



Queensland Alliance for Agriculture and Food Innovation

Honours Projects 2024

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QAAFI Honours Projects 2024





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

Contents

Centre for Animal Science Projects	3
Centre for Nutrition and Food Sciences Projects	31
Centre for Horticultural Science Projects	51
Centre for Crop Science Projects	77

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





Centre for Animal Science Projects

CAS 1 Project	1) <u>Bovine campylobacteriosis metagenomics, biomarkers and diagnostics</u>
Prof Ala Tabor A/Prof Pat Blackall Dr Conny Turni	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 <i>Campylobacter fetus</i> subspecies <i>venerealis</i> from other organisms. Genomic sequencing has identified new diagnostic targets to separate this subspecies from the closely related species <i>C. fetus</i> subspecies <i>fetus</i> . We have also been examining the reproductive metagenome and using Nanopore long read technologies in an adaptive and/enrichment format. 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.
Prof Ben Hayes	Calf loss Sequence alignments
Advisors	 Prof Ala Tabor, a.tabor@ug.edu.au +61 334 62176
contact	 Associate Advisor: A/Prof Pat Blackall, <u>p.blackall@uq.edu.au</u> +61 7 344 32466 Associate Advisor: Dr Conny Turni, <u>c.turni1@uq.edu.au</u> +61 7 344 32463 Associate Advisor: Prof Ben Hayes, <u>b.hayes@uq.edu.au</u> +61 7 334 62173
Location	QBP, Building 80, St Lucia campus
Webpage	https://qaafi.uq.edu.au/profile/492/ala-tabor
Useful majors	Microbiology / biotechnology / molecular biology / bioinformatics





CAS 2	2) Biomarkers and bovine genetics to identify cattle tick
Project	resistance markers
Prof Ala Tabor	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 have identified biomarkers for tick resistance. Opportunities for molecular biology, RNA seq, proteomics, bovine genetics, biomarker detection, and bioinformatics analyses for research are available in our laboratory – the angle of the project can be negotiated to suit the candidate.
	Image: Second
Advisors contact	 Prof Ala Tabor, <u>a.tabor@uq.edu.au</u> +61 334 62176 Associate Advisor: Dr Ali Raza, <u>a.raza@uq.edu.au</u> +61 7 334 62317
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Useful majors	Microbiology / biotechnology / molecular biology / bioinformatics

QAAFI Centre for Animal Science





CAS 3 Project	3) <u>Title – Optimising Oxford Nanopore sequencing for arthropod</u> genome sequencing with large repetitive content
Prof Ala Tabor	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.
Advisor(s) contact	 Professor Ala Tabor, <u>a.tabor@uq.edu.au</u> 07 334 62176 Associate Advisors: Dr Hannah Siddle, h.siddle@uq.edu.au
Location	QBP, Building 80, St Lucia campus
Webpage	https://qaafi.uq.edu.au/profile/492/ala-tabor
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biotechnology





CAS 4 Project	4) <u>Evaluating forage quality changes using environmental and</u> <u>satellite data in northern Australia</u>
Dr Luis Prada e Silva Dr Kieren McCosker	Are you interested in ruminant nutrition, environmental science, and precision agriculture? This honours project offers a unique opportunity to explore the interaction between environmental factors and forage quality in Northern Australia. Project Overview : This project aims to evaluate changes in forage quality by analysing satellite data (pasture total standing dry matter and fractional cover) alongside environmental data from weather stations and forage quality assessments using collected samples. The goal is to better understand how environmental factors influence forage quality across different seasons and locations. What You Will Learn: - Analysis of forage quality using data from faecal NIRS and direct forage samples Use of satellite data to assess pasture conditions Exploration of the relationship between environmental conditions (rainfall, temperature) and forage quality Data handling, statistical analysis, and interpretation. Project Requirements: Interest in animal science, agriculture, or environmental science. Basic understanding of data analysis (training will be provided). Enthusiasm for fieldwork and remote data collection. This project is a great fit for students looking to gain experience in applied research with a direct impact on sustainable cattle production.
	The set of
Advisors contact	 Dr Luis Prada e Silva, <u>l.pradaesilva@uq.edu.au</u>+61 421 833 376 Dr Kieren McCosker, <u>k.mccosker@uq.edu.au</u>+61 447 828 315
Location	UQ Gatton Campus
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Useful majors	Animal Science/Animal and Veterinary Bioscience/Animal Agricultural Biotechnology/Agronomy





5) 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.
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6) <u>Combining omics: Examining genome structure and function</u>
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.











CAS 5 to 16	8) Form and Function: Novel isoform discovery
Project Prof Ben Hayes Dr Elizabeth Ross	New technology now allows the sequencing to hundreds of thousands of full length transcripts (expressed genes) from a single sample. A dataset of 10 tissues has been generated using isoseq - a method that can sequence the full length expressed isoforms in a sample. This project will analyse that isoseq data and identify novel isoforms including those for genes at are known to of industry importance. This information will provide a deeper understanding of the genetic variation in the Australian northern beef industry and be used to inform large genome wide association studies and discovery of mutations controlling gene expression studies. The project focuses on bioinformatics and analysis skills in a fast developing area of research.
Dr Loan Nguyen	E1 E2 E3 E4 E5
CAS 5 to 16 Project	9) Predicting age using methylated sites
	utilized as an accurate biomarker for aging. In cattle, biological age prediction based
Prof Ben Haves	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
Dr Elizabeth	been under during its lifetime. However, relatively little is known about DNA methylation patterns in cattle. Students will use cutting edge data sources including
Ross	reduce representation bisulphite sequencing data,
Dr Loan	sequencing and human methylation data to
Nguyen	identify differentially methylated regions between
	with modern molecular technologies. This project
	will require skills in bioinformatics as well as
	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 5 to 16 Project	10) <u>FastStack - evolutionary computing to stack desirable alleles</u> <u>in wheat</u>
Prof Ben Hayes Dr Kai Voss-Fels Dr Eric Dinglasan	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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Webpage	https://qaafi.uq.edu.au/centre-for-animal-science
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics / Agriculture
CAS 5 to 16 Project	11) <u>Reducing methane emissions through improved</u> <u>understanding of the rumen microbiome</u>
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.
Advisors contact	 Prof Ben Hayes, b.hayes@uq.edu.au +61 7 334 62173 Dr Elizabeth Ross, e.ross@uq.edu.au +61 7 334 62162
Location	QBP, Building 80, St Lucia campus
Webpage	https://qaafi.uq.edu.au/centre-for-animal-science
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Microbiology / Agriculture / Veterinary Medicine
CAS 5 to 16 Project Prof Ben Hayes Dr Bailey Engle	 12) <u>Cow fertility through the ages</u> 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	13) Genes impacting female fertility
Project Prof Ben Hayes Dr	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.
Elizabeth Ross Dr Loan Nguyen	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.
Dr Bailey Engle	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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Webpage	https://qaafi.uq.edu.au/centre-for-animal-science
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Agriculture / Veterinary Medicine
CAS 5 to 16 Project	14) <u>The need for speed in Genomic research: Comparing</u> <u>algorithms to estimate polygenic effects in tropically adapted</u> <u>beef cattle</u>
Prof Ben Hayes Dr Roy Costilla	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 5 to 16	15) <u>Improving genotype imputation in the tropics: using Bos</u> indicus reference populations for tropically adapted beef
Project	<u>cattle</u>
Prof Ben Hayes Dr Roy Costilla	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.
	00- TropComp2 Brahman
	-0.010 -0.005 0.000 0.005 0.010 0.015 0.020 PC1

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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics
CAS 5 to 16 Project	16) Exploring TSS-enhancer correlations and identification of novel mutations in TSS-enhancer regions in Bos indicus species
Prof Ben Hayes Dr Mehrnush Forutan	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 $Gene1$ $Gene1$ $Gene2$ $Gene3$ Ge
Advisors contact	 Prof Ben Hayes, b.hayes@uq.edu.au +61 7 334 62173 Dr Mehrnush Forutan, m.forutan@uq.edu.au
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics





CAS 17 Project	17) Harnessing trehalulose formation by stingless bees
Dr Natasha Hungerford Dr Loan Nguyen	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 aim to harness the synbio of these tropical insects, for example, to produce a unique and novel way to yield trehalulose.
	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. <i>Scientific Reports</i> 10 , 12128. <u>https://doi.org/10.1038/s41598-020-68940-0</u>
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Webpage	https://about.uq.edu.au/experts/20086 https://about.uq.edu.au/experts/22854
Useful Majors	Biochemistry & Molecular Biology / Bioinformatics / Chemistry / Genetics





CAS 18	18) CRISPER-CAS system in bacterial pathogen diagnosis and
Project	typing
Dr Lida Omaleki Dr Conny Turni Dr. Noman Naseem	Chicken is the most consumed meat in Australia. Fowl cholera caused by <i>P. multocida</i> is one of the major bacterial diseases in the chicken industry. The lipopolysaccharide (LPS) outer structure of <i>P. multocida</i> is the key immunogenic factor in killed whole cell vaccine. This projects seeks to use CRISPR/Cas system to enrich for the LPS outer core biosynthesis loci of <i>P. multocida</i> isolates and then sequence it on a Oxford Nanopore Technologies (ONT) platform. CRISPR/Cas is a pair of molecular scissors which can be used to sense genomic material of a pathogen and enrich it within a sample. This system together with long read sequencing technology offered by Oxford Nanopore Technologies (ONT) provides a rapid and reliable diagnostic and typing technique. The basic principle of this method is to excise the targeted genomic region/virulence gene of the pathogen (the CRISPR-Cas step) and then determine the genetic sequence via DNA sequencing on an ONT MinION device.
Advisor(s) contact	 Dr Lida Omaleki, I.omaleki@uq.edu.au Associate Advisor: Dr Conny Turni, c.turni1@uq.edu.au Associate Advisor: Dr. Noman Naseem: m.naseem@uq.edu.au
Location	EcoSciences Precinct, Dutton Park
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology





CAS 19 Project	19) Pangenome analysis of avian Pasteurella multocida
Dr Conny Turni Dr Lida Omaleki	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 <i>P. multocida</i> . 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 used for pangenome analysis and compare the major virulence factors.
Advisor(s) contact	 Dr Lida Omaleki, I.omaleki@uq.edu.au Associate Advisor: Dr Conny Turni, c.turni1@uq.edu.au Associate Advisor: Dr. Noman Naseem: m.naseem@uq.edu.au
Location	EcoSciences Precinct, Dutton Park
Webpage	https://researchers.uq.edu.au/researcher/2477
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology





CAS 20 Project	20) Phenotypic and genotypic aspects of antimicrobial resistance
-,	In porcine Pasteurella multocida
Dr Lida Omaleki Dr Conny Turni	Pasteurella multocida is associated with porcine respiratory disease complex, a disease complex that is associated with high morbidity and mortality. In Australia <i>P. multocida</i> 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 <i>P. multocida</i> was done in 2014. A further study was done in that year to look at the antimicrobial resistance genes of 20 isolates of <i>P. multocida</i> via PCR and the whole genome of one isolate was explored. This project seeks to address the gaps in our knowledge. Our laboratory is the national reference center for this pathogen and holds an extensive culture collection from around Australia. A representative set of isolates will be screened by a standardized phenotypic method for antimicrobial resistance. Isolates that show resistance will then be screened for resistance genes, principally by PCR but also by whole genome sequencing. The knowledge gained from this project will be an important support tool for the Australian pig industry.
Advisor(s)	 Dr Lida Omaleki, I.omaleki@ug.edu.au
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

QAAFI Centre for Animal Science





CAS 21 Project 21) Is Pasteurella multocide the primary pathogen in outbreaks of swine diseases?

