trace different foods. Data fusion and multivariate data analysis techniques are also applied to increase the effectiveness of these approaches. The aim of this project is to develop protocols and test analytical methods based in vibrational spectroscopy sensors combined with multivariate data analysis to trace and authenticate the value and provenance of foods of economic importance in order to ensure the integrity of the food value chain.
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CNAFS 17 Project

Prof Louw Hoffman

Prof Eugeni Roura

A/Prof Daniel Cozzolino

17) Is chicken breast becoming spaghetti meat?

In 2019-20, Australia produced 1.2 million tonnes of poultry meat (carcass weight) with a gross value of $2.9 billion per annum. Unfortunately, a new phenomenon (woody breast / white stripping / spaghetti meat) that is affecting the breast meat quality of broilers has become more and more prevalent world-wide. Wooden breast syndrome is a muscle-quality disorder that affects only broiler chickens, rendering their pectoral muscles (i.e., breast meat) tough and chewy. Wooden breast syndrome is a muscle myopathy that has been identified as an emerging quality defect. Macroscopically, woody breast is characterized by palpably hard, pale ridge-like disorder that affects only broiler chickens, rendering their pectoral muscles (i.e., breast meat) tough and chewy. The Australian industry has no knowledge of what the incidence rate of this syndrome is.

The aim of this study is to carry out a preliminary evaluation of the incidence of woody breast and related muscle abnormalities in retail outlets. Specific samples will be collected and analysed for their effect on the quality of the breasts. Laboratory techniques will be used to determine proximate (moisture, proteins, fat, dietary fibre, ash), and physical quality aspects of the raw and cooked breasts. The student will work as part of a larger team in QAAFI/SAFS working in the poultry team which brings together industry, research, and the community to capitalise on Australia's poultry industry.

Figure 1 A chicken breast showing the woody breast syndrome.

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CNAFS 18 Project

Prof Louw Hoffman

Dr Deirdre Mikkelsen

18) Black soldier fly fit for nutrition

Most of Australia's 7 million tons of waste come from post-consumer waste streams with most of it is going to landfill. With the global drive to up-stream this waste, scientists are evaluating different systems to utilize these waste by-products. A system that has shown great promise is utilizing the larvae from the black soldier fly to transform the waste into a utilizable product; black soldier fly larvae and frass. The safety of the use of the larvae as animal feed or human food, when the larvae are grown in biological by-products, is of paramount importance. One method to ensure the safety of the product is post-harvest treatments of the larvae.

The aim of this study is to carry out a preliminary evaluation of black soldier fly larvae and frass when treated under different temperature and drying regimes. Laboratory techniques will be used to determine proximate (moisture, proteins, fat, dietary fibre, ash), minerals and trace elements, and microbial levels on these two products after the different treatments have been applied. The student will work as part of a larger team in QAAFI/SAFS working on the Fight Food Waste Cooperative Research Centre (FFW-CRC) which brings together industry, research and the community to capitalise on Australia's food waste opportunities.

Figure 1 Black soldier fly larvae at point of harvest.

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Centre for Horticultural Science Projects

CHS 1 Project *Dr Lilia Costa Carvalhais* *Prof Andre Drenth* *Dr Alistair McTaggart* *Dr Vivian Rincon-Florez*	**1) <u>Sex in banana fungi</u>** 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.  
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CHS 2 Project

Dr Louisa Parkinson

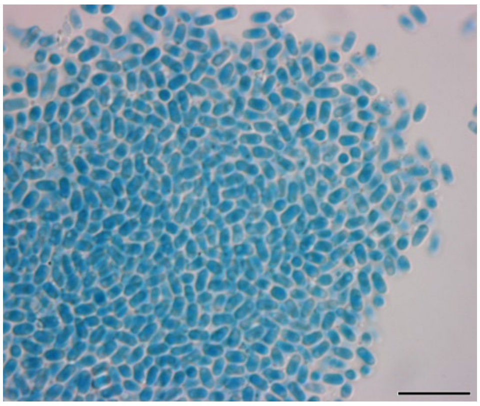
Prof Roger Shivas

A/Prof Andrew Geering

2) Phylogeny and taxonomy of Claviceps associated with ergot of native grasses in Australia

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.

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CHS 3 Project

Dr Louisa Parkinson

A/Prof Andrew Geering

A/Prof Elizabeth Dann

3) 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.

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CHS 4
Project

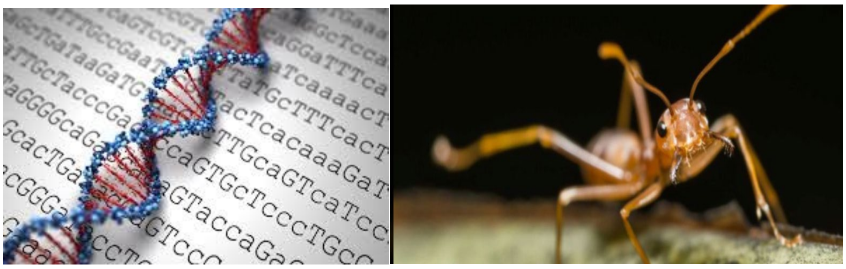
Prof Neena Mitter

Dr Karishma Mody

4) 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.

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CHS 5 Project

Dr Karishma Mody

Prof Neena Mitter

Prof Tim Mahony

5) 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.

