



THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA

**QAAFI**  
Queensland Alliance for  
Agriculture and Food Innovation

The Queensland Alliance for Agriculture and Food Innovation

# HONOURS PROGRAM



Queensland  
Government

[qaafi.uq.edu.au](http://qaafi.uq.edu.au)  
[qaafi@uq.edu.au](mailto:qaafi@uq.edu.au)  
+61 7 3346 0550



# Participate in an honours program at UQ with QAAFI

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

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

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

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

Duration: 1 year full-time

For more information about Honours at QAAFI and available projects, visit: [qaafi.uq.edu.au/honours](https://qaafi.uq.edu.au/honours)

## Honours Co-ordinator

Dr Vijaya Singh

[v.singh@uq.edu.au](mailto:v.singh@uq.edu.au)

To register your interest, scan here:



## Join the QAAFI Student Association



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

QSA aims to:

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

For more information about Honours at QAAFI and available projects, visit: [qaafi.uq.edu.au/honours](https://qaafi.uq.edu.au/honours)

## QAAFI Student Association:

[qaafi.uq.edu.au/qa](https://qaafi.uq.edu.au/qa)

[qa@uq.edu.au](mailto:qa@uq.edu.au)

To join the QSA, scan here:



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

**Yastika Banerjee – QAAFI Honours Student**

**Project:** Cloning and expression of conserved Mycoplasma bovis antigenic sequences into the BoHV-1 vaccine vector - Development of a BHV – M. bovis bivalent vaccine.

**Supervisors:** Dr. Karl Robinson and Prof. Timothy Mahony



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

**Da Wei (David) Chia – QAAFI Honours Student**

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



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

**Tatiana Briody – QAAFI Honours Student**

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



THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA

**QAAFI**  
Queensland Alliance for  
Agriculture and Food Innovation

# Queensland Alliance for Agriculture and Food Innovation

## Honours Projects 2023

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



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

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

## Contents

<b>Centre for Animal Science Projects .....</b>	<b>3</b>
<b>Centre for Nutrition and Food Sciences Projects .....</b>	<b>29</b>
<b>Centre for Horticultural Science Projects .....</b>	<b>47</b>
<b>Centre for Crop Science Projects.....</b>	<b>75</b>

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

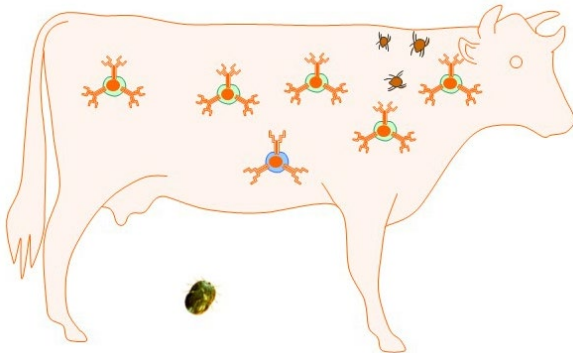





# Centre for Animal Science Projects



<p><b>CAS 1 Project</b></p> <p><i>Prof Ala Tabor</i></p> <p><i>A/Prof Pat Blackall</i></p> <p><i>Dr Conny Turni</i></p> <p><i>Prof Ben Hayes</i></p>	<p><b>1) <u>Bovine campylobacteriosis metagenomics, biomarkers and diagnostics</u></b></p> <p>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.</p> <div data-bbox="344 840 630 1055" data-label="Image"></div> <p>Calf loss</p> <div data-bbox="646 875 1374 1055" data-label="Figure"> </div> <p>Sequence alignments</p>
<p>Advisors contact</p>	<ul style="list-style-type: none"> <li>• <b>Prof Ala Tabor</b>, <a href="mailto:a.tabor@uq.edu.au">a.tabor@uq.edu.au</a> +61 334 62176</li> <li>• Associate Advisor: A/Prof Pat Blackall, <a href="mailto:p.blackall@uq.edu.au">p.blackall@uq.edu.au</a> +61 7 344 32466</li> <li>• Associate Advisor: Dr Conny Turni, <a href="mailto:c.turni1@uq.edu.au">c.turni1@uq.edu.au</a> +61 7 344 32463</li> <li>• Associate Advisor: Prof Ben Hayes, <a href="mailto:b.hayes@uq.edu.au">b.hayes@uq.edu.au</a> +61 7 334 62173</li> </ul>
<p>Location</p>	<p>QBP, Building 80, St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/492/ala-tabor">https://qaafi.uq.edu.au/profile/492/ala-tabor</a></p>
<p>Useful majors</p>	<p>Microbiology / biotechnology / molecular biology / bioinformatics</p>