Dr Conny Turni

Dr Lida Omaleki *Pasteurella multocida* causes an extensive range of economically important diseases in different livestock species. These diseases include fowl cholera in birds, atrophic rhinitis in pigs, haemorrhagic septicemia in cattle and snuffles in rabbits. While *P. multocida* is typically regarded as a secondary pathogen of pigs, we have collection of isolates of this organism from a number of disease outbreaks where the field and the laboratory evidence suggest that the disease was primarily caused by *P. multocida*. Thus, it was hypothesized that the virulence factor profiles of these *P. multocida* isolates might be different from those considered secondary pathogens. The objective of this study is to compare the virulence factors profile of porcine *P. multocida* isolates from disease outbreaks where the organism appears to be the primary pathogen with isolates from disease outbreaks where no primary role of *P. multocida* isolates was demonstrated. The work would focus on the use of whole genome sequencing and bioinformatic analysis to compare and contrast the two populations with a focus on the virulence factor profile of the isolates.



QAAFI Centre for Animal Science





Useful	Biochemistry & Molecular Biology / Bioinformatics / Microbiology
majors	

CAS 22 Project	22) Discovering methane reducing pathways in seaweed	
Prof Ben Hayes Dr Loan Nguyen Dr Elizabeth Ross	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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Location	Queensland Alliance for Agriculture and Food Innovation, St Lucia campus	
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics	





CAS 23 Project	23) <u>Title – Understanding host biology to cattle tick infestation</u>
Dr Ali Raza Professor Ala Tabor	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.
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biotechnology





CAS 24 to 28 Projects

Prof Tim Mahony

24) <u>The application of gene editing to improve animal</u> <u>resistance to infections</u>

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.

25) <u>Construction of bovine herpesvirus 5 infectious clone</u>

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.

26) <u>Characterisation of bovine herpesvirus 2 genome</u>

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.

27) <u>The application of synthetic biology to large DNA viral</u> <u>genomes</u>

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.

28) <u>The development of strand-specific sequencing</u> <u>methodologies double-stranded DNA viral genomes</u>

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 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.







CAS 29 Proiect

29) <u>Development of Isothermal LAMP Assay for Point of</u> <u>Management (POM) Detection of Swine Colibacillosis</u>

Dr Noman Naseem

Escherichia coli are one of the major causative agents of enteric colibacillosis in pigs, leading to death in suckling and weaned pigs worldwide. Enteric colibacillosis causes heavy economic losses to the pork industry in terms of decreased weight gain, increased mortality and high cost for treatments and control. Colibacillosis is caused by colonization of the small intestine by enterotoxigenic strains of Escherichia coli. These pathogenic strains produce varying combinations of enterotoxins that act locally to induce fluid and electrolyte secretion into the intestinal lumen, resulting in diarrhea, dehydration and metabolic acidosis. Early diagnosis of the causative agent is an essential factor in the effective control of disease and related losses. This project aimed to develop an isothermal LAMP assay for the early detection of swine colibacillosis. It was envisaged to perform this test on-farm with minimal equipment and technical skills required. Because the present study is focusing on using piggery effluent as a sample, it would make this novel LAMP assay an excellent tool for herd health monitoring. This study would be a part of a bigger project focusing on developing POM assays for pig diseases funded by Australian Pork Limited (APL).



QAAFI Centre for Animal Science





	Diagnostic Droid by Botella Lab	
Advisor(s) contact	 Dr Noman Naseem (<u>m.naseem@uq.edu.au</u>) Associate Advisor - Dr Conny Turni Dr Lida Omaleki 	
Location	EcoSciences Precinct, Dutton Park	
Webpage	https://qaafi.uq.edu.au/profile/5083/noman-naseem	
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology	

CAS 30	30) <u>Development of Isothermal LAMP Assay for Point of</u>
Project	<u>Management (POM) Detection of Swine Colibacillosis</u>
Dr Noman Naseem	<i>Escherichia coli</i> are one of the major causative agents of enteric colibacillosis in pigs, leading to death in suckling and weaned pigs worldwide. Enteric colibacillosis causes heavy economic losses to the pork industry in terms of decreased weight gain, increased mortality and high cost for treatments and control. Colibacillosis is caused by colonization of the small intestine by enterotoxigenic strains of <i>Escherichia coli</i> . These pathogenic strains produce varying combinations of enterotoxins that act locally to induce fluid and electrolyte secretion into the intestinal lumen, resulting in diarrhea, dehydration and metabolic acidosis. Early diagnosis of the causative agent is an essential factor in the effective control of disease and related losses. This project aimed to develop an isothermal LAMP assay for the early detection of swine colibacillosis. It was envisaged to perform this test on-farm with minimal equipment and technical skills required. Because the present study is focusing on using piggery effluent as a sample, it would make this novel LAMP assay an excellent tool for herd health monitoring. This study would be a part of a bigger project focusing on developing POM assays for pig diseases funded by Australian Pork Limited (APL).





	Image: Additional of the sector of the sec	
Advisor(s) contact	 Dr Noman Naseem (<u>m.naseem@uq.edu.au</u>) Associate Advisor - Dr Conny Turni Dr Lida Omaleki 	
Location	EcoSciences Precinct, Dutton Park	
Webpage	https://qaafi.uq.edu.au/profile/5083/noman-naseem	
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology	

CAS 31 Project	31) <u>Determining bioactive release rates for slow degrading</u> biocomposites for methane mitigation in cattle
Dr Natasha Hungerford Dr Viviene Santiago	This industry-focused Honours project will focus on chemical analysis of bioactive in both novel composites and in solution to determine release rates in different situations and over time. The composites represent a novel delivery system for bioactive components to reduce methane emission in livestock. Once located in the cattle rumen, such biocomposites will degrade over time through surface erosion, delivering sustained active dosing of animals both in extensive pastures and/or in feedlot situations. This project, funded by Meat and Livestock Australia, engages with both government and industry to have maximum impact on the CN30 goal for Northern Australian beef herds.
	Scholars will gain experience in sample preparation and chemical analysis of bioactive levels in fermentation samples and other matrices. Quantification will use HPLC-UV and/or LC-MS/MS, or other novel methods. They will gain experience in data analysis of results.





	bioactive release from biopolymer Time
Advisor(s)contact	• Dr Natasha Hungerford, <u>n.hungerford@uq.edu.au</u> +61 7 344 32473
	 Dr Viviene Santiago, <u>v.santiago@uq.edu.au</u> +61 7 344 36288
Location	Health and Food Sciences Precinct, Coopers Plains
Webpage	https://about.uq.edu.au/experts/20086 https://about.uq.edu.au/experts/43714
Useful majors	Chemical Sciences / Chemistry / Biochemistry & Molecular Biology

CAS 32 Project	32) <u>DNA methylation patterns in the bone of pre and post-</u> pubertal heifers
Dr Loan	Early puberty is essential for the lifetime reproductive performance of cattle.
Nguyen	However, Brahman cattle, a breed of the Bos indicus sub-species, which can withstand
	hostile conditions in northern production systems, are often older and heavier at
Dr Elizabeth	puberty than <i>Bos taurus</i> breeds. As reaching the age of puberty is an important event
Ross	major aim for <i>Bos indicus</i> breeders for efficient herd productivity.
	Bone growth is most remarkable during puberty. To enhance our understanding of puberty-related bone function, this project will perform methylome analyses of bone





	samples from six pre- and six post-pubertal Brahman heifers (<i>Bos indicus</i>). The project aims are to perform differential expression analyses and co-expression analyses to derive a regulatory methylation network associate with puberty.
Advisor(s) contact	 Dr Loan Nguyen, <u>t.nguyen3@uq.edu.au</u> Dr Elizabeth Ross, <u>e.ross@uq.edu.au</u>
Location	St Lucia campus
Webpage	
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Biophysics / Chemical Sciences / Chemistry / Computational Science / Genetics / Microbiology

CAS 33 Project	33) Low coverage Nanopore sequencing for traceability
Dr Loan Nguyen & Dr Elizabeth Ross	This project offers an exciting opportunity to delve into the cutting-edge field of low- coverage Nanopore sequencing and its application in traceability within the food supply chain. Students will have hands-on experience analyzing sequence data from 46 diverse samples, including those from farms, abattoirs, and butcher shops with unknown identities. Through this research, students will explore the innovative potential of low-coverage sequencing to trace the origin of food products, contributing to advancements in food safety and transparency. This project provides practical skills in bioinformatics and genomics.
Advisor(s) contact	 Dr Loan Nguyen, <u>t.nguyen3@uq.edu.au</u> Dr Elizabeth Ross, <u>e.ross@uq.edu.au</u>
Location	St Lucia campus
Webpage	
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Biophysics / Chemical Sciences / Chemistry / Computational Science / Genetics / Microbiology

CAS 34	34) <u>Mapping nutrient sensors in the gastrointestinal tract of</u>
Project	young pigs
Dr. Maximiliano Müller	The gastrointestinal tract (GIT) helps maintain energy and amino acid homeostasis, in part through nutrient sensors and the subsequent activation of signalling molecules (e.g., endocrine and neural components) capable of interacting with the central nervous system to





Prof. Eugeni Roura Dr. Xinle Tan	modulate nutrient utilization via digestive, metabolic, and satiating effects. While a considerable amount of research on nutrient sensors has been done in rodents and humans, only recently has chemosensory science been more thoroughly explored in pigs. Better understanding which receptors play a pivotal role on the sensing of carbohydrates, fats, and amino acids, as well as their location throughout the GIT, may help optimize pig's feed formulations to improve growth and gut health, particularly during critical points of the production cycle (e.g., post weaning period). This project aims to survey the location of the main nutrient sensors, known to date, along the GIT and evaluate the impact that current nutritional trends have on the expression of these mechanisms as well as microbiome (i.e., hindgut bacteria) diversity in young pigs.
Advisor(s) contact	 Dr. Maximiliano Müller, <u>m.mullerbravo@uq.edu.au</u>, +61 481 381 349 Associate Advisors:
	 Prof. Eugeni Roura, <u>e.roura@uq.edu.au</u>, +61 7 3365 2526 Dr. Xinle Tan, <u>xinle.tan@uq.edu.au</u>, +61 414 695 759
Location	St Lucia Campus (Hartley Teakle building #83)
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Useful majors	Biochemistry & Molecular Biology / Microbiology