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CHS 6 Project *Dr Chris O'Brien* *Dr Alice Hayward* *Prof Neena Mitter*	**6) <u>From Freezer to Field - Cryostasis for Conservation!</u>** Plants possess the incredible ability of cell totipotency, with each cell having potential to generate complete new plants. Taking advantage of this property, The Mitter lab is dedicated to developing cryopreservation (cryostorage at -196C) protocols for recalcitrant plants that do not survive seed-banking – including the high-value species avocado. This technology allows us to safely freeze plant cells and tissues at -196C and then revive them to grow into whole new plants. This provides an insurance bank to conserve incredible genetic diversity of precious species including crops and endangered species that cannot be seed-banked. This is becoming <u>really important</u> in the face of climate change, new weather extremes and disease risks including pandemics like myrtle rust. We have three projects in this space. **Three Projects are available in this space!** 1. Development of a cryopreservation regeneration media for different avocado cultivars. 2. Cryopreservation of Australian native macadamia. 3. Cryopreservation of an endangered Queensland plant – *Gossia gonoclada* 
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CHS 7 Project *Dr Alice Hayward* *Prof Neena Mitter* *Dr Jayeni Hiti-Bandaralage*	**7) <u>Novel Tissue Culture Systems for Plant Production</u>** The Mitter Lab has received global media coverage for developing the ***world's first*** tissue-culture production system for avocado plants - the world's most instagrammed fruit. This is important as a ***sustainable, cost-effective and climate-secure*** way to produce plants. Dedicated students will be part of our expanding research in a new $20M tissue-culture facility at UQ, developing systems for other crop species as well as endangered or high value native species where prior research is lacking or proved too challenging. Students will work with industry and research partners will value-add student experience. **A number of Projects available:** 1. World's-first tissue culture production of macadamia plants for industry. 2. Tissue culture propagation for the native nursery species, *Lomandra.* 3. Tissue culture propagation of high-value crops vanilla and cocoa. 
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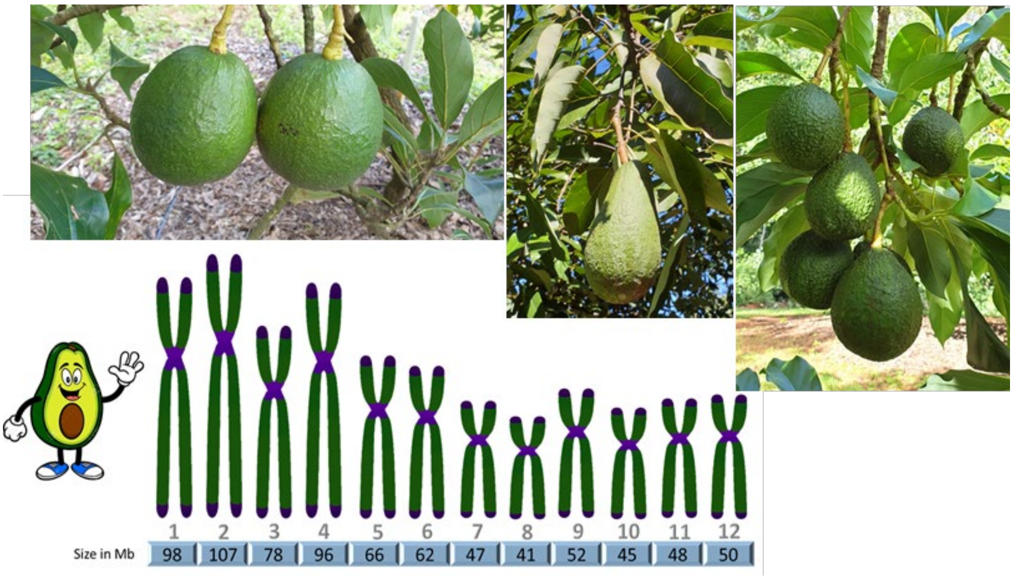
CHS 8 Project *Dr Alice Hayward* *Mr Stephen Fletcher* *Prof Neena Mitter*	**8) Genomics and DNA Markers for Australian Avocado** The Mitter Lab and QAAFI has been part of a large effort sequencing the genomes of major sub-tropical fruit crops including avocado. We have developed a DNA marker set that can distinguish avocado cultivars available in Australia – this is important for industry to be able to rapidly identify and track plants. This project will test these markers across a large number of seedling plants to provide confidence for industry in the system. The student will day-travel around QLD and N-NSW for sample collection, extract DNA, run our marker assay and critically analyse results, with valuable connections to industry and academia. The student will also have a chance to be involved in analysis of the avocado genome sequence and identification of useful candidate genes of interest to the crop. 
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CHS 9 Project

A/Prof Femi Akinsanmi

9) 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.

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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

CHS 10 Project

Dr Inigo Auzmendi

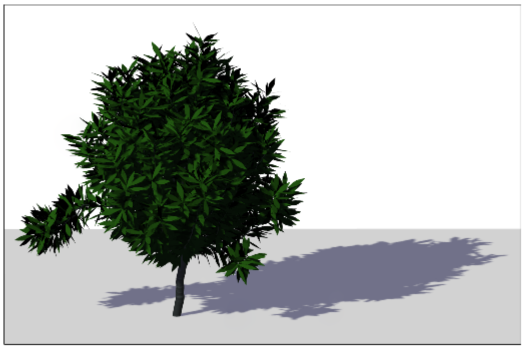
10) Simulating fruit tree growth and development

Functional-structural plant models simulate organ development and growth 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 development and 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 one of four areas: tree architecture, light interception, vegetative vigour and crop load. Our final aim is to improve management practices, e.g. training, pruning, fruit thinning, limb bending, planting density and tree size that will allow better yields in fruit and nut trees.

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



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Useful majors	Biochemistry & Molecular Biology / Biophysics / Computational Science / Plant Science / Horticulture

CHS 11 Project *Dr Craig Hardner* *Dr Elizabeth Ross* *Dr Robyn Cave* *Dr Mulsuew Fikere*	**11) 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.
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Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Bioinformatics, (Agriculture, Horticulture, Plant breeding)

CHS 12 Project *Dr Craig Hardner* *Dr Vivi Arief* *Dr Robyn Cave* *Prof Bruce Topp* *Shane Mulo*	**12) <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**, craig.hardner@uq.edu.au +61 7 334 69465 • Potential Associate Advisor: Dr Vivi Arief • Potential Associate Advisor: Dr Robyn Cave, r.cave@uq.edu.au +61 7 546 01 240 • Potential Associate Advisor: Prof Bruce Topp, b.topp@uq.edu.au +61 7 538 11373 • Potential Associate Advisor: Shane Mulo (QDAF)
Location	St Lucia campus
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Useful majors	Genetics, Plant breeding, Agricultural economics

CHS 13 Project *Dr Craig Hardner*	**13) 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. 
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Location	St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Bioinformatics, Social history

CHS 14 Project *Dr Craig Hardner* *A/Prof Mark Dieters* *Dr Vivi Arief*	**14) 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.
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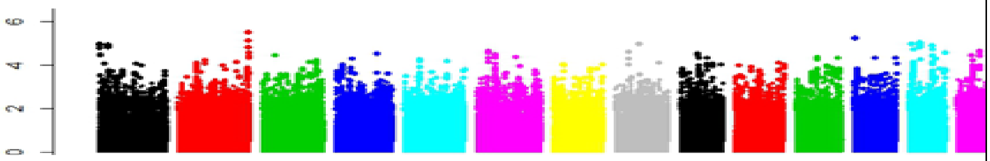
Location	St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Quantitative genetics, statistics, poly-ploid genetics