<b>CAS 2 Project</b>  <i>Prof Ala Tabor</i>	<p><b>2) <u>Biomarkers and bovine genetics to identify cattle tick resistance markers</u></b></p> <p>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.</p> <div></div> <p>N.B. ticks and immune cells not to scale</p>
Advisors contact	<ul style="list-style-type: none"><li>• <b>Prof Ala Tabor</b>, <a href="mailto:a.tabor@uq.edu.au">a.tabor@uq.edu.au</a> +61 334 62176</li><li>• Associate Advisor: Dr Ali Raza, <a href="mailto:a.raza@uq.edu.au">a.raza@uq.edu.au</a> +61 7 334 62317</li></ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/profile/492/ala-tabor">https://qaafi.uq.edu.au/profile/492/ala-tabor</a>
Useful majors	Microbiology / biotechnology / molecular biology / bioinformatics





<b>CAS 3 Project</b>  <i>Prof Ala Tabor</i>	<p><b>3) Title – Optimising Oxford Nanopore sequencing for arthropod genome sequencing with large repetitive content</b></p> <p>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.</p> <div></div>
Advisor(s) contact	<ul style="list-style-type: none"><li>• <b>Professor Ala Tabor</b>, <a href="mailto:a.tabor@uq.edu.au">a.tabor@uq.edu.au</a> 07 334 62176</li><li>• Associate Advisors: Dr Hannah Siddle, <a href="mailto:h.siddle@uq.edu.au">h.siddle@uq.edu.au</a></li></ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/profile/492/ala-tabor">https://qaafi.uq.edu.au/profile/492/ala-tabor</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biotechnology




<p><b>CAS 4 Project</b></p> <p><i>Dr Luis Prada e Silva</i></p>	<p><b>4) <u>Nitrogen recycling as determinant for feed efficiency of Bos indicus cattle</u></b></p> <p>To thrive in northern Australia, cattle depend on the capacity of efficiently extract nutrients during periods of restricted availability. Therefore, the ability to recycle nitrogen (N) back to the rumen, instead of eliminating in the urine, is crucial. This project is testing four relevant hypotheses: 1) feed efficiency in low-protein diets is associated with N recycling and not correlated with feed efficiency in nutrient abundant diets; 2) rumen efficiency can be practically measured and incorporated into genetic selection; 3) N utilization efficiency (NUE) can be measured by isotopic analysis in animal tissues; and 4) differences in rumen efficiency reflect differences in rumen microbial populations. Ninety Bos indicus steers are being evaluated over 60 days receiving a diet supplying only 70% of the rumen degradable protein (RDP) requirements, followed by 60 days on a diet providing 100% of the RDP. After each period, efficiency of microbial protein production is measured in metabolism crates, using purine derivatives in urine and N recycling is quantified with infusion of 15N-enriched urea. Rumen contents are collected for rumen microbiome and transcriptome analysis. Tail hair has been used to evaluate a less-invasive approach to estimate NUE.</p> 
<p>Advisors contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Luis Prada e Silva</b>, <a href="mailto:l.pradaesilva@uq.edu.au">l.pradaesilva@uq.edu.au</a> +61 334 62166</li> <li>• Associate Advisor: Dr Diogo Costa</li> <li>• Associate Advisor: Dr Sarah Meale, <a href="mailto:s.meale@uq.edu.au">s.meale@uq.edu.au</a> x50614</li> </ul>
<p>Location</p>	<p>QBP, Building 80, St Lucia campus and/or Building 8150, Gatton campus</p>
<p>Webpage</p>	<p><a href="http://researchers.uq.edu.au/researcher/16777">http://researchers.uq.edu.au/researcher/16777</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Chemical Sciences / Chemistry / Genetics / Microbiology</p>