Centre for Nutrition and Food Sciences Projects

CNAFS 1	1) Nutritional and bioactive properties of Australian boab
Project	(Adansonia gregorii): an emerging functional food ingredient
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, <u>y.sultanbawa@uq.edu.au</u>+61 7 344 32471 Dr Anh Phan, a.phan1@uq.edu.au +61 7 344 32476
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QAAFI Centre for Nutrition and Food Science





Useful majors	Biochemistry, Chemistry, Microbiology, Agriculture, Food Science
CNAFS 2 Project	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
Yasmina Sultanbawa Dr Oladapo Olukomaiya	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.
Advisor(s)	 A/Prof Yasmina Sultanbawa, <u>v.sultanbawa@uq.edu.au</u>+61 7 344 32471 Dr Oladapo Olukomaiya, <u>uqooluko@uq.edu.au</u>
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Useful	Chemistry, Microbiology, Food Science
majors	





CNAFS 3 Project	3) Food applications of native plant foods and ingredients
A/Prof Heather Smyth	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.
Advisor(s)	A/Prof Heather Smyth, h.smyth@uq.edu.au +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
Webpage	www.qaafi.uq.edu.au
	www.uniquelyaustralianfoods.org
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	4) Impact of processing on honey quality
A/Prof Heather Smyth	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.
Advisor(s)	A/Prof Heather Smyth, <u>h.smyth@uq.edu.au</u> +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
Webpage	www.qaafi.uq.edu.au
	www.uniquelyaustralianfoods.org
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Microbiology / Agriculture / Food Science / Entomology





CNAFS 5 Project	5) Flavour chemistry of tropical fruits
A/Prof Heather Smyth Dr Thoa Nguyen	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.
Advisor(s)	 A/Prof Heather Smyth, <u>h.smyth@uq.edu.au</u>+61 7 344 32469 Dr Thoa Nguyen, <u>thoa.nguyen@uq.edu.au</u>
Location	Elkhorn Building, Long Pocket Campus
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Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Food Science / Psychology

QAAFI Centre for Nutrition and Food Science




CNAFS 6 Project	6) Individual human variation and sensory experience
A/Prof Heather Smyth	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.
Advisor(s)	A/Prof Heather Smyth, h.smyth@uq.edu.au +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
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	7) <u>Plant protein – towards better tasting meatless burgers</u>
A/Prof Heather Smyth	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.
Advisor(s)	A/Prof Heather Smyth, https://www.historiangle.edu.au +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
Webpage	www.qaafi.uq.edu.au
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Chemical Engineering / Agriculture / Food Science / Psychology





CNAFS 8 Project	8) <u>The effect of popping on carotenoid content in zeaxanthin-</u> biofortified popcorp
Dr Tim O'Hare	 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.
	Nutritious project. Nutritious project. $i = \int_{C} $
Advisor(s)	Dr Tim O'Hare, <u>t.ohare@uq.edu.au</u> +61 7 535 15068
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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 9 Project	9) <u>Fresh and cooked purple sweetcorn aroma, chemical</u> <u>components and influence on flavour volatiles</u>
Dr Tim O'Hare	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.
	(a new sweetcorn established by Tim O'Hare's research group), compared to commercial yellow sweetcorn using GC-MS. The student will work as part of a larger team in QAAFI working on Naturally Nutritious project.
Advisor(s)	Dr Tim O'Hare, <u>t.ohare@uq.edu.au</u> +61 7 535 15068
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Useful majors	Biochemistry & Molecular Biology / Chemistry / Agriculture / Horticulture / Food Science





CNAFS 10	10) Exploring the nutritional value of Saltbush, an Australian
Project	indigenous edible Halophyte
Dr Michael Netzel Dr Olivia Wright Dr Hung Trieu Hong Prof Yasmina Sultanbawa	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, <u>m.netzel@uq.edu.au</u> M: 0400 887 072 Dr Olivia Wright, <u>o.wright@uq.edu.au</u> +61 7 336 56116 Dr Hung Trieu Hong, <u>h.trieu@uq.edu.au</u> Prof Yasmina Sultanbawa, <u>y.sultanbawa@uq.edu.au</u> +61 7 344 32471
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Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Agriculture / Food Science





CNAFS 11	11) Metabolic resilience to heat stress in lactating sows
Project	
Project Dr Marta Navarro Prof Eugeni Roura	Heat waves are predicted to be increase in frequency, length, and intensity as climate change conditions keep progressing. Modern pig lines have become more sensitive to hot temperatures as a result of the genetic selection to improve performance parameters (but not heat resilience). On the contrary, modern pig genetics characterised by fast and lean weight gain, is associated with a high internal heat production that jeopardizes adaptations to a challenging high ambient temperature environment. Thus, pig's hyperthermia episodes are considered one of the main welfare and economic problems in modern pig production. However, a large variation exists between individuals regarding heat tolerance. This project aims to determine metabolic biomarkers and microbiome signatures that differentiate resilient to high sensitivity to hyperthermia in sows. During lactation nutritional requirement peak to high pushing the maintenance of metabolic homeostasis to the limit particularly under heat stress. It is anticipated that the identification of metabolic biomarkers and microbiome profiles associated with heat tolerance in lactating sows will result in novel nutrition and management intervention strategies to improve sow welfare under heat stress events.
Advisor(s)	 Dr Marta Navarro, <u>m.navarrogomez@uq.edu.au</u> 0458 999 192 Prof Eugeni Roura, <u>e.roura@uq.edu.au</u> +61 7 336 52526
Location	St Lucia or Gatton campus
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Useful	Animal or Veterinary Sciences/ Nutrition / Biomedical Science / Computational
majors	Science / Microbiology





CNAFS 12	12) Peri-hatching programs that naturally improve chicken gut
Project	<u>health</u>
Dr Shahram Niknafs Prof Eugeni Roura	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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Useful	Animal or Veterinary Sciences/ Nutrition / Biomedical Science / Computational
	Secrec / Microbiology

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CNAFS 13 Project	13) Dietary fibre involvement in gut-brain dialogues
Dr Shahram Niknafs Prof Eugeni Roura	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.
	High-fiber diet
Advisor(s) contact	 Dr Shahram Niknafs, s.niknafs@uq.edu.au 0468 691 705 Prof Eugeni Roura, <u>e.roura@uq.edu.au</u>, +61 7 336 52526
Location	St Lucia or Gatton campuses
Webpage	http://researchers.uq.edu.au/researcher/24913 https://qaafi.uq.edu.au/profile/429/eugeni-roura
Useful majors	Animal or Veterinary Sciences/ Nutrition / Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science/ Genetics / Microbiology





CNAFS 14	14) How to make antibiotics in pig feed redundant, naturally
Project Dr Marta Navarro Prof Eugeni Roura	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.
Advisor(s) contact	 Dr Marta Navarro, <u>m.navarrogomez@uq.edu.au</u> 0458999192 Prof Eugeni Roura, <u>e.roura@uq.edu.au</u> +61 7 336 52526
Location	St Lucia or Gatton campus
Webpage	https://researchers.ug.edu.au/researcher/26066
	https://qaafi.uq.edu.au/profile/429/eugeni-roura
Useful majors	Animal or Veterinary Sciences/ Nutrition/ Biochemistry & Molecular Biology / Biomedical Sciences/ Immunology/ Microbiology





CNAFS 15 Project	15) <u>Non-invasive and non-destructive analytical methods for</u> <u>food evaluation</u>
A/Prof Daniel Cozzolino Prof Louw Hoffman	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.
Advisor(s) contact	 A/Prof Daniel Cozzolino, <u>d.cozzolino@uq.edu.au</u>+61 7 336 52144 Associate Advisors: Prof Louw Hoffman, louwrens.hoffman@uq.edu.au +61 7 344 32602
Location	St Lucia Campus or Gatton Campus
Webpage	https://qaafi.uq.edu.au/profile/6668/daniel-cozzolino
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Biophysics / Chemical Sciences / Chemistry / Computational Science / Genetics / Microbiology





CNAFS 16 Project	16) Sensors and math to assure value and provenance in the food chain
A/Prof Daniel Cozzolino Prof Louw Hoffman	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.
Advisor(s) contact	 A/Prof Daniel Cozzolino, <u>d.cozzolino@uq.edu.au</u>+61 7 336 52144 Associate Advisors: Prof Louw Hoffman, louwrens.hoffman@uq.edu.au +61 7 344 32602
Location	St Lucia Campus or Gatton Campus
Webpage	https://qaafi.uq.edu.au/profile/6668/daniel-cozzolino
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Biophysics / Chemical Sciences / Chemistry / Computational Science / Genetics / Microbiology





CNAFS 17 Project	17) Is chicken breast becoming spaghetti meat?
Prof Louw Hoffman Prof Eugeni Roura A/Prof Daniel Cozzolino	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.
Advisor(s)	 Prof Louw Hoffman, Louwrens.hoffman@uq.edu.au +61 7 344 32602 Associate Advisors: Prof Eugeni Roura, e.roura@uq.edu.au +61 7 336 52526 Associate Advisors: A/Prof Daniel Cozzolino, d.cozzolino@uq.edu.au +61 7 336 52144
Location	St Lucia or Gatton campus
Webpage	https://qaafi.uq.edu.au/profile/4974/louw-hoffman
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Microbiology / Agriculture / Animal Science

QAAFI Centre for Nutrition and Food Science





QAAFI Centre for Nutrition and Food Science

Honours Projects 2024





CNAFS 18 Project	18) Black soldier fly fit for nutrition
Prof Louw Hoffman Dr Deirdre Mikkelsen	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.
Advisor(s)	 Prof Louw Hoffman, Louwrens.hoffman@uq.edu.au +61 7 344 32602 Associate Advisors: Dr Deirdre Mikkelsen, <u>d.mikkelsen@uq.edu.au</u> +61 7 334 69642
Location	St Lucia or Gatton campus
Webpage	https://qaafi.uq.edu.au/profile/4974/louw-hoffman
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Microbiology





Centre for Horticultural Science Projects

CHS 1 1) Sex in banana fungi Project Bananas are the fourth most important food crop worldwide, surpassed only by Dr Lilia crops such as rice, maize and wheat. The production, consumption and trade can Costa be greatly affected by pests and mainly fungal diseases such as Sigatoka leaf spot Carvalhais 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 Prof Andre particular race. However, new pathogens strains are constantly emerging, such as Drenth the tropical race 4 (TR4) which has been devastating banana plantations after invasion. The origins of diversity in fungal pathogens usually stem from sexual Dr Alistair reproduction and the objective of the project you will be involved in is to gain **McTaggart** knowledge concerning the genetic mechanisms that create diversity in Fusarium oxysporum f.sp. cubense and Pseudocercospora musae, the causal agents of Dr Vivian Fusarium wilt and yellow Sigatoka, respectively. The specific aims of this study are: Rincon-1) to obtain cultures and DNA from banana fungal pathogens, 2) to screen isolates Florez of banana fungal pathogens for the presence of mating type sequences, 3) evaluate whether mating type genes are transcribed during vegetative growth. Advisor(s) Dr Lilia Costa Carvalhais, l.carvalhais@uq.edu.au 0426 197 372 contact Associate Advisor: Prof Andre Drenth, a.drenth@ug.edu.au +61 7 344 32460 Associate Advisor: Dr Alistair McTaggart, a.mctaggart@uq.edu.au Associate Advisor: Dr Vivian Rincon-Florez, v.rinconflorez@ug.edu.au x32454 Location **Ecosciences Precinct, Dutton Park** Webpage https://qaafi.uq.edu.au/profile/3177/lilia-costa-carvalhais Useful Microbiology/Genetics majors