CHS 15 Project *Dr Mobashwer Alam* *Prof Bruce Topp*	**15) Molecular investigation on the phenotypic variability in flowering time in macadamia** Flowering is a phenological trait, which is important for orchard management and productivity. Planting cultivars with known time of flowering will assist farmers in orchard management decisions regarding fertilization, irrigation, establishment of pollinators and pest control. Over the last few decades, the Australian industry breeding program has developed and phenotypically characterized a large collection of cultivated and wild germplasm and multi-parental seedling populations. A quantitative genetic analysis of the phenotypic data will be useful to select progeny with known flowering time. However, the conventional tree breeding approach is time consuming, and laborious. Genomic approach offers potential to increase breeding efficiency through marker-assisted selection. Discovering molecular markers involved in the variability in flowering will help breeders to develop an efficient selection tool. This project was aimed to explore the variability and inheritance pattern of flowering phenology in macadmaia germplasm and to identify genomic regions associated with the trait variation. Using high-throughput DNA marker, a genome-wide association study will be conducted on a colelction of wild genetic resources. Identified markers can be use in future marker assisted selection of breeding progeny.  
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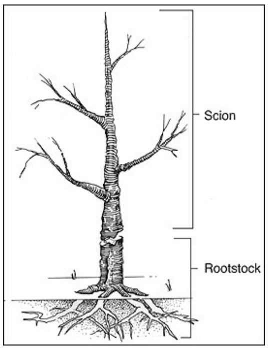
Useful majors	Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 16 Project *Dr Mobashwer Alam* *Prof Bruce Topp*	**16) Investigating macadamia rootstock genetics on the variability in scion architecture and branching.** The management of excessive vigour through pruning and hedging is a major expense in commercial macadamia orchards. Recently, Queensland Department of Agriculture and Fisheries (QDAF) and the University of Queensland (UQ) took initiatives to control scion vigour by using rootstocks through two consecutive Horticulture Innovation (HI) Australia funded projects: “Transforming subtropical/tropical tree crop productivity” (AI 13004) and National Tree Crop Intensification in Horticulture Program (AS18000). A diverse range of germplasm of macadamia rootstocks were planted at Nambour with a single scion cultivar. Investigating the effect of rootstocks on the variability in the architectural traits and branching pattern of the scion will be useful to select rootstocks for vigour management. In this project, the scholar will collaborate with a research higher degree student and measure growth traits and branching pattern of a common scion. A branching index equation will be developed to characterise trees for the variability in branching. Statistical analysis will be conducted to find out the effect of rootstock genotypes on scion vigour.   
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Useful majors	Please select from: Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 17 Project

Dr Mobashwer Alam

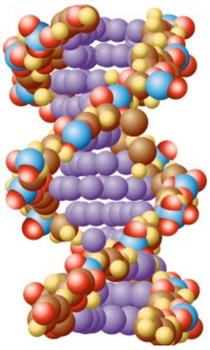
Prof Bruce Topp

17) Molecular investigation to determine species composition and extent of genetic base of Australian elite selections of Macadamia

Macadamia is an Australian native crop and is highly valued for its kernel. Using the available cultivars as parents, Australian national macadamia breeding program generated >15,000 breeding progeny and selected 53 elites through first and generation of progeny evaluation. Most of the parents of these selections belong to Macadamia integrifolia or M. tetraphylla or their hybrids. Although pedigree information of the 53 selections is available, species identity is still unexplored.

This project is aimed to investigate the genetic patterns in 53 elite selections and will identify species composition using high-throughput markers. Genetic information from wild species will be used in species composition analysis. Genetic diversity of the selected accessions will be compared with the diversity within cultivated and wild gene pools.



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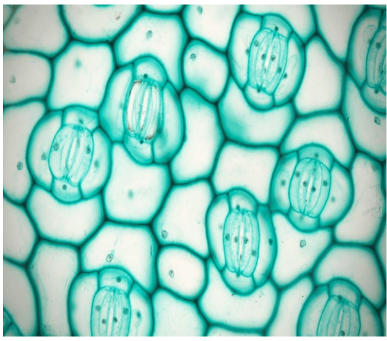
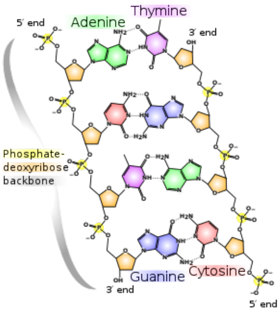
Useful majors	Please select from: Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 18 Project *Dr Mobashwer Alam* *Prof Bruce Topp*	**18) <u>Investigating genetic architecture of stomatal traits to exploit in climate change adaptation</u>** 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. A genome-wide association study on wild and cultivated gene-pool will be conducted to identify markers associated with the traits. The inheritance pattern of the traits can be useful for future breeding decisions and planning. 
Advisor(s) contact	**Dr Mobashwer Alam**, m.alam@uq.edu.au 0753 811 371 Associate Advisor: Prof Bruce Topp, b.topp@uq.edu.au +61 7 538 11373
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Useful majors	Please select from: Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 19 Project *Prof Bruce Topp* *Prof Jose Chaparro* *Dr Mobashwer Alam*	**19) Investigating genetic diversity in feral peach** Feralisation is a complex process that involves domestic populations reverting to wild phenotypes. In the absence of human interruption, feral plants may show adaptation to new environments and display characteristics of their wild ancestors. We have collected 30 accessions of feral peach from Queensland and New South Wales which have been propagated and planted at Stanthorpe. This project will investigate the genetic and morphological variation in these feral accessions and compare them to commercial cultivars. Flowering, fruiting and vegetative growth traits will be measured. SSR markers will be used to study genetic diversity. Depending on the availability of funding, the student may have an opportunity to visit the laboratory of Prof Jose Chaparro of the University of Florida, USA.   
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Useful majors	Please select from: Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 20 Project

Prof Bruce Topp

Prof Jose Chaparro

Dr Mobashwer Alam

20) Investigating rootstock effect on scion vigour, flowering, and fruiting in low chill peach

Rootstocks play a vital role on the performance of horticultural crops. As a part of a dual plant system, rootstocks translocate water and nutrients to the above ground scion and thereby, regulate resource supply for growth and development of vegetative and reproductive parts. In several tree crops, rootstocks have been widely used to manage the size and vigour of the scion. Although extensive studies have been conducted previously in peach, but the investigation on low-chill rootstock effect on low chill peach cultivars is limited. In this project, the scholar will collect data on growth, flowering and fruit quality traits of 3 low-chill scion cultivars grafted onto 7 different low chill rootstocks. Statistical analysis will be conducted to identify best vigour managing rootstocks.

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Useful majors	Please select from: Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 21 Project

A/Prof Andrew Geering

A/Prof John Thomas

Dr Kathy Crew

21) 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.