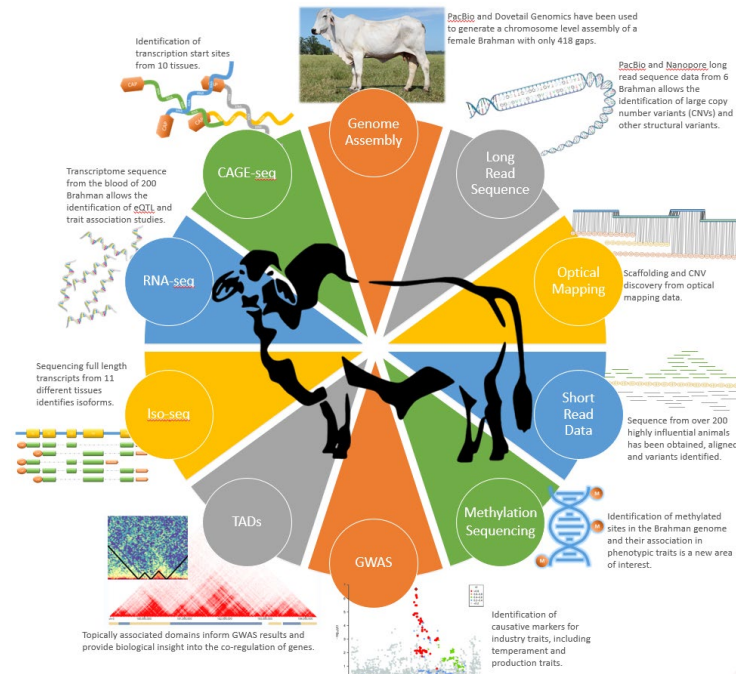
<p><b>CAS 5 Project</b></p> <p><i>Dr Luis Prada e Silva</i></p>	<p><b>5) <u>Nutritional modulation of the transfer of passive immunity in tropically adapted cattle</u></b></p> <p>This experiment aims to clarify factors associated with the nutritional modulation of colostrum secretion and transfer of passive immunity from cows to calves. Proper colostrogenesis and transfer of passive immunity is certainly a major factor for calf survival, it is our overall hypothesis that protein metabolism during late gestation with its consequent effects on hormonal and metabolic profile are important factors modulating colostrum secretion and quality. The project aims is to determine the effect of protein and prebiotic feeding during the transition period on the transfer of passive immunity. Factors measured will include metabolite and hormonal changes in the cow around calving, colostrum quality, and calf vigour, health, and growth in the first two weeks. The practical objective is the development of efficient supplementation strategies to minimize stress and calf loss in commercial herds. The results obtained in the present study could be used to improve adoption of more efficient supplementation strategies alleviating the nutritional stress around parturition, preventing the substantial loss of calves currently occurring in parts of Queensland, and reducing the use of antibiotics in cattle.</p> <div data-bbox="363 887 708 1267"> </div> <div data-bbox="715 887 1139 1267"> </div> <div data-bbox="1145 887 1410 1267"> </div>
<p><b>Advisors contact</b></p>	<ul style="list-style-type: none"> <li>• <b>Dr Luis Prada e Silva</b>, <a href="mailto:l.pradaesilva@uq.edu.au">l.pradaesilva@uq.edu.au</a> +61 334 62166</li> <li>• Associate Advisor: Dr Geoffry Fordyce, <a href="mailto:g.fordyce@uq.edu.au">g.fordyce@uq.edu.au</a> 0428 109 062</li> <li>• Associate Advisor: Dr Diogo Costa</li> </ul>
<p><b>Location</b></p>	<p>QBP, Building 80, St Lucia campus and/or Building 8150, Gatton campus</p>
<p><b>Webpage</b></p>	<p><a href="http://researchers.uq.edu.au/researcher/16777">http://researchers.uq.edu.au/researcher/16777</a></p>
<p><b>Useful majors</b></p>	<p>Biochemistry &amp; Molecular Biology / Chemical Sciences / Chemistry / Genetics / Microbiology</p>