CHS 2 Project	2) Topical application of RNAi for management of Fire Ants
Prof Neena Mitter Dr Karishma Mody	Fire ants are a serious pest because they have the potential to cause major social, environmental and economic impacts in Queensland and Australia. Fire ants were first detected in Brisbane in 2001, and in September that year the National Red Imported Fire Ant Eradication Program was formed in partnership with State governments. The current project is aimed at investigating RNA interference (RNAi) as a tool to manage fire ants. RNAi targeting neuropeptides and pheromones resulted in increased fire ant mortality (Choi et al. 2012 and Qiu et al. 2017). In this project, the RNAi platform will be further explored to develop novel targets to control fire ants. Students in both Themes can learn valuable techniques in cloning, PCR, qRTPCR, sequencing, RNA/DNA extractions, bioinformatics and RNAi biology. The student will work closely with other members of the Mitter laboratory and industry partners to develop scientific outcomes and a highly productive research.
Advisor(s) contact	 Prof Neena Mitter, <u>n.mitter@uq.edu.au</u> +61 7 334 66513 Associate Advisor: Dr Karishma Mody, <u>k.mody@uq.edu.au</u> +61 7 334 62318
Location	QBP, Building 80, St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/1427
Useful majors	Biochemistry & Molecular Biology / Bioinformatics





CHS 3 Project	3) <u>Clay innovation: sustainable alternative to pesticides for</u> protecting Queensland's livestock
Dr Karishma Mody Prof Neena Mitter Prof Tim Mahony	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
	NO HARMFUL RESIDUES IN LIVESTOCK Image: State of the stat
	further explored to develop novel targets to control both blowfly and lice. Students in both Themes can learn valuable techniques in cloning, PCR, qRTPCR, sequencing, RNA/DNA extractions, bioinformatics and RNAi biology. The student will work closely with other members of the Mitter laboratory and industry partners to develop scientific outcomes and a highly productive research.
Advisor(s)	• Dr Karishma Mody, k.mody@uq.edu.au +61 7 334 62318
contact	 Associate Advisor: Prof Neena Mitter, <u>n.mitter@uq.edu.au</u>+61 7 334 66513 Associate Advisor: Prof Tim Mahony, t.mahony@uq.edu.au +61 7 334 66505
Location	QBP, Building 80, St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/23229
Useful majors	Biochemistry & Molecular Biology / Bioinformatics





CHS 4 Project	4) From Freezer to Field - Cryostasis for Conservation!
Dr Chris O'Brien Dr Alice Hayward Prof Neena Mitter	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!
	 Development of a cryopreservation regeneration media for different avocado cultivars. Cryopreservation of critically endangered native myrtaceae species Cryopreservation of critically endangered <i>Macadamia jansenii</i>
	ten total a series of the seri
Advisor(s) contact	 Dr Chris O'Brien, <u>c.obrien4@uq.edu.au</u> Dr Alice Hayward, <u>a.hayward@uq.edu.au</u> Dr Albert Wong, <u>albertchernsun.wong@uq.edu.au</u> Prof Neena Mitter, <u>n.mitter@uq.edu.au</u>
Location	QBP, Building 80 Level 3 South, St Lucia campus
Webpage	https://qaafi.uq.edu.au/honours
Useful majors	Biochemistry & Molecular Biology / Plant Biology/ Botany/ Horticulture / Conservation





CHS 5 Project	5) <u>Novel Tissue Culture Tools for Ginger Breeding</u>
Dr Alice Hayward Prof Neena	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 <i>sustainable, cost-effective and climate-secure</i> way to produce plants.
Mitter Dr Jayeni Hiti- Bandaralag e	Dedicated students will be part of our expanding research in a new \$20M tissue- culture facility at UQ. Students will work with industry and research partners to value-add student experience. This project will focus on ginger – an import crop facing many disease issues in industry, and where in vitro tools to breed new or improved varieties are sought after. Protoplast extraction and regeneration will be optimised, with opportunity for fusion to create new hybrids, or gene editing using CRISPR.
Advisor(s) contact	 Dr Alice Hayward, <u>a.hayward@uq.edu.au</u> Dr Jayeni Hiti-Bandaralage, <u>j.hitibandalarage@uq.edu.au</u> Prof Neena Mitter, <u>n.mitter@uq.edu.au</u>
Location	QBP, Building 80 Level 3 South, St Lucia campus
Webpage	https://qaafi.uq.edu.au/honours
Useful majors	Biochemistry & Molecular Biology / Plant Biology/ Botany / Microbiology/ Horticulture





CHS 6 Project	6) Genomics and DNA Markers for Australian Avocado
Dr Alice Hayward Mr Stephen Fletcher Prof Neena Mitter	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.
	1 2 3 4 5 6 7 8 9 10 11 12 Sze in Mi 98 107 78 96 66 62 47 41 52 48 50
Advisor(s) contact	 Dr Alice Hayward, <u>a.hayward@uq.edu.au</u> Mr Stephen Fletcher, <u>s.fletcher@uq.edu.au</u> Prof Neena Mitter, <u>n.mitter@uq.edu.au</u>
Location	QBP, Building 80 Level 3 South, St Lucia campus
Webpage	https://qaafi.uq.edu.au/honours
Useful majors	Biochemistry & Molecular Biology / Plant Biology/ Horticulture/ Genetics/ Bioinformatics





CHS 7 Project	7) <u>Agroecological Crop Protection</u>
A/Prof Femi Akinsanmi Dr Vivian Rincon- Florez,	 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 fruit and nut crop: 1. Pathogen biology: Characterization of the biology of causal agents of major foliar and soilborne diseases
	 Notecular epidemiology: Spatial and temporal analysis of dynamics of fungal pathogens in agricultural ecosystems Sustainable solutions: Develop new alternative solutions to synthetic chemical pesticides to manage fungal diseases in horticultural crops
	Scholars will join the pathology team and have opportunity to contribute to publications arisen from the research.
	Leffblight with yellow halb Clestabliopsis leaf disease) Leffblight with yellow halb Clestabliopsis leaf disease) Leffblight with yellow halb Leffblight with yellow halb Cleation of the stabliopsis leaf disease) Leffblight with yellow halb Leffblight with
Advisor(s) contact	 A/Prof Femi Akinsanmi, <u>o.akinsanmi@uq.edu.au</u> +61 7 344 32453 Dr Vivian Rincon-Florez, <u>v.rinconflorez@uq.edu.au</u> Tel: +61 (0)7 3443 2762
Location	Ecosciences Precinct, 41 Boggo Road, Dutton Park (10-min walk from St Lucia campus)
Webpage	https://qaafi.uq.edu.au/profile/186/femi-akinsanmi
Useful majors	Agriculture / Biotechnology / Molecular Biology / Microbiology





CHS 8 Project	8) <u>Simulating fruit tree growth and development</u>
Dr Inigo Auzmendi Dr Emma Carrie	Functional-structural plant models <u>simulate</u> 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 <u>four areas</u> : 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.
Advisor(s) contact	 Dr Inigo Auzmendi, <u>i.auzmendi@uq.edu.au</u> +61 7 344 32702 Associate Advisor: Dr Emma Carrie, <u>e.carrie@uq.edu.au</u>
Location	St Lucia campus
Webpage	https://qaafi.uq.edu.au/profile/762/inigo-auzmendi
Useful majors	Biochemistry & Molecular Biology / Biophysics / Computational Science / Plant Science / Horticulture





CHS 9 Project	9) <u>Genomics of horticultural tree crops</u>
Dr Craig Hardner Dr Elizabeth Ross	View of the second seco
Dr Robyn Cave	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
Dr Mulsuew Fikere	 Robustness of Japanese genomic prediction models for mandarin fruit quality in Australian germplasm Chromosome structural variation in citrus using nanopore technology Global prediction of sweetness in peach Selection for timing of fruit maturity for adaption of cherry to changing environment Student in these projects will collaborate with local and international research groups in Japan, US and Europe. Projects in citrus, peach and cherry will to use genomic prediction methods to connect data collected from across the global with results. The citrus project will explore if chromosome structural variation can account for variation among sweet-orange varieties. Student will develop skills in field assessment, big-data management, bioinformatics, molecular and quantitative genetics, and scientific writing. All projects are aimed at producing manuscripts for submission to peer-reviewed journals.
Advisor(s) contact	 Dr Craig Hardner, craig.hardner@uq.edu.au +61 7 334 69465 Potential Associate Advisor: Dr Elizabeth Ross, <u>e.ross@uq.edu.au</u> +61 7 334 62162 Potential Associate Advisor: Dr Robyn Cave, <u>r.cave@uq.edu.au</u> +61 7 546 01 240 Potential Associate Advisor: Dr Mulsuew Fikere
Location	St Lucia campus
Webpage	https://researchers.ug.edu.au/researcher/1973
Useful majors	Genetics, Bioinformatics, (Agriculture, Horticulture, Plant breeding)





CHS 10 Project	10) Optimising horticultural tree crops breeding
Dr Craig Hardner Dr Vivi	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
Arief Dr Bohyn	 Bio-economic models for trait evaluation in macadamia or coffee Modelling apple, macadamia, mango breeding strategies
Cave	Student will collaborate with local and international research groups. Student will develop skills in systems modelling, economics, plant breeding, quantitative
Prof Bruce Topp	submission to peer-reviewed journals.
Shane Mulo	
Advisor(s)	• Dr Craig Hardner, craig.hardner@uq.edu.au +61 7 334 69465
Contact	 Potential Associate Advisor: Dr Vivi Arief Potential Associate Advisor: Dr Robyn Cave, <u>r.cave@uq.edu.au</u> +61 7 546 01 240
	 Potential Associate Advisor: Prof Bruce Topp, <u>b.topp@ug.edu.au</u> +61 7 538 11373
	Potential Associate Advisor: Shane Mulo (QDAF)
Location	St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Plant breeding, Agricultural economics





CHS 11 Project	11) <u>Genomic platform for understanding the population genetics</u> of pre-colonisation distribution of Bunya pine
Dr Craig Hardner	
	Bunya pine is a special Queensland forest tree. While widespread prior to European colonisation, the only remnant large population occurs in Bunya mountains with isolated individual trees distributed throughout SEQ Queensland. Anthropogenic dispersal by first nations people may have had a major role in the distribution of the species. This proposed aims of this project are the development and evaluation of molecular tools for studying the distribution of these species, and survey the remnant Bunya population and individuals throughout SEQ Queensland investigate the spatial relationship between the remnant population at Bunya Mountains and the isolated trees.
Advisor(s) contact	 Dr Craig Hardner, craig.hardner@uq.edu.au +61 7 334 69465 Potential Associate Advisors: To be advised
Location	St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Genetics, Bioinformatics, Social history