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Useful majors	Biochemistry & Molecular Biology / Microbiology

CHS 22 Project *A/Prof Andrew Geering* *A/Prof John Thomas* *Dr Kathy Crew*	**22) Population genetics of Alternanthera mosaic virus and development of an infectious clone** Alternanthera mosaic virus (AltMV) was discovered in Australia but is thought to have been introduced into Australia in the early 20th Century in fodder shipments from the USA. In this project, research will be done to investigate sequence variation of this virus in Australia and to compare with isolates of the virus from the USA and Europe. AltMV shows great potential to be used as a gene expression vector and as a first step towards this goal, an infectious clone of the virus will be prepared. Full length genome constructs will need to be prepared and linked to a transcription promoter to allow infection of plants by mechanical transmission of the plasmid constructs. 
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Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology

CHS 23 Project

A/Prof Andrew Geering

A/Prof John Thomas

Dr Nga Tran

23) Epidemiology of a new nepovirus associated with buffalo grass yellows

Buffalo grass (*Stenotaphrum secundatam*) is the most valuable turfgrass species in Australia, and is also an important pasture species. Over the last few years, turf farmers along the eastern seaboard of Australia have been affected by an enigmatic disease called buffalo grass yellowing. High throughput sequencing was done to identify viruses infecting the diseased plants, and a new nepovirus was discovered and shown to be widely distributed in Australia. Virtually nothing is known about the biology of this virus, including its host range, impact on growth of buffalo grass, and mode of transmission. In this project, a broad diversity of experimental work (laboratory, glasshouse and field) will be done to provide a better understanding of the epidemiology of this virus. It is also hypothesised that the nepovirus synergistically interacts with other buffalo grass viruses to cause a worse disease than either virus would alone, and experiments will be done to test this hypothesis.

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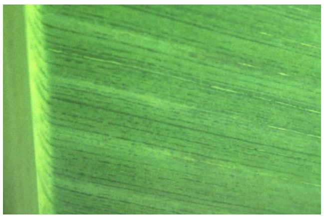
Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology

CHS 24 Project *A/Prof John Thomas* *A/Prof Andrew Geering* *Dr Kathy Crew* *Dr Megan Vance* *Mr Ric Webb*	**24) Cytopathology and sites of replication of banana bunchy top virus**   Banana bunchy top virus causes a devastating disease of bananas, and threatens food security in sub-Saharan Africa. One of the characteristic symptoms of infection is dark green dot-dash flecking of leaves and stem sheaths, and the dot-dashes are associated with the proliferation in the phloem of small cells with abundant chromatophores. In this project, thin sections of diseased leaf tissue will be immunolabelled with fluorophore and examined under a confocal microscope to investigate the distribution of the virus relative to the abnormal cells. If time allows, more sophisticated techniques such as thin section electron microscopy, laser capture microdissection and high throughput sequencing will be done to investigate changes in the cytology and transcriptome of these cells.
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Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology

CHS 25 Project *Dr Louisa Parkinson* *A/Prof Andrew Geering*	**25) <u>Developing molecular diagnostic tests for rapid detection of Phytophthora and Phytopythium spp. causing root rot of avocado</u>** 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 +61 7 344 32457 • Associate Advisor: A/Prof Andrew Geering, a.geering@uq.edu.au +61 7 344 32459
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Useful majors	Please select from: Biochemistry & Molecular Biology / Bioinformatics / Microbiology / Plant Pathology

CHS 26 Project *A/Prof Elizabeth Dann* *Dr Akila Prabhakaran*	**26) 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 +61 7 344 32455 • Associate Advisor: Dr Akila Prabhakaran, a.prabhakaran@uq.edu.au
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Useful majors	Please select from: Agriculture/Horticulture/ Microbiology/ Plant Pathology/ Agronomy/Molecular Biology

CHS 27 Project

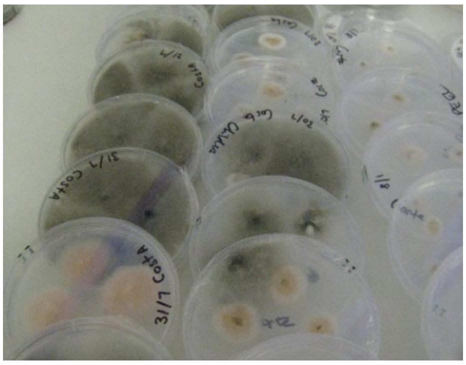
A/Prof Elizabeth Dann

Kaylene Bransgrove

27) Monitoring efficacy of postharvest disease management strategies in avocado

Species of *Colletotrichum* fungi are responsible for anthracnose disease of many horticultural crops, including avocado and mango. Fungi infect throughout the fruit development period, however symptoms are not commonly observed until fruit have been harvested and ripen in distribution facilities or consumers' fruit bowls. The fruit rot can be so severe that consignments in the market could be rejected, and/or consumers are disappointed in their purchase.

Successful management practices include conventional and "bio" fungicide sprays in orchards. It is pertinent to check from time to time that the commonly used industry fungicides are effective, and that populations of *Colletotrichum* have not evolved resistance to those fungicide groups. This project will investigate sensitivity to key fungicides amongst a large number of *Colletotrichum* isolates collected from avocado orchards across Australia, including unsprayed organic orchards. The research will involve culturing fungi and screening for sensitivity, molecular analyses for mutations responsible for fungicide resistance, and testing a range of isolates for their relative pathogenicity (ability to cause disease) in avocado fruit. The outcomes of this project are extremely important for the avocado industry and will have immediate relevance.



Advisor(s) contact	• **A/Prof Elizabeth Dann**, e.dann@uq.edu.au, +61 7 344 32455 • Associate Advisor: Kaylene Bransgrove, k.bransgrove@uq.edu.au
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Webpage	https://qaafi.uq.edu.au/profile/477/elizabeth-dann
Useful majors	Agriculture/Horticulture/Plant Pathology/ Biochemistry & Molecular Biology