<p><b>CAS 6 to 17 Project</b></p> <p><i>Prof Ben Hayes</i></p> <p><i>Dr Elizabeth Ross</i></p> <p><i>Dr Loan Nguyen</i></p>	<p><b>6) <u>Structural Issues: Identification of large structural variants in the bovine genome using real time long read sequencing</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p> 
<p><b>CAS 6 to 17 Project</b></p> <p><i>Prof Ben Hayes</i></p> <p><i>Dr Elizabeth Ross</i></p> <p><i>Dr Loan Nguyen</i></p>	<p><b>7) <u>Combining omics: Examining genome structure and function for health and welfare</u></b></p> <p>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.</p>



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



**CAS  
6 to 17  
Project**

*Prof Ben  
Hayes*

*Dr  
Elizabeth  
Ross*

*Dr Loan  
Nguyen*

## 8) Filling the gap: completing the Brahman reference assembly

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

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



**CAS  
6 to 17  
Project**

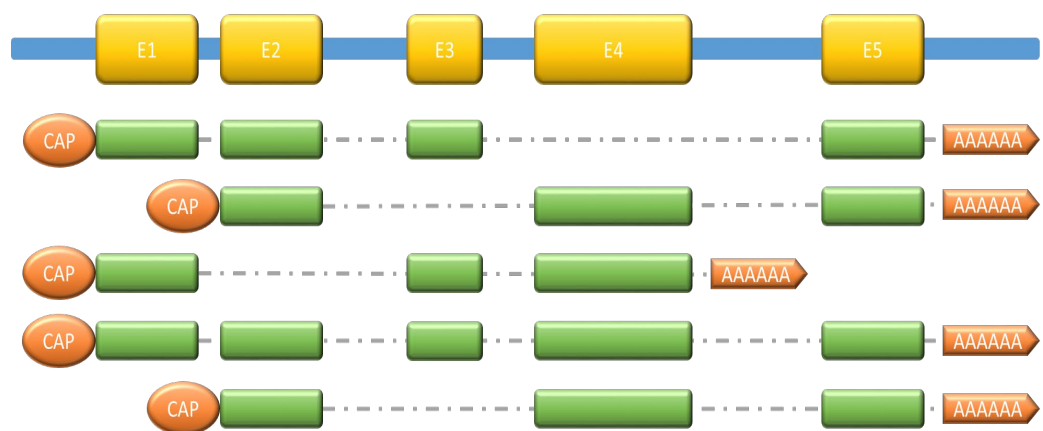
*Prof Ben  
Hayes*

*Dr  
Elizabeth  
Ross*

*Dr Loan  
Nguyen*

## 9) Form and Function: Novel isoform discovery

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



**CAS  
6 to 17  
Project**

*Prof Ben  
Hayes*

*Dr  
Elizabeth  
Ross*

*Dr Loan  
Nguyen*


## 10) Predicting age using methylated sites

In humans, the methylation state of CpG sites changes with age and can therefore be utilized as an accurate biomarker for aging. In cattle, biological age prediction based on methylation status could provide key information for genetic improvement programs. Additionally, comparing chronological age with biological age (based on methylation status) can provide important information about the stress an animal has been under during its lifetime. However, relatively little is known about DNA methylation patterns in cattle. Students will use cutting edge data sources including reduce representation bisulphite sequencing data, whole genome bisulphite sequencing, long read sequencing and human methylation data to identify differentially methylated regions between old and young animals and validate those regions with modern molecular technologies. This project will require skills in bioinformatics as well as molecular biology. Students will learn how to manage very large sequence data sets.









Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, <a href="mailto:b.hayes@uq.edu.au">b.hayes@uq.edu.au</a> +61 7 334 62173</li> <li>• <b>Dr Elizabeth Ross</b>, <a href="mailto:e.ross@uq.edu.au">e.ross@uq.edu.au</a> +61 7 334 62162</li> <li>• <b>Dr Loan Nguyen</b>, <a href="mailto:t.nguyen3@uq.edu.au">t.nguyen3@uq.edu.au</a> +61 7 334 62179</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaaifi.uq.edu.au/centre-for-animal-science">https://qaaifi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Agriculture / Veterinary Medicine
<b>CAS 6 to 17 Project</b>  <i>Prof Ben Hayes</i>  <i>Dr Kai Voss-Fels</i>  <i>Dr Eric Dinglasan</i>	<p><b>11) <u>FastStack - evolutionary computing to stack desirable alleles in wheat</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p> <p>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).</p> 
Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, <a href="mailto:b.hayes@uq.edu.au">b.hayes@uq.edu.au</a> +61 7 334 62173</li> <li>• <b>Dr Kai Voss-Fels</b>, <a href="mailto:k.vossfels@uq.edu.au">k.vossfels@uq.edu.au</a> +61 7 334 62288</li> <li>• <b>Dr Eric Dinglasan</b>, <a href="mailto:e.dinglasan@uq.edu.au">e.dinglasan@uq.edu.au</a></li> </ul>




Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaaifi.uq.edu.au/centre-for-animal-science">https://qaaifi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics / Agriculture
<b>CAS 6 to 17 Project</b>  <i>Prof Ben Hayes</i>  <i>Dr Elizabeth Ross</i>	<p><b>12) <u>Reducing methane emissions through improved understanding of the rumen microbiome</u></b></p> <p>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.</p> <p>In this project students will develop molecular genetics, bioinformatics, quantitative genetics, and analysis skills in a fast developing area of research.</p> 
Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, <a href="mailto:b.hayes@uq.edu.au">b.hayes@uq.edu.au</a> +61 7 334 62173</li> <li>• <b>Dr Elizabeth Ross</b>, <a href="mailto:e.ross@uq.edu.au">e.ross@uq.edu.au</a> +61 7 334 62162</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaaifi.uq.edu.au/centre-for-animal-science">https://qaaifi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Microbiology / Agriculture / Veterinary Medicine
<b>CAS 6 to 17 Project</b>  <i>Prof Ben Hayes</i>  <i>Dr Bailey Engle</i>	<p><b>13) <u>Cow fertility through the ages</u></b></p> <p>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.</p> <p>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</p>

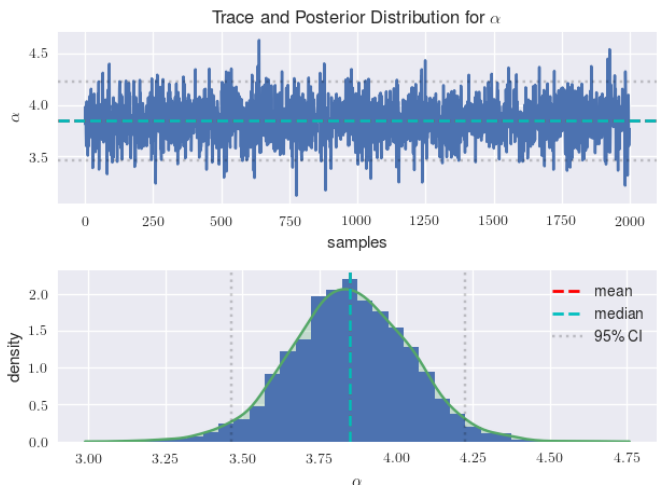
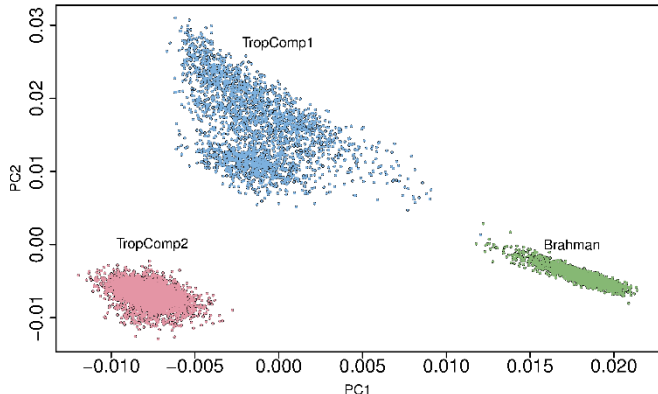