CHS 12 Project	12) <u>General recursive equations for estimating relationship</u> <u>coefficients in auto-polyploid organisms</u>
Dr Craig Hardner	
A/Prof Mark Dieters Dr Vivi	
Arief	The aim of this project is to extend general recursive equations used to estimate relationship coefficients for genetic effects in diploids to account for the more complicated inheritance pattern in auto-polyploid organisms. This project will involve development of probabilistic models of identical-by-descent of genes in diploid and auto-polyploid genetic systems, simulation of multiple population structures under varying polyploidy to validate relationship coefficients, analysis of existing phenotypic data with alternative genetic models to evaluate differences in accuracy of predict genetic values, and preparation of a manuscript for publication in high impact journal.
Advisor(s) contact	 Dr Craig Hardner, craig.hardner@uq.edu.au +61 7 334 69465 Potential Associate Advisor: A/Prof Mark Dieters, <u>m.dieters@uq.edu.au</u> x 57410 Potential Associate Advisor: Dr Vivi Arief
Location	St Lucia campus
Webpage	https://researchers.uq.edu.au/researcher/1973
Useful majors	Quantitative genetics, statistics, poly-ploid genetics





CHS 13 Project	13) Molecular investigation on the phenotypic variability in
FIOJECI	flowering time in macadamia
Dr Mobashwer Alam Prof Bruce Topp	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.
Advisor(s) contact	 Dr Mobashwer Alam, <u>m.alam@uq.edu.au</u> 0753 811 371 Associate Advisor: Prof Bruce Topp, <u>b.topp@uq.edu.au</u> +61 7 538 11373
Location	Maroochy Research Facility, 47 Mayers Rd, Nambour (Student can be based at st lucia, but needs to travel to Nambour, Tairo and Bundaberg for data/sample collection)
Webpage	https://researchers.uq.edu.au/researcher/13285
	https://researchers.uq.edu.au/researcher/2467
Useful majors	Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology





CHS 14 Project	14) <u>Investigating macadamia rootstock genetics on the</u> variability in scion architecture and branching.
Dr Mobashwer Alam Prof Bruce Topp	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.
	Image: Scient of the scient
Advisor(s) contact	 Dr Mobashwer Alam, <u>m.alam@uq.edu.au</u> 0753 811 371 Associate Advisor: Prof Bruce Topp, <u>b.topp@uq.edu.au</u> +61 7 538 11373
Location	Maroochy Research Facility, 47 Mayers Rd, Nambour (Student can be based at St Lucia, but needs to travel to Nambour for data/sample collection)
Webpage	https://researchers.uq.edu.au/researcher/13285 https://researchers.uq.edu.au/researcher/2467
Useful majors	Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology





CHS 15	15) Molecular investigation to determine species composition
Project	and extent of genetic base of Australian elite selections of
Dr Mobashwer Alam Prof Bruce Topp	MacadamiaMacadamia 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.Image: Image:
Advisor(s) contact	 Dr Mobashwer Alam, <u>m.alam@uq.edu.au</u> 0753 811 371 Associate Advisors: Prof Bruce Topp, <u>b.topp@uq.edu.au</u> +61 7 538 11373
Location	Maroochy Research Facility, 47 Mayers Rd, Nambour (Student can be based at St Lucia, but needs to travel to Nambour, Tairo and Bundaberg for data/sample collection)
Webpage	https://researchers.uq.edu.au/researcher/13285 https://researchers.uq.edu.au/researcher/2467
Useful	Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding
majors	/Environmental Science/ Ecology
CHS 16	16) <u>Investigating genetic architecture of stomatal traits to</u>
Project	<u>exploit in climate change adaptation</u>
Dr	To cope with global climate change, one of the key focuses of the plant breeding
Mobashwer	program is to develop climate-smart varieties with efficient water use and
Alam	photosynthesis. Finding out heritable and simple traits associated with less water
Prof Bruce	loss and high photosynthesis can help breeders to select drought and high
Topp	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, <u>m.alam@uq.edu.au</u> 0753 811 371 Associate Advisor: Prof Bruce Topp, <u>b.topp@uq.edu.au</u> +61 7 538 11373
Location	Maroochy Research Facility, 47 Mayers Rd, Nambour (Student can be based at st lucia, but needs to travel to Nambour, Tairo and Bundaberg for data/sample collection)
Webpage	https://researchers.uq.edu.au/researcher/13285
	https://researchers.uq.edu.au/researcher/2467
Useful majors	Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 17 Project	17) Investigating genetic diversity in feral peach
Prof Bruce	Feralisation is a complex process that involves domestic populations reverting to
Торр	wild phenotypes. In the absence of human interruption, feral plants may show
	adaptation to new environments and display characteristics of their wild ancestors.
Prof Jose	We have collected 30 accessions of feral peach from Queensland and New South
Chaparro	Wales which have been propagated and planted at Stanthorpe. This project will
	investigate the genetic and morphological variation in these feral accessions and
Dr	compare them to commercial cultivars. Flowering, fruiting and vegetative growth
Mobashwer	traits will be measured. SSR markers will be used to study genetic diversity.
Alam	





	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.
Advisor(s) contact	 Prof Bruce Topp, <u>b.topp@uq.edu.au</u> +61 7 538 11373 Associate Advisor: Prof Jose Chaparro Associate Advisor: Dr Mobashwer Alam, <u>m.alam@uq.edu.au</u> 0753 811 371
Location	Nambour at the Maroochy Research Facility (Student will need to travel to Stanthorpe for data/sample collection)
Webpage	https://researchers.uq.edu.au/researcher/2467
	https://hos.ifas.ufl.edu/people/on-campus-faculty/jose-x-chaparro/
	https://researchers.uq.edu.au/researcher/13285
Useful majors	Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 18	18) Investigating rootstock effect on scion vigour, flowering,
Project	and fruiting in low chill peach
Prof Bruce Topp Prof Jose Chaparro Dr Mobashwer Alam	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.





Advisor(s) contact	 Prof Bruce Topp, <u>b.topp@uq.edu.au</u>+61 7 538 11373 Associate Advisor: Prof Jose Chaparro Associate Advisor: Dr Mobashwer Alam, <u>m.alam@uq.edu.au</u> 0753 811 371
Location	Nambour at the Maroochy Research Facility (Student may need to travel to Stanthorpe for data/sample collection)
Webpage	https://researchers.uq.edu.au/researcher/2467 https://hos.ifas.ufl.edu/people/on-campus-faculty/jose-x-chaparro/ https://researchers.uq.edu.au/researcher/13285
Useful majors	Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology

CHS 19 Project	19) <u>3-D imaging of badnaviral replication structures</u>
A/Prof	Badnaviruses are some of the most common viral pathogens in the tropics and
Andrew	infect a range of economically important plants such as banana, citrus, cacao,
Geering	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
A/Prof John	of replication structures (viroplasms) in the cytoplasm of infected cells. This project,
Thomas	a collaboration between QAAFI and the Centre for Electron Microscopy and
	Microanalysis, will utilize cryosectioning and transmission electron microscopy to
Dr Kathy	image multiple layers of an infected cell, which will then be integrated using
Crew	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,





	<image/>
Advisor(s) contact	 A/Prof Andrew Geering, <u>a.geering@uq.edu.au</u> +61 7 344 32459 Associate Advisor: A/Prof John Thomas, <u>j.thomas2@uq.edu.au</u> +61 7 325 54393 +61 7 344 32461 Associate Advisor: Dr Kathy Crew, <u>kathleen.crew@uq.edu.au</u>
Location	Centre for Electron Microscopy and Microanalysis, Ecosciences Precinct, Dutton Park
Webpage	https://qaafi.uq.edu.au/profile/81/andrew-geering
Useful majors	Biochemistry & Molecular Biology / Microbiology

CHS 20	20) <u>Population genetics of Alternanthera mosaic virus and</u>
Project	<u>development of an infectious clone</u>
A/Prof Andrew Geering A/Prof John Thomas	Alternanthera mosaic virus (AltMV) was discovered in Australia but is thought to have been introduced into Australia in the early 20 th 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





Dr Kathy Crew	transcription promoter to allow infection of plants by mechanical transmission of the plasmid constructs.
Advisor(s)	 A/Prof Andrew Geering, <u>a.geering@uq.edu.au</u> +61 7 344 32459 Acception Advisory A (Prof John Themas, it themas) @ug.edu.au +61 7 325
CONTACT	 Associate Advisor: A/Prof John Thomas, <u>I.thomas2@ud.edu.au</u> +61 7 325 54393 +61 7 344 32461
	 Associate Advisor: Dr Kathy Crew, <u>kathleen.crew@uq.edu.au</u>
Location	Ecosciences Precinct, Dutton Park
Webpage	https://qaafi.uq.edu.au/profile/81/andrew-geering
Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology

CHS 21 Project	21) <u>Cytopathology and sites of replication of banana bunchy top</u> <u>virus</u>
A/Prof John Thomas	
A/Prof Andrew Geering	





Dr Kathy Crew Dr Megan Vance Mr Ric Webb	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.
Advisor(s) contact	 A/Prof John Thomas, j.thomas2@uq.edu.au, +61 7 325 54393 +61 7 344 32461 Associate Advisor: A/Prof Andrew Geering, <u>a.geering@uq.edu.au</u> +61 7 344 32459 Associate Advisor: Dr Kathy Crew, <u>kathleen.crew@uq.edu.au</u> Associate Advisor: Dr Megan Vance, <u>m.vance@uq.edu.au</u> +61 7 344 32456 Associate Advisor: Mr Ric Webb, <u>r.webb@uq.edu.au</u>
Location	Ecosciences Precinct, Dutton Park
Webpag e	https://qaafi.uq.edu.au/profile/228/john-thomas
Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology





CHS 22	22) <u>Title: Protecting the Australian avocado industry</u>
Project	from exotic pests and pathogens
Project Dr Nga Tran A/Prof. Andrew Geering	from exotic pests and pathogens Abstract: Avocado is one of the most economically important horticultural industries in Australia with farmgate value over \$570 million (2023). In the last decade, the industry has undergone rapid expansion to meet the increased demand in domestic consumption and favourable market prices. The growth of the Australian avocado industry has also been seen in many other nations around the world. Several major diseases and pests of avocado, such as laurel wilt (Harringtonia lauricola), Persea mite (Oligonychus perseae), and large seed weevil (Heilipus lauri) have emerged and expanded their geographic ranges. Australia has strict biosecurity laws and has managed to keep many of these pests and pathogens out. However, there are risks of these exotic pests and pathogens entering Australia through a mixture of both legal and illegal pathways. This research aims to improve the biosecurity diagnostic capacity and capability as part of the Australian avocado industry's preparedness if an incursion event was to occur. The student/s will have the opportunity to improve their knowledge and skills in plant pathology, entomology, molecular biology and bioinformatics, industry connections through being involved in research to investigate the population genetics and developing molecular diagnostic assays for the high priority exotic pests of the Australian avocado industry, including O. perseae and H. lauri.
	 Figure 1. Avocado fruit infested by large seed weevils (<i>Heilipus lauri</i>) (A and B), the adult weevil is indicated by the red arrow (B), and avocado leaf infested by Persea mite (<i>Oligonychus perseae</i>). Note that multiple projects on different exotic pests and pathogens of Australian avocados are available, please contact the supervisors to discuss your interests.
Advisor(s)	Dr Nga Tran Email: <u>n.tran3@uq.edu.au</u> Phone: 07 3443 2454
Location	A/Prot. Andrew Geering Email: <u>a.geering@uq.edu.au</u> Phone: 07 344 32459 Ecosciences Precinct, Dutton Park 4102
Webpage	https://researchers.uq.edu.au/researcher/22053 https://researchers.uq.edu.au/researcher/1587




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

CHS 23-24 Project A/Prof Craig Hardner	 23) 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. 24) 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

CHS 25 project	25) Molecular Physiology of Root Formation in Macadamia
	Adventitious root (AR) formation is critical for the efficient propagation of elite





Dr Albert Wong & Dr Alice Hayward	horticultural and forestry crops. ARs can initiate from internodes, callus formed at the base of cuttings, or the hypocotyl of herbaceous plants. Despite many rooting successes from cuttings and in vitro cultures of many horticultural crops, the cellular processes and molecular mechanisms underlying AR induction in woody plants remain obscure. However, as for other plants, there is a key role for the hormone auxin. This project aims to investigate stem anatomy of in vitro macadamia cultures under the effects of auxin. The secondary aims are to investigate auxin pathway genes (e.g. receptors and auxin transporters that determine polar auxin response, transport and auxin gradients) present in macadamia via bioinformatic tools and design future experiments to evaluate gene expression profiles. If time permits, the student can learn to design CRISPR/Cas9 gene editing constructs
Advisor(s) contact	 Dr Albert Wong, <u>albertchernsun.wong@uq.edu.au</u> Dr Alice Hayward, <u>a.hayward@uq.edu.au</u>
Location	UQ Long Pocket (10 min from St Lucia), Building 1024
Webpage	https://qaafi.uq.edu.au/honours
Useful majors	Biochemistry & Molecular Biology / Plant Biology/ Horticulture/ Genetics/ Bioinformatics

CHS 26 project	26) RNA-based fungicides for ginger
Dr Anne Sawyer	
Prof Neena Mitter	
Prof Elizabeth Aitken	





	The soilborne diseases Pythium Soft Rot (PSR) and Fusarium yellows caused by <i>Pythium</i> sp. and <i>Fusarium oxysporum f.sp. zingiberi (Foz)</i> respectively, significantly limit yield and profitability for the Australian ginger industry. Both diseases impact ginger yield and quality throughout all growing and harvesting stages and under conducive conditions cause losses of ~30-90%. Several chemicals are available to control <i>Pythium</i> in ginger but their intensive use as a seed treatment or in-field application has environmental and social consequences for the industry. There are no chemicals currently registered for the control of <i>Foz</i> and growers are totally reliant on management practices. The aim of this project is to develop RNA-based fungicides as a novel environmentally friendly disease management strategy for ginger, extending on the successful use of BioClay TM to control plant viruses and insect pests.
Advisor(s)	Dr Anne Sawyer, <u>a.sawyer@uq.edu.au</u> , 3346 2295
contact	 Associate Advisor: Prof Neena Mitter, <u>n.mitter@uq.edu.au</u>, 3346 6513 Associate Advisor: Prof Elizabeth Aitken, <u>e.aitken@uq.edu.au</u>, 33654775
Location	Location: Queensland Bioscience Precinct, St Lucia
Webpage	https://about.uq.edu.au/experts/23842
Useful majors	Plant Science / Biochemistry & Molecular Biology / Bioinformatics / Genetics / Microbiology







	Figure. (A) Typical hairy root phenotype observed after genetic transformation using Agrobacterium rhizogenes. (B) GFP reporter expression in transgenic hairy roots.
	In this project you will produce hairy root transgenic lines of citrus and the model plant <i>Nicotiana benthamiana</i> to test their ability to harbour CTV and to identify suitable mild cross-protection strains. In this project you will undertake a variety of plant molecular biology techniques such as gene construct cloning, RT-PCR, Agrobacterium rhizogenes root transformation, and virus detection and quantification.
	This project will be based at the Ecosciences Precinct at Dutton Park. You will work with expert scientists from the Queensland Alliance for Agriculture and Food Innovation (QAAFI) and the Queensland Department of Agriculture and Fisheries (DAF). This project will suit students interested in novel genetic solutions for plant biosecurity.
	For more information, please see the review article: Folimonova SY (2013) Developing an understanding of cross-protection by Citrus tristeza virus. Front. Microbiol. 4:76. doi: 10.3389/fmicb.2013.00076
Advisor(s) contact	 Dr Mark Jackson (<u>m.jackson1@uq.edu.au</u>) Associate Professor Andrew Geering (<u>a.geering@uq.edu.au</u>)
Location:	Ecosciences Precinct, Dutton Park 4102
Useful majors	Biochemistry & Molecular Biology / Genetics / Microbiology





Centre for Crop Science Projects

CCS 1	1) Title: Proximal sensing of soil water for root phenotyping
Project Prof Daniel Rodriguez Dr Dongxue Zhao Dr Peter deVoil	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)	 Prof Daniel Rodriguez, <u>d.rodriguez@uq.edu.au</u> +61 7 535 15091
contact	 Dr Dongxue Zhao, <u>dongxue.zhao@uq.edu.au</u> Dr Peter deVoil, <u>p.devoil@uq.edu.au</u> +61 7 535 15087
Location	Gatton or St Lucia Campus
Webpage	https://www.qld-fsr.info/
Useful majors	Bioinformatics / Biophysics / Computational Science / Agronomy





CCS 2 Project	2) Need for speed: growing plants fast to feed the world
A/Prof Lee Hickey Dr Millicent Smith	We need more robust and productive crops to feed the world but developing new crop varieties is slow using traditional plant breeding approaches.
Prof Graeme Hammer	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, <u>l.hickey@uq.edu.au</u> +61 408 210 286 Associate Advisor: Dr Millicent Smith, millicent.smith@uq.edu.au Associate Advisor: Prof Graeme Hammer, <u>g.hammer@uq.edu.au</u> +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	3) Developing Herbicide Resistant Pigeonpea and Mung Bean
A/Prof Bhagirath Chauhan	Pigeonpea and Mung Bean have great potential as legume rotation crops in cereal farming systems in subtropical Australia. Due to the high demand in the international market, Australian growers have shown interest in cultivating both of these species. Weeds are one of the most important biotic factors that can adversely affect legumes





Dr Bradley Campbell Dr Guoquan Liu	as options for controlling broadleaf weeds in the crop are very limited. Up to 90% yield losses have been reported in pigeonpea due to weed infestations and to a lesser extent mung bean.
	Herbicide-resistant pigeonpea and mung bean could be an effective way of controlling weeds in this crop. However, such products are not available commercially. Therefore, this project will evaluate herbicide resistance mechanisms in these legumes.
	The student will conduct an Ethyl methanesulfonate (EMS) experiment to mutagenize seed from pigeonpea (long duration crop) and mung bean (short duration crop) at the labs in St Lucia (UQ). The mutant populations will then be screened for herbicide resistance via seedling assays and field trials (to be conducted at Gatton). The student will develop important skills in experimental design, chemical safety, plant physiology, phenotyping and data analysis. If time permits, bioinformatic analysis to understand the resistance mechanism may occur.
	EMS
	Mutagenesis
Advisor(s) contact	 Professor Bhagirath Chauhan; <u>b.chauhan@uq.edu.au</u>; +61 7 535 15092 Associate Advisors: Dr Bradley Campbell; <u>b.campbell2@uq.edu.au</u> & Dr Guoquan Liu; <u>g.liu2@uq.edu.au</u>
Location	Lab based work will be conducted at St Lucia (UQ), while field-based work will be conducted at Gatton.
Webpage	https://researchers.uq.edu.au/researcher/10189
Useful majors	Biochemistry & Molecular Biology, Genetics





CCS 4	4) Matching adapted chickpea genotypes with soil and climate
Project	to maximise yield and profit: Field experimentation
Prof Daniel Rodriguez Dr Fer Dreccer	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.
Dr Jeremy Whish	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)	 Prof Daniel Rodriguez, <u>d.rodriguez@uq.edu.au</u> +61 7 535 15091
contact	 Dr Fer Dreccer (CSIRO), Dr Jeremy Whish (CSIRO),
Location	Gatton campus
Webpage	https://www.qld-fsr.info/
	nitips.//yaan.uy.edu.au/prome/4/1/damei-rodriguez
Useful majors	Agriculture, crop physiology, agronomy





CCS 5 Project	5) Matching adapted pulse genotypes with soil and climate to maximise yield and profit: Cropping systems modelling
Prof Daniel Rodriguez Dr Peter deVoil	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.
Dr Jeremy Whish	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).
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Advisor(s) contact	 Prof Daniel Rodriguez, <u>d.rodriguez@uq.edu.au</u> +61 7 535 15091 Dr Peter deVoil, <u>p.devoil@uq.edu.au</u> +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