CHS 28-29 Project *A/Prof Craig Hardner*	**28) New technologies for efficient genomic prediction in horticultural tree crops** Prediction of phenotype based on DNA marker information has become a fundamental approach to support breeding in the 21st century. Horticultural tree crops produce premium fruit and nuts with high nutritional value and may benefit the most from this technology due to long juvenile phase and high assessment costs. This project will examine new genotyping technologies and associated bioinformatics to evaluate new approaches to revolutionise the adoption of genomic-based selection methods in horticultural tree crops. Haplotagging is a new low-cost method for genotyping and phase genomes to improve prediction accuracy that has recently been evaluated at UQ for use in tree crops. This project will build on a 2021 proof-of-concept project to study segregation in a biparental mango family to support implementation of haplotagging in breeding programs. **29)** Nanopore is a new low cost while-genome sequencing technology used across humans, animals and some plants. A 2nd possible project will evaluate and extend to mango methods developed in animals for low depth sequencing using Nanopore. A $5,000 scholarship will be offered for a high-quality student to undertake either of these projects.
Advisor(s) contact	• **A/Prof Craig Hardner,** craig.hardner@uq.edu.au +61 7 334 69465
Location	St Lucia campus
Webpage	https://qaafi.uq.edu.au/profile/48/craig-hardner
Useful majors	Plant biology, genetics, molecular genetics, bioinformatics

Centre for Crop Science Projects

CCS 1 Project *Prof Daniel Rodriguez* *Dr Dongxue Zhao* *Dr Peter deVoil*	**1) Title: Proximal sensing of soil water for root phenotyping** Crop phenotyping is a rapidly advancing field of research due to the widespread availability of sensors and analysis tools. However, most applications focus on the above-ground parts of crops, ignoring a “hidden half”: the rooting system and its activity. We recently developed a new approach to produce 3D characterizations of crop water use and root activity in large field genotype (G) by environment (E) by management (M) sorghum experimentation, using an electromagnetic induction (EMI) instrument. We have also produced a root activity factor (R) derived as a function of water use, water availability and crop demand, that represents the presence and activity of roots in different soil layers in the soil profile. We would be happy to have students to join the team that is now applying the technology in chickpeas as. The work could involve running surveys, collecting plant material, and desktop data analysis and modelling.  DualEM 21S being used to survey root activity in a sorghum crop, at UQ’s Gatton Campus.
Advisor(s) contact	**Prof Daniel Rodriguez**, d.rodriguez@uq.edu.au +61 7 535 15091 **Dr Dongxue Zhao**, dongxue.zhao@uq.edu.au **Dr Peter deVoil**, p.devoil@uq.edu.au +61 7 535 15087
Location	Gatton or St Lucia Campus
Webpage	https://www.qld-fsr.info/
Useful majors	Please select from: Bioinformatics / Biophysics / Computational Science / Agronomy

CCS 2 Project *A/Prof Lee Hickey* *Dr Millicent Smith* *Prof Graeme Hammer*	**2) <u>Need for speed: growing plants fast to feed the world</u>**  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 Advisor: Dr Millicent Smith, millicent.smith@uq.edu.au • Associate Advisor: Prof Graeme Hammer, g.hammer@uq.edu.au +61 7 334 69463
Location	St Lucia or Gatton campus
Webpage	https://qaafi.uq.edu.au/profile/108/lee-hickey
Useful majors	Biochemistry & Molecular Biology / Genetics / Plant Science

CCS 3 Project *A/Prof Bhagirath Chauhan* *A/Prof Andries Potgieter*	**3) <u>Mapping and estimating weeds using drones</u>** Drones have emerged as an innovative technology to provide spatio-temporal information about weed species in crop fields. Such information is critical for any site-specific weed management program. This project will map and estimate weeds in chickpeas and/or mungbean. 
Advisor(s) contact	• **A/Prof Bhagirath Chauhan**, b.chauhan@uq.edu.au 0427 923 272 • Associate Advisor: A/Prof Andries Potgieter, a.potgieter@uq.edu.au +61 7 535 15085
Location	Gatton campus
Webpage	https://researchers.uq.edu.au/researcher/10189 https://researchers.uq.edu.au/researcher/2466
Useful majors	Computational Science / Engineering

CCS 4 & 5 Project *A/Prof Bhagirath Chauhan*	**4) Genetic diversity in turnip weed (Rapistrum rugosum)** Turnip weed is becoming a problematic weed in the eastern cropping region of Australia. Genetic diversity is important for understanding the ability of weeds to adapt to different environments and the impact of herbicide selection on weed populations. The objective of the project is to characterize genetic variation in turnip weed biotypes collected from different regions of Queensland and New South Wales. **5) Weed management in an aerobic rice system** Rice has the potential to be grown as a summer crop in aerobic conditions in north Australia. However, weeds are the main biotic constraints in aerobic rice systems because of the lack of standing water and availability of effective herbicides. This project will evaluate different management options for weed control in rice grown in aerobic conditions.
Advisor(s) contact	• **A/Prof Bhagirath Chauhan**, b.chauhan@uq.edu.au 0427 923 272
Location	Gatton Campus
Webpage	https://researchers.uq.edu.au/researcher/10189
Useful majors	Molecular biology (genetic diversity) Agriculture (weed management in rice)

CCS 6 Project

Prof Daniel Rodriguez

Dr Fer Dreccer

Dr Jeremy Whish

Dr Joe Eyre

6) Matching adapted chickpea genotypes with soil and climate to maximise yield and profit: Field experimentation

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**, d.rodriguez@uq.edu.au +61 7 535 15091 • **Dr Fer Dreccer** (CSIRO), • **Dr Jeremy Whish** (CSIRO), • **Dr Joe Eyre**, j.eyre@uq.edu.au +61 7 535 15083
Location	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

Dr Peter deVoil

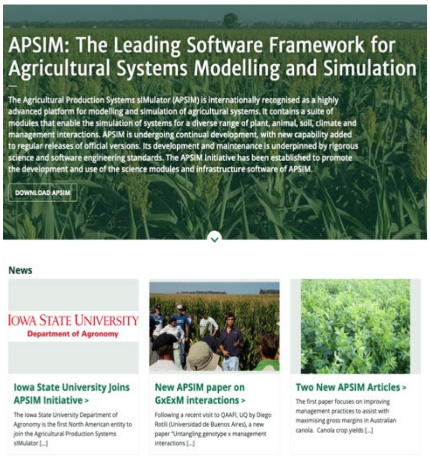
Dr Jeremy Whish

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**, d.rodriguez@uq.edu.au +61 7 535 15091 **Dr Peter deVoil**, p.devoil@uq.edu.au +61 7 535 15087 **Dr Jeremy Whish** (CSIRO)
Location	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

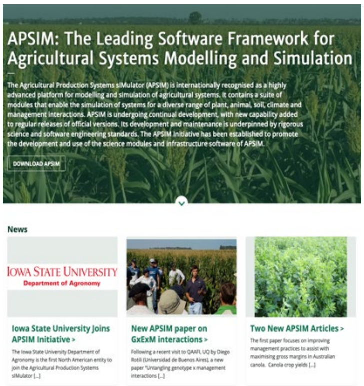
Prof Daniel Rodriguez

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.