	C) M/interregions and the second department and future
Project	6) Winter sown sorghum as an adaptation to present and future
	climates
Prof Daniel Rodriguez	Water stress and extreme heat at flowering are becoming common abiotic stresses limiting sorghum production across the Northern Grains Region. These stresses can only be expected to increase in frequency and intensity as our climate changes. Winter sown sorghum has been proposed as a practice to increase sowing opportunities, avoid heat and water stress at flowering, and increase the frequency of double cropping i.e. planting a winter crop after a short summer fallow following the winter sown sorghum. As part of a collaborative effort between UQ-QAAFI Centre for Crop Sciences, NSW DPI and QDAF, this project aims to assess the likely benefits of the practice using datasets from a network of trials run over the last two years across NSW and QLD, APSIM-Sorghum (www.apsim.info), and climate projections from a wide range of global circulation models.
	This Honours project will focus on desktop activities that will analyse existing experimental data, parameterise and run simulation models. The student will join a team of crop physiologist, APSIM programmers and climate modellers, using QAAFI's facilities at UQ's Gatton Campus. Frequent travelling to the field and working outdoors in farmers' fields might be possible if interested.
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Advisor(s) contact	 Prof Daniel Rodriguez, <u>d.rodriguez@uq.edu.au</u> +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 7 Project	7) Revolutionizing Turf Management: Optimizing Gene Editing for Resilient Bermuda Grass
Dr Karen Massel Dr Bradley Campbell	Turfgrass is an essential component of landscaping, sports fields, and golf courses worldwide. Maintaining a healthy and attractive turfgrass is a challenging task, as it requires constant management, including fertilization, irrigation, and pest control. Despite advances in turfgrass management techniques, genetic improvement of turfgrasses remains an unexplored field. The development of a gene editing system for turfgrass can revolutionize the industry, providing more efficient and sustainable turfgrass management practices. Gene editing technologies such as CRISPR/Cas9 have revolutionized the way we understand and manipulate DNA. By using CRISPR/Cas9, researchers can precisely modify specific genes, opening the door to a new era of plant breeding. Developing a gene editing system for turfgrass can help improve stress tolerance, disease resistance, and aesthetic qualities, leading to better-performing turfgrass varieties. Furthermore, gene editing can provide an eco-friendly alternative to conventional turfgrass management practices, such as excessive pesticide use and fertiliser applications. Gene editing can reduce the need for these chemicals, leading to better environmental outcomes.
	This project involves optimising a CRISPR/Cas9 transformation system for Bermuda grass (<i>Cynodon dactylon</i>). Phytoene Desaturase (PDS) will be the gene of choice for editing. It is recommended a student have a background in genetics and molecular biology for this project.
Advisor(s) contact	 Dr Karen Massel; <u>k.massel@uq.edu.au</u>; 61+ 420 676 979 Associate Advisors: Dr Bradley Campbell; <u>b.campbell2@uq.edu.au</u>
Location	John Hines Building (62); St Lucia Campus (UQ)
Webpage	https://qaafi.uq.edu.au/profile/6037/karen-massel
Useful majors	Biochemistry & Molecular Biology / Biomedical Science / Genetics / Microbiology





CCS 8 Project	8) Fascinating fasciation via gene editing
Dr Karen Massel	 Background: Fasciation is a phenomenon in which plant stems, leaves, or flowers become flattened, elongated, or distorted due to abnormal growth. Although it is often considered a deformity, fasciation can also be harnessed for crop improvements. This project focuses on a fasciated sorghum mutant created through gene editing approaches targeting a key receptor involved in signalling cascade for stem cell maintenance. The fasciated sorghum mutant shows unique phenotypes which are not always found in other highly related crops which warrants further research. Approach: Gene editing will be performed targeting the key ligand that binds to the receptor for an alternative approach to disrupt this signalling cascade. Due to the time constraints on creating a transgenic sorghum line, this project will also further our understanding of the outcomes of the receptor mutant. This receptor is known to function as a heterodimer. Therefore, we will use biomolecular fluorescence complementation assays in tobacco to understand its receptor-receptor interactions. The outcomes will be compared to transcriptomic data to understand when and where these interactions may occur during development. Thus, the selected honours student will learn and apply foundational molecular tools as well as have the opportunity to utilise innovative biotechnological approaches to study
	gene networks.
	Supernumerary flored organs
	Image: Stigmas 2 4 1 2 1 3 WT Mutant Mutant Polyembryony 05 02 02 WT 05 02 02 02 WT 05
Advisor(s) contact	Dr Karen Massel k.massel@ug.edu.au
Location	Rm 319, John Hines (62), St Lucia campus
Webpage	https://qaafi.uq.edu.au/
Useful majors	Biochemistry & Molecular Biology Genetics / Biotechnology





CCS 9 Project	9) Sustaining food production on the face of climate change through crop root adaptation
Dr Jack Christopher Dr Karine Chenu	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, <u>i.christopher@uq.edu.au</u> +61 7 452 91413 Associate Advisor: Dr Karine Chenu, <u>karine.chenu@uq.edu.au</u> +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 10 Project	10) Increased food production on constrained soils
Dr Jack Christopher Dr Yash Dang	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, <u>v.dang@uq.edu.au</u>
Location	Leslie Research Facility, Toowoomba
Webpage	https://qaafi.uq.edu.au/
Useful majors	Biochemistry & Molecular Biology / Agriculture





CCS 11 Project	11) Determining soil moisture from high-resolution satellite imagery (Sentinel-2)
A/Prof Andries Potgieter Dr Yan Zhao	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.
	Skills in machine learning and remote sensing utilised in this research study will enhance the candidate's knowledge in creating novel solutions to real-world problems in agriculture and remote sensing technologies.
	$ \begin{array}{c} 800 \\ 600 \\ 19 \\ 100 \\ 200 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$
	Spectral Index from Satellite
	Moisture related spectral index derived from satellite dataPossible relationships between soil moisture and remotely sensed indices
Advisor(s contact	 A/Prof Andries Potgieter, <u>a.potgieter@uq.edu.au</u> +61 7 535 15085 Associate Advisor: Dr Yan Zhao, <u>yan.zhao@uq.edu.au</u> +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	Statistics /Mathematics / Biophysics / Computational Science





CCS 12 Project	12) Predicting Plant Success - Big Data for Small Plants
Dr Owen	Data Creation & Collection Big Data & Artifical Intelligence Translate Success
Powell	555 1000
Dr Francois Barbier Prof Mark Cooper Prof Christine Beveridge	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, <u>o.powell2@uq.edu.au</u> Associate Advisor: Dr Francois Barbier, SBS, f.barbier@uq.edu.au Associate Advisor: Prof Mark Cooper, <u>mark.cooper@uq.edu.au</u> +61 7 334 62778 Associate Advisor: Prof Christine Beveridge, SBS, <u>c.beveridge@uq.edu.au</u> +61 7 336 57525
Location	St Lucia campus
Webpage	https://qaafi.uq.edu.au/profile/7515/owen-powell
Useful majors	Molecular Biology / Genetics/ Computational Science





CCS 13-18 Project	13) Mapping the genes controlling grain density in sorghum
A/Prof Emma Mace Prof David Jordan	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.
Ms Geetika Geetika	<u>14) Genetic diversity of genes involved in pollen fertility</u> <u>restoration in sorghum</u>
	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.
	15) 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.
	<u>16) Correlation of lignin content in midrib versus stem in</u>
	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.





	 17) 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 components 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. 18) 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
Advisor(s) contact	 A/Prof Emma Mace, emma.mace@uq.edu.au +61 7 454 26729, +61 7 336 54368 Prof David Jordan, <u>David.jordan@uq.edu.au</u> +61 7 454 26722, +61 7 336 54367 Ms Geetika Geetika, <u>g.geetika@uq.edu.au</u> x54366
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





CCS 19	19) 3D mapping of plant available water capacity
Project Dr Dongxue Zhao Prof Daniel Rodriguez Dr Peter deVoil	The amount of soil water available to crops – plant available water capacity (PAWC) is the main soil property required to assess the amount and distribution of plant available water (PAW) – is a key determinant of potential yield in dryland agriculture. Plant available water capacity (PAWC) is the main soil property required to assess the amount and distribution of plant available water (PAW), used to inform pre-planting, planting, and in-crop management decisions. Having access to reliable spatial maps of PAWC and PAW can also help inform cost- benefit analyses of investments in precision agriculture technologies and their applications. This project will combine geophysical electromagnetic induction technology with crop modelling to i) spatially map PAWC and PAW across fields and ii) to inform decisions such as: whether to sow or to wait, optimum nitrogen rates across the field, achievable yield, as well as decisions on a combination of cultivar and density. This project will involve running field surveys, desktop data analysis and modelling. The student will develop experience in applying advanced proximal sensing technologies (e.g., electromagnetic induction and visible near-infrared spectroscopy) for precision agriculture.
Advisor(s) contact	 Dr Dongxue Zhao Email: <u>dongxue.zhao@uq.edu.au</u> Prof Daniel Rodriguez Email: <u>d.rodriguez@uq.edu.au</u> Dr Peter deVoil Email: <u>p.devoil@uq.edu.au</u>
Location	Gatton or St Lucia Campus
Webpage	https://www.qld-fsr.info/ https://qaafi.uq.edu.au/profile/9642/dongxue-zhao
Useful majors	Plant Science / Soil Science / Computational Science / Agronomy





CCS 20 Project	20) Breaking the Barriers: Developing a Protoplast System for Genetic Advancement of Taro and Boot Crops
Project Dr Bradley Campbell Dr Karen Massel	<text><text><text><text></text></text></text></text>
Advisor(s)	Dr Bradley Campbell; <u>b.</u> campbell2@ug.edu.au: 61+ 412 648 391
contact	Associate Advisors: Dr Karen Massel; <u>k.massel@uq.edu.au</u>
Location	John Hines Building (62), St Lucia Campus (UQ)
Webpage	https://www.abc.net.au/gardening/how-to/future-proofing-taro/13881562
Useful majors	Biochemistry & Molecular Biology / Biomedical Science / Chemical Sciences / Genetics / Microbiology





CCS 21 21) What is the value of increased sorghum grain quality to grain Project growers and cattle producers?

Sorghum is one of the most important crops across the semi-arid tropics worldwide Dr Joseph with economic, environmental, and social benefits both from grain and stover at the crop and cropping systems levels. However, immediate economic benefits from grain sales for animal feedstock, human consumption and ethanol conversion are limited by inconsistent quality threatening the entire cropping system Dr Karen sustainability. Understanding the genetic and environmental drivers of grain quality Harper will inform when and how to grow high value sorghum to benefit short-term cash flow from grain sales and longer-term system drought resilience, environmental sustainability and cropping systems profitability.

A/Pro Daniel Cozzolino

Eyre

The objective of this project is to quantify the value of available white, red and waxy type hybrid sorghums to grain growers and livestock producers when grown in farmers' fields across heat and water stress gradients. The value to grain grower will be evaluated at the sorghum crop (productivity and economics) and cropping systems (water balance) levels with a view to understanding the whole cropping system drought resilience.

Our previous research showed that new grain sorghums have greater value to livestock per hectare (Digestible Energy [DE], MJ/ha) than industry stand hybrids. However, the grain weight to energy conversion factors were established for crops grown in conditions not representative of Australia's commercial sorghum cropping systems i.e. non-adapted germplasm grown on a research station. For example, poultry feed rations developed based on established grain sorghum quality analysis performed well below expectation in 2017 suggesting a grain quality variation is not adequately captured in current grain energy models. Our results also showed that the new sorghum mean grain size was lower and screenings higher than industry standards in some sites and this may have greater negative impacts on livestock performance than grain composition benefits.

Total starch, amylose content and protein digestibility explain 94% of the variation in sorghum grain digestibility (Wong et al. 2010). Total ethanol, fermentation rate and conversion efficiency of sorghum grain is similarly influenced by total starch, amylose to amylopectin ratio, protein content and protein composition (Wu et al. 2008; Zhao et al. 2008; Fox and Manley 2009; Wu et al. 2010; Li et al. 2015). The genes influencing grain quality are affected by high temperatures resulting in 8 to 9% reduction in energy conversion. Finally, market demand, end user willingness to pay premiums and ability to differentiate specialist grain sorghums is unresolved

Topics for honours project within this program include;

- 1- Field crop agronomy Grain density distribution of waxy, white and red sorghum types and the morphological attributes,
- 2- Cattle nutrition Effect of sorghum grain density and genotype on in-vitro digestible energy.
- 3- Grain quality analysis MIR/NIRs methods to quantify grain sorghum quality,





	 4- Crop-physiology – Environmental drivers of grain sorghum quality variability for selected waxy, white and red sorghum types. 5- Crop modelling – Simulation modelling sorghum and maize production systems.
	Scholars will be expected to provide Joseph Eyre <u>i.eyre@uq.edu.au</u> with a ½ to 1 page statement on their motivation for a specific topic within this project and their CV. An appropriate work plan will be developed between the research team and the incumbent based on experience, motivations and demonstrated learning capacity.
Advisor(s) contact	 Principle advisor: Dr Joseph Eyre j.eyre@uq.edu.au Associate Advisors: Dr Karen Harper <u>karen.harper@uq.edu.au</u>; A/Pro Daniel Cozzolino <u>d.cozzolino@uq.edu.au</u>
Location	Gatton and St Lucia Campus
Webpage	
Useful majors	Agronomy / Crop physiology / Biochemistry / Computational Science

CCS 22 Project	22) Economic thresholds for managing fall armyworm damage in sorghum and maize				
Dr Joseph Eyre	The decision to control pre-anthesis FAW infestations in sorghum and maize requires information on crop yield and loss potential. Existing control thresholds for FAW are based on crop defoliation levels, but defoliation has a poor correlation with yield loss. FAW only feed on leaves developing inside the whorl with few cost-efficient control options available once the full extent of crop damage becomes evident. Identifying the most susceptible crop growth stages to yield limiting FAW infestation				
Melina Miles	will inform the timing of effective control options. Understanding crop management practices and environmental conditions influence on the likelihood and potential magnitude of yield limiting FAW infestation will inform the most cost-effective FAW control action.				
Roslyn Gleadow	Previous experiments showed 20 to 30% yield losses when sorghum and maize crops with 3 expanded leaves was infested with FAW until the crop had 12 expanded leaves at Ayr or Gatton in 2022. Yields were correlated with FAW defoliation quantified as the fraction of intercepted photosynthetically active radiation (fiPAR) at anthesis and the population density of fertile plants. The effects of FAW infestation during the canopy expansion and growth stage on yields could be simulated with APSIM by attenuating model co-efficient for the potential largest leaf size until fiPAR matched observed values. This means that yield loss was either a result of direct FAW reduction of immature leaves size, indirectly through limiting photosynthate supply to developing leaves or both resulting in reduced total canopy size.				







Barrenness due to direct effects of FAW feeding or shading of FAW stunted plants by neighbouring plants was a secondary contribution to yield loss.

Pre-flowering FAW infestations elsewhere show a highly variable yield loss and the cause of this variability remain unclear. While many ecological factors affect the FAW population density and infestation persistence within the crop, this study focuses on crop physiological aspects. Previous research has shown that crop growth rate relative to pest growth rate, crop health, crop growth cycle duration and host plant defences most frequently attenuate pest damage magnitude.

Here we conduct empirical research to develop relationships between FAW population density and timing on potential canopy size then estimate crop loss variability by incorporating new FAW canopy attenuation routines into a process-based crop modelling (APSIM <u>https://www.apsim.info/</u>) to predict crop losses across different agro-ecologies and seasons.

Empirical field trials will test the hypothesis that the most sensitive canopy development stage to FAW infestation is consistent regardless of temperature, radiation, plant growth and development rates. The effects of canopy size and crop growth rate on the relationship between timing of FAW infestations relative to crop canopy development stage on potential sorghum yield formation. Growth rate treatments will be imposed by manipulating the photo-thermal quotation with levels of shading and sowing date.

Crop canopy attenuation routines that represent the effect of pre-anthesis FAW infestations on canopy size potential will be incorporated into the APSIM sorghum & maize modules based on empirical trial findings. Simulations validated against on-farm trials will then be run to quantify the potential crop losses across Australian production environments and systems.

A database of simulated FAW crop losses for sorghum and maize production scenarios will be delivered to the economic threshold tool design team. This team will develop a web tool so that farmers and consultants can input their own crop and FAW status to inform economic value of control options by interrogating the simulation database.

Topics for honours project within this program include

- 1- Field crop agronomy The effect of FAW infestation on sorghum and maize yield components,
- 2- Entomology The relationship between FAW larvae infestation and crop damage ratings,
- 3- Crop-physiology The effect of FAW infestation and plant population density on crop growth rates.
- 4- Crop modelling Simulation modelling sorghum and maize production systems.

Scholars will be expected to provide Joseph Eyre <u>i.eyre@uq.edu.au</u> with a ½ to 1 page statement on their motivation for a specific topic within this project and their CV. An appropriate work plan will be developed between the research team and the incumbent based on experience, motivations and demonstrated learning capacity.





Advisor(s) contact	 Principle advisor: Dr Joseph Eyre j.eyre@uq.edu.au Associate Advisors: Melina Miles <u>Melina.Miles@daf.qld.gov.au</u> Roslyn Gleadow <u>ros.gleadow@monash.edu.au</u> 				
Location	Gatton Campus				
Webpage					
Useful majors	Agronomy / Crop physiology / Biochemistry / Computational Science				

CCS 23	23) What is the influence of sustainability frameworks on					
Project	grower/producer decision making?					
Dr Joseph Eyre Melina Miles	Opportunities to establish broadacre cropping across northern Australian are well known yet the landscape remains dominated by extensive grazing systems due to failure to adequately address production risks. High land and commodity prices, climate variability, cattle biosecurity and market risk, emerging carbon markets and policy settings has sparked renewed interest in revaluation of cropping risks. This project brings together experienced public and private researchers and value chain actors in a coordinated approach to enable cotton led farm diversification as part of a sustainable cropping systems that benefits cattle producers.					
Roslyn Gleadow	Critical to successful development of a Northern Australian cropping sector is the need for a unified vision for agricultural led agricultural development. Natural resource management stewardship is increasingly needed to establish social licence for a unified vision with local communities, agri-business and the three levels of government. Here we have an opportunity to involve these stakeholders in co-designing sustainable integrated crop and livestock systems.					
	Co-design of agricultural systems is shown to benefit from design team exposure to different perspectives and solutions through an emersion tour. That is, a tour that takes the members away from their daily routines and experiences and affords them the ability to see problems and solutions beyond their own worldview. Emersion tours also connect participants on a personal level, increase mutual trust and confidence to positively challenge one another's thinking beyond "business as usual solutions".					
	During the emersion tour the project team will conduct surveys with stakeholders including farmers, community leaders, agri-business and government representatives to;					
	 Benchmark farmers' current sustainable practices Understand farmers' interpretation of the term 'sustainability' Explore farmers' views on the sustainability of Australian agriculture, both now and in the future 					





	 Gauge awareness of, and participation in, industry frameworks or schemes that demonstrate sustainability Identify expectations and concerns around premium payments for frameworks or schemes and explore compliance issues 					
	Honours scholars will have access to this survey dataset to complete a thesis on topics such as;					
	 Review of sustainability frameworks and best practice guidelines in mixed-farming systems, What is the influence of industry sustainability frameworks on farmers decision making? What can we learn from farmers learning? What are the bridging points for improving farming practices as well as tailoring sustainability framework for tracking and improving sustainability outcomes. Scholars will be expected to provide Associate Professor Sudhir Yadav <u>sudhir.yadav@uq.edu.au</u> with a ½ to 1 page statement on their motivation for a specific topic within this project and their CV. An appropriate work plan will be developed between the research team and the incumbent based on experience, mativations and domenstrated learning capacity. 					
Advisor(s)	Principle advisor: Associate Professor Sudhir Vaday sudhir vaday@ug.edu.au					
contact	 Associate Advisors: Dr Joseph Eyre j.eyre@uq.edu.au 					
Location	Remote					
Webpage						
Useful majors	Agronomy / Crop physiology / Biochemistry / Computational Science					

CCS 24 Project	24) Biomass Quality Indices for Renewable Energy
A/Profess or Sudhir Yadav & Dr Bruno Moreira	This research program is part of an ongoing project focused on developing biomass quality indices to enhance renewable energy generation in Australia. Our objective is to create functional biomass models by integrating physicochemical properties from agriculture, forestry, and urban sectors, using data from the CSIRO's Biomass and Waste-to-Energy Database and other relevant resources. The project aims to establish practical quality indices that consider both individual properties and their interplay, providing analytical tools to better inform biomass selection and mitigate issues related to thermal conversion inefficiencies and maintenance costs in biomass- burning equipment. The focus will be on identifying, calculating, and modelling quality indices such as the Volatile Fuel Index and Fouling/Slagging Index for various biomass types. The student's roles include systematically reviewing the literature, organising





	data from relevant resources, and contributing to the creation of functional and graphical models to compare and select the most suitable biomass types for solid fuel production.
Advisor(s)	 A/Professor Sudhir Yadav; sudhir.yadav@uq.edu.au, +61 7 334 62199
contact	Associate Advisors: Dr Bruno Moreira; <u>b.moreira@uq.edu.au</u>
Location	St Lucia
Webpage	
Useful majors	Chemical Sciences / Chemistry / Computational Science/Environmental Science

CCS 25	25) <u>Environmental Footprint Assessment of</u>
Project	Alternative Food Sources
A/Professor Sudhir Yadav & Dr Cresha Nadar	This project focuses on evaluating the sustainability of emerging food production technologies through life cycle assessments (LCA). With advancements in biotechnology, alternative food sources such as lab-grown meat, plant-based proteins, and insect farming are being explored to meet global nutrition demands. However, the environmental impacts of these technologies vary depending on the processes involved, making it essential to assess their sustainability accurately. The primary objectives are to introduce honours students to the core principles of LCA and provide practical experience in running simulation scenarios. Students will model the environmental footprints of various food production technologies, analysing factors such as energy use, water consumption, greenhouse gas emissions, and land use. By comparing these impacts, students will gain insights into the sustainability of different food systems and compare the environmental impacts of alternative food sources. The outcomes will inform the selection and optimisation of food



QAAFI Gueensland Alliance for Agriculture and Food Innovation

	production technologies with lower environmental footprints, supporting transition to more sustainable food systems.						orting the	
	Waste feedstock	Fermentation type	Microbe type	Fermentation technology	Operating parameters	Output	Quality	
	Lignocellulosic biomass Free sugars Gases Others Others	Solid Liquid Gases	Bacteria Fungi Veast Mix Veast	Traditional fermentation Biomass fermentation Precision fermentation	Temperature	Protein	Amino acids	
Advisor(s)co ntact	 A/Professor Sudhir Yadav; <u>sudhir.yadav@uq.edu.au</u>, +61 7 334 62199 Associate Advisors: Dr Cresha Nadar; <u>c.nadar@uq.edu.au</u> 							
Location	St Lucia							
Webpage								
Useful majors	Food Science, Biotechnology, Biochemistry, Environmental science							