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.

DOWNLOAD APSIM

News

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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**, d.rodriguez@uq.edu.au +61 7 535 15091
Location	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

Dr Bradley Campbell

Dr Millicent Smith

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	• **Prof Ian Godwin**, i.godwin@uq.edu.au, +61 409 582 481 • Associate Advisor: Dr Bradley Campbell, b.campbell2@uq.edu.au +61 7 336 52504 • Associate Advisor: Dr Millicent Smith, millicent.smith@uq.edu.au
Location	Lab 319, John Hines Building (62), 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

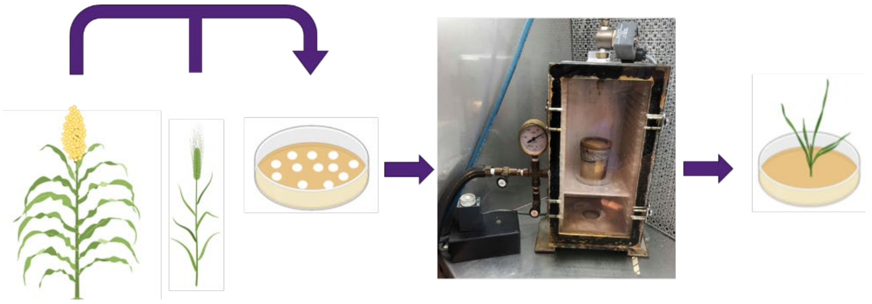
Dr Karen Massel

Prof Ian Godwin

A/Prof Lee Hickey

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**, a.borrell@uq.edu.au, +61 7 454 26740, 0445 426 740 **Dr Karen Massel**, k.massel@uq.edu.au x52504 Associate Advisor: Prof Ian Godwin, i.godwin@uq.edu.au +61 409 582 481 Associate Advisor: A/Prof Lee Hickey, l.hickey@uq.edu.au +61 408 210 286
Location	Room 319, John Hines Building (62), St Lucia
Webpage	https://qaafi.uq.edu.au/profile/234/andrew-borrell https://qaafi.uq.edu.au/profile/384/ian-godwin https://qaafi.uq.edu.au/profile/108/lee-hickey https://qaafi.uq.edu.au/profile/6037/karen-massel
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Genetics

CCS 11 Project *Dr Jack Christopher* *Dr Karine Chenu*	**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**, j.christopher@uq.edu.au +61 7 452 91413 • Associate Advisor: Dr Karine Chenu, karine.chenu@uq.edu.au +61 7 452 94252 +61 7 535 15084
Location	Leslie Research Facility, Toowoomba
Webpage	https://qaafi.uq.edu.au/
Useful majors	Biochemistry & Molecular Biology / Agriculture

CCS 12 Project *Dr Jack Christopher* *Dr Yash Dang*	**12) <u>Increased food production on constrained soils</u>** 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**, j.christopher@uq.edu.au +61 7 452 91413 • Associate Advisor: Dr Yash Dang, SAFS, y.dang@uq.edu.au
Location	Leslie Research Facility, Toowoomba
Webpage	https://qaafi.uq.edu.au/
Useful majors	Biochemistry & Molecular Biology / Agriculture

CCS 13 Project

Prof Andrew Borrell

Dr Karen Massel

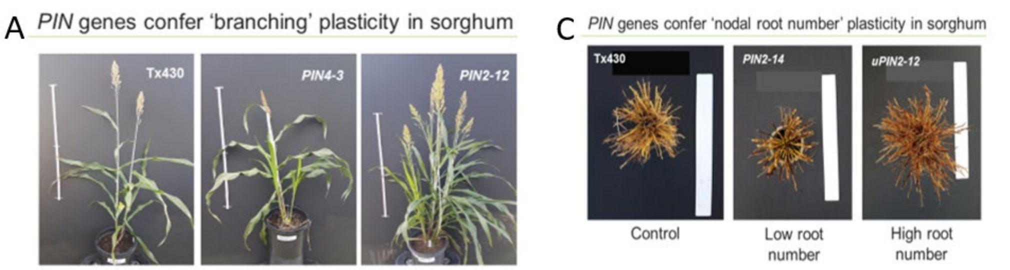
A/Prof Lee Hickey

Prof Ian Godwin

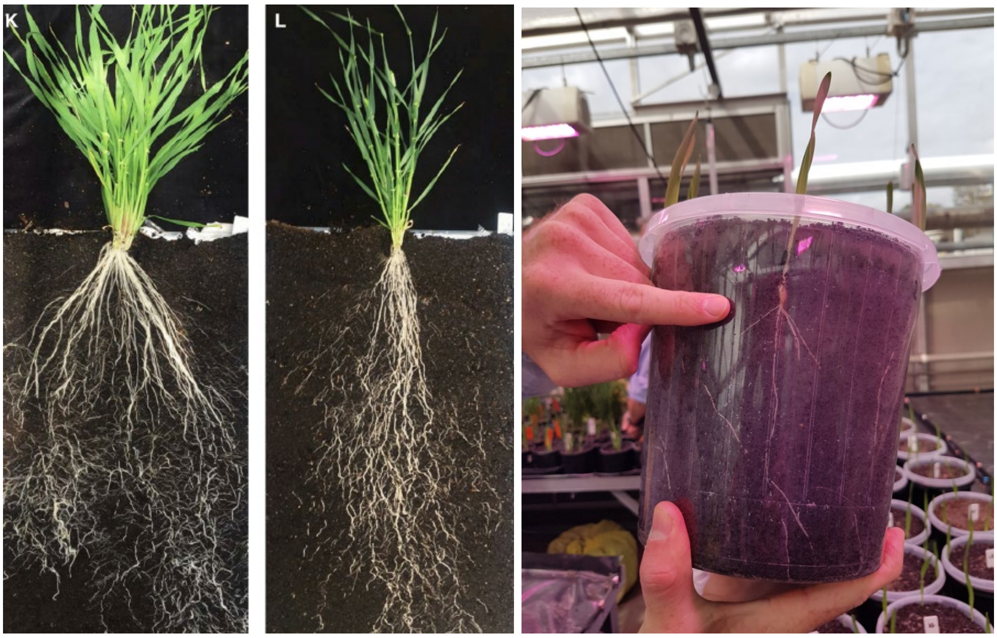
13) Enhancing drought adaptation in sorghum through gene editing

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 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.



Advisors contact	- **Prof Andrew Borrell**, a.borrell@uq.edu.au +61 7 454 26740, 0445 426 740 - Associate Advisor: Dr Karen Massel, k.massel@uq.edu.au x52504 - Associate Advisor: A/Prof Lee Hickey, l.hickey@uq.edu.au +61 408 210 286 - Associate Advisor: Prof Ian Godwin, i.godwin@uq.edu.au, +61 409 582 481
Location	John Hines Building (62), St Lucia
Webpage	https://researchers.uq.edu.au/researcher/1239

CCS 14 Project *Prof Andrew Borrell* *Dr Karen Massel* *A/Prof Lee Hickey* *Prof Ian Godwin*	**14) <u>Enhancing drought adaptation in barley 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 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	- **Prof Andrew Borrell**, a.borrell@uq.edu.au +61 7 454 26740, 0445 426 740 - Associate Advisor: Dr Karen Massel, k.massel@uq.edu.au x52504 - Associate Advisor: A/Prof Lee Hickey, l.hickey@uq.edu.au +61 408 210 286 - Associate Advisor: Prof Ian Godwin, i.godwin@uq.edu.au, +61 409 582 481
Location	John Hines Building (62), St Lucia
Webpage	https://researchers.uq.edu.au/researcher/1239

CCS 15 Project

Dr Alex Wu

Dr Erik van Oosterom

15) Discovering how plants adapt to water limited environments

C_4 plants have evolved to be more water use efficient, meaning they can produce more biomass per unit of water transpired. This gives C_4 plants strong advantages in dry environments. Understanding processes that underpin water use efficiency will help identify targets for improving crop production.

Evidence suggest there are variations in the amount of biomass produced per water used at the whole-plant level, that is the transpiration efficiency, and variations in photosynthetic CO_2 assimilation rate by stomatal conductance at the leaf level that is the intrinsic water use efficiency. However, the link between what determines better whole-plant transpiration efficiency and what happens at the leaf-level remains unclear.

This project aims to understand the link across these biological scales by combining leaf gas-exchange with structural and anatomical leaf obersavtions as inputs into a mathematical model that predicts how leaf-level processes integrate through to the whole-canopy level. Students will be trained in both theoretical and experimental plant physiology and generate new knowledge that would benefit crop improvement.

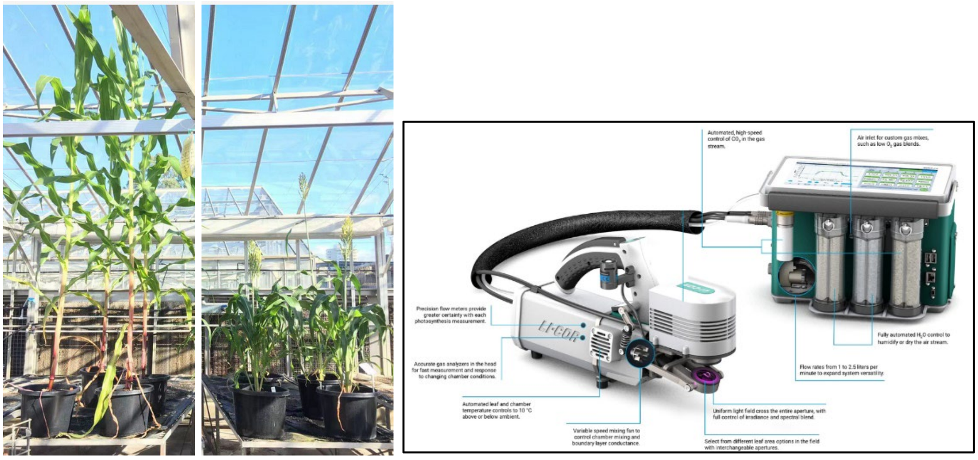
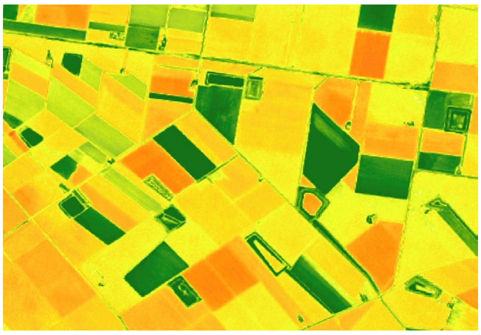
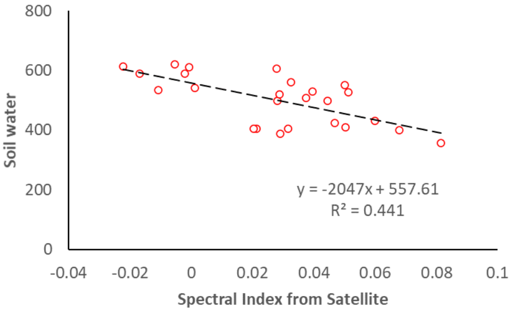
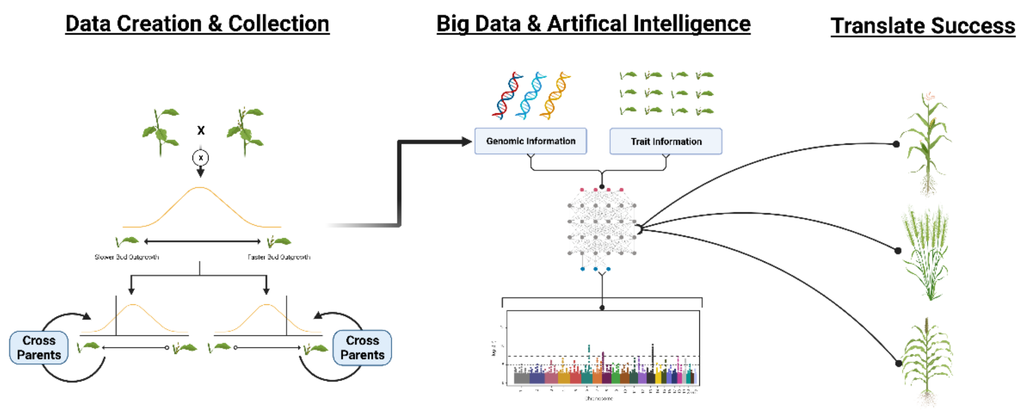


Figure 1: Left (maize), middle (sorghum), right (LI-6800 portable photosynthesis system)

Advisor(s) contact	- **Dr Alex Wu**, c.wu1@uq.edu.au +61 7 334 62780 - Associate Advisor: Dr Erik van Oosterom, erik.van.oosterom@uq.edu.au +61 7 334 69464
Location	St Lucia or Gatton campus
Webpage	https://qaafi.uq.edu.au/profile/405/alex-wu
Useful majors	Plant/crop physiology and/or math

CCS 16 Project *A/Prof Andries Potgieter* *Dr Yan Zhao*	**16) <u>Determining soil moisture from high-resolution satellite imagery (Sentinel-2)</u>** Growers are facing significant and increasing drought risks. Soil moisture is a key variable indicating the presence of droughts and regulating crop growth. This project aims to evaluate the performance of globally and freely available satellite data in revealing pixel scale soil moisture variations across fields. Sufficient moisture data measured in-situ have been accumulated for fields across Australia cropping region. Their relationships with parameters derived from both multispectral (Sentinel 2) and microwave (Sentinel 1) satellite sensors will be explored in this project. By implementing well-designed statistical algorithms, it is expected this project would generate operational predictive models to retrieve soil moisture at high spatial resolution and with high accuracy. Outputs form this project will benefit growers with informed crop management strategies.  Moisture related spectral index derived from satellite data  Possible relationships between soil moisture and remotely sensed indices
Advisor(s) contact	- **A/Prof Andries Potgieter**, a.potgieter@uq.edu.au +61 7 535 15085 - Associate Advisor: Dr Yan Zhao, yan.zhao@uq.edu.au +61 7 336 56529
Location	St Lucia & Gatton (at least 1 day per week using UQ bus service)
Webpage	https://qaafi.uq.edu.au/profile/465/andries-potgieter
Useful majors	Please select from: Statistics /Mathematics / Biophysics / Computational Science

CCS 17 Project *Dr Owen Powell* *Dr Francois Barbier* *Prof Mark Cooper* *Prof Christine Beveridge*	**17) Predicting Plant Success - Big Data for Small Plants**  This project offers to opportunity for a student to gain experience and skills in gene discovery, data science, predictive methods (machine learning/artificial intelligence) as part of a research pipeline to deliver real-world impact. The work is related to agriculture, but the skills learned are transferable to plant, animal and human research. As part of a collaboration between staff in QAAFI's Predictive Agriculture Theme, the School of Biological Sciences and the ARC Centre of Excellence for Plant Success in Nature and Agriculture, data will be collected on shoot branching behaviour in thousands of Arabidopsis plants. This project will aid in this data collection and perform computational analyses to detect associations between regions of the genome and plant architecture. Skills and experience will be gained in data collection, quality control, curation, and analysis. The specific tasks could include measurements taken in growth chambers and glasshouses, software analyses of associations between genetic fingerprints (DNA markers) and plant measurements. The time split between data collection and computer work can be adjusted to suit the student. Potential for inclusion of student in research publications.
Advisor(s) contact	• **Dr Owen Powell**, o.powell2@uq.edu.au • Associate Advisor: Dr Francois Barbier, SBS, f.barbier@uq.edu.au • Associate Advisor: Prof Mark Cooper, mark.cooper@uq.edu.au +61 7 334 62778 • Associate Advisor: Prof Christine Beveridge, SBS, c.beveridge@uq.edu.au +61 7 336 57525
Location	St Lucia campus
Webpage	https://qaafi.uq.edu.au/profile/7515/owen-powell
Useful majors	Please select from: Molecular Biology / Genetics/ Computational Science

CCS 18-23 Project

A/Prof Emma Mace

Prof David Jordan

Ms Geetika Geetika

18) Mapping the genes controlling grain density in sorghum

The density of sorghum grain is an important factor in determining its potential grain yield and quality. While previous research has focussed on nutritional quality and use of sorghum, there is a lack of understanding of genes controlling sorghum grain density amongst the genotypes. This information is essential for ensuring yield gains and ease of post-harvest processing. Hence, this project will use existing phenotypic data to map the genes controlling grain density in sorghum, with potential applications to increasing yields.

19) Genetic diversity of genes involved in pollen fertility restoration in sorghum

Cytoplasmic male sterility genes and the associated nuclear restorer genes are critical for the production of commercial hybrid cultivars. Cytoplasmic male sterility has evolved many times in different plant species because of a genetic arms race between the cytoplasmically inherited mitochondrial genome and the restorer genes in the nuclear genome. This project will involve analysis of sequence data of restorer genes, which controls mitochondrial dysfunctions, from a range of ecologically diverse populations of sorghum.

20) Genetic diversity of genes involved in lignin biosynthesis in sorghum

Lignin plays a critical role in plant growth by providing a key structural basis element and many of the key genes involved in the trait are known. In sorghum there is considerable variation in the trait associated with adaptation to various types of stresses. This project will make use of a large set of sequenced data from 1000 sorghum lines from all around the world to investigate genetic variation in key genes in the lignin biosynthesis pathway with a view to help plant breeders develop sorghum genotypes with optimal lignin content.

21) Correlation of lignin content in midrib versus stem in sorghum

Lignin is one of the major components of lignocellulosic biomass, making up the plant cell wall and hence, determines the stem strength. Hence, lignin is an important contributor to preventing sorghum plants from falling over (lodging) prior to harvest. At present it is difficult to rapidly measure lignin content of sorghum stems because of the extensive mechanical processing and time-consuming laboratory procedures. Using a large set of fully sequenced sorghum lines from all around the world, this project will determine the lignin content of the leaf midrib and attempt to develop a prediction for determining lignin content of the stems, based on mid-rib estimates.

22) Investigating genetic variation in lignin content in sorghum

Lignocellulosic substance's such as lignin, cellulose and hemi-cellulose are components that make up the plant cell wall. Stem strength is comprised of varying amounts of these components. Lignin, is one of the major component of lignocellulosic biomass, and hence, determines the stem strength. Stem strength and likelihood of lodging are negatively associated and genotypes with weaker stem

	more likely to lodge. Increasing resistance to lodging is complicated due to the trade-off between lodging resistance and grain yield and is determined genetically. Hence, investigating the genetic effects on lignin content in sorghum would enable us to identify genotypes that may be useful in creating lodging resistant lines in future. This project will utilise several genotypes from the diversity to panel to examine the variations in stem lignin content in sorghum. **23) Investigating genetic control of Johnsons grass mosaic virus in sorghum** Johnsons grass mosaic virus is a significant disease of sugarcane, sorghum and maize. In this project the student would screen a range of genotypes for resistance to this disease and contribute to mapping and cloning the genes underlying this trait.
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Location	St Lucia or Gatton campus – data collection may occur at Gatton and Warwick. Project 23 could be located at the Bogo road Ecosciences Precinct Brisbane
Webpage	https://qaafi.uq.edu.au/profile/333/emma-mace https://qaafi.uq.edu.au/profile/222/david-jordan https://qaafi.uq.edu.au/profile/2088/geetika-geetika
Useful majors	Agricultural science/ Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Genetics