	<p>genetics, and industry relevance to help improve cow fertility in the north Australian beef industry.</p> <p>In this project students will develop data analysis and quantitative genetics skills, and will learn techniques to handle extremely large biological data sets. Students will have the opportunity to learn genomic selection techniques.</p> 
Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, <a href="mailto:b.hayes@uq.edu.au">b.hayes@uq.edu.au</a> +61 7 334 62173</li> <li>• <b>Dr Bailey Engle</b>, <a href="mailto:b.engele@uq.edu.au">b.engele@uq.edu.au</a> +61 7 334 66506</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/centre-for-animal-science">https://qaafi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics / Agriculture / Veterinary Medicine
<b>CAS 6 to 17 Project</b>  <i>Prof Ben Hayes</i>  <i>Dr Elizabeth Ross</i>  <i>Dr Loan Nguyen</i>  <i>Dr Bailey Engle</i>	<p><b>14) <u>Genes impacting female fertility</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p>

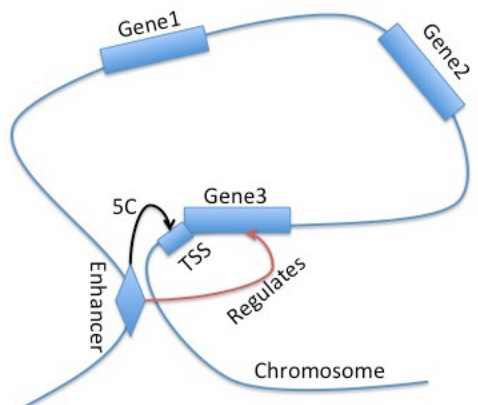




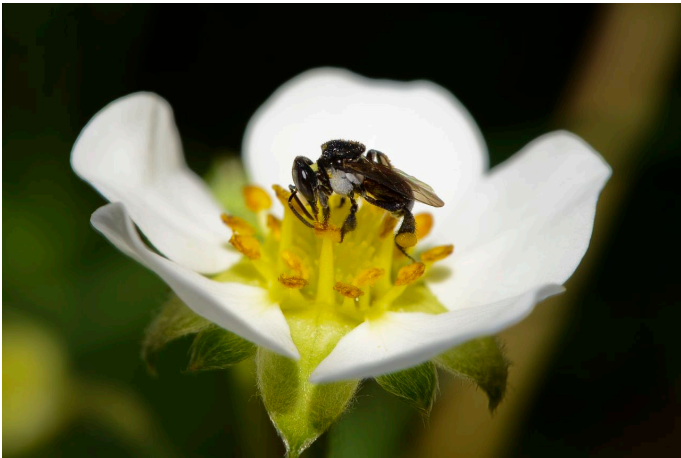
	
Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, b.hayes@uq.edu.au +61 7 334 62173</li> <li>• <b>Dr Elizabeth Ross</b>, e.ross@uq.edu.au +61 7 334 62162</li> <li>• <b>Dr Loan Nguyen</b>, t.nguyen3@uq.edu.au +61 7 334 62179</li> <li>• <b>Dr Bailey Engle</b>, b.engle@uq.edu.au +61 7 334 66506</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/centre-for-animal-science">https://qaafi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Computational Science / Genetics / Agriculture / Veterinary Medicine
<b>CAS 6 to 17 Project</b>  <i>Prof Ben Hayes</i>  <i>Dr Roy Costilla</i>	<p><b>15) <u>The need for speed in Genomic research: Comparing algorithms to estimate polygenic effects in tropically adapted beef cattle</u></b></p> <p>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.</p>

	<p>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.</p> 
<p><b>CAS 6 to 17 Project</b></p> <p><i>Prof Ben Hayes</i></p> <p><i>Dr Roy Costilla</i></p>	<p><b>16) <u>Improving genotype imputation in the tropics: using Bos indicus reference populations for tropically adapted beef cattle</u></b></p> <p>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.</p> <p>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.</p>  




Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, b.hayes@uq.edu.au +61 7 334 62173</li> <li>• <b>Dr Roy Costilla</b>, r.costilla@uq.edu.au +61 7 334 62179</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/centre-for-animal-science">https://qaafi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics
<b>CAS 6 to 17 Project</b>  <i>Prof Ben Hayes</i>  <i>Dr Mehrnush Forutan</i>	<p><b>17) <u>Exploring TSS-enhancer correlations and identification of novel mutations in TSS-enhancer regions in Bos indicus species</u></b></p> <p>Next generation sequencing technologies including Cap-Analysis of Gene Expression (CAGE) have made it possible to accurately identify and quantify transcriptional start sites (TSSs) and enhancer throughout the genome. Having access to both TSSs and enhancers in a single experiment makes CAGE well suited for studying many aspects of transcriptional regulation, for example TSS-enhancer correlations, super enhancer identification, mutation discovery in TSS-enhancer regions, etc. This study will analyse the CAGE-tags mapped to the Bos taurus reference genome to identify CAGE-enhancer and explore the TSS-enhancer correlation and discovery of novel mutation in TSS and enhancer. In this project students will develop molecular genetics, bioinformatics, quantitative genetics, and analysis skills in a fast developing area of research.</p> 
Advisors contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, b.hayes@uq.edu.au +61 7 334 62173</li> <li>• <b>Dr Mehrnush Forutan</b>, m.forutan@uq.edu.au</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/centre-for-animal-science">https://qaafi.uq.edu.au/centre-for-animal-science</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Computational Science / Genetics



<p><b>CAS 18 Project</b></p> <p><i>Prof Mary Fletcher</i></p> <p><i>Dr Natasha Hungerford</i></p> <p><i>Dr Tobias Smith</i> (School of Biological Sciences)</p>	<p><b>18) <u>Investigation of trehalulose content of different stingless bee species</u></b></p> <p>Stingless bee honey has recently been shown to contain high levels of the unusual disaccharide sugar trehalulose (Fletcher et al 2020). Trehalulose is known to have beneficial properties such as having a low glycaemic index (low GI) and being acariogenic (tooth friendly). Trehalulose is an isomer of sucrose and has not previously been found as a major component in any other food, so the presence of this sugar in high proportions in Australian stingless bee honey is an exciting discovery. This project will examine the level of trehalulose in honey from related stingless bee species in Brazil.</p>  <p>This project will be located in laboratories at Health and Food Sciences Precinct, Coopers Plains (Brisbane) and utilise Ion Chromatography (IC-PAD) and also Liquid Chromatography Mass Spectrometry (LC-MS).</p> <p><b>Reference:</b> 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> <b>10</b>, 12128. <a href="https://doi.org/10.1038/s41598-020-68940-0">https://doi.org/10.1038/s41598-020-68940-0</a></p>
<p>Advisors contact</p>	<ul style="list-style-type: none"> <li>• <b>Prof Mary Fletcher</b>, <a href="mailto:mary.fletcher@uq.edu.au">mary.fletcher@uq.edu.au</a> +61 7 344 32479</li> <li>• <b>Dr Natasha Hungerford</b>, <a href="mailto:n.hungerford@uq.edu.au">n.hungerford@uq.edu.au</a> +61 7 344 32473</li> <li>• <b>Dr Tobias Smith</b>, <a href="mailto:t.smith5@uq.edu.au">t.smith5@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Health and Food Sciences Precinct, Coopers Plains</p>
<p>Webpage</p>	<p><a href="http://researchers.uq.edu.au/researcher/235">http://researchers.uq.edu.au/researcher/235</a></p> <p><a href="https://researchers.uq.edu.au/researcher/20086">https://researchers.uq.edu.au/researcher/20086</a></p> <p><a href="https://biological-sciences.uq.edu.au/profile/804/tobias-smith">https://biological-sciences.uq.edu.au/profile/804/tobias-smith</a></p>
<p>Useful Majors</p>	<p>Chemistry/ Chemical sciences/ Biochemistry &amp; Molecular Biology</p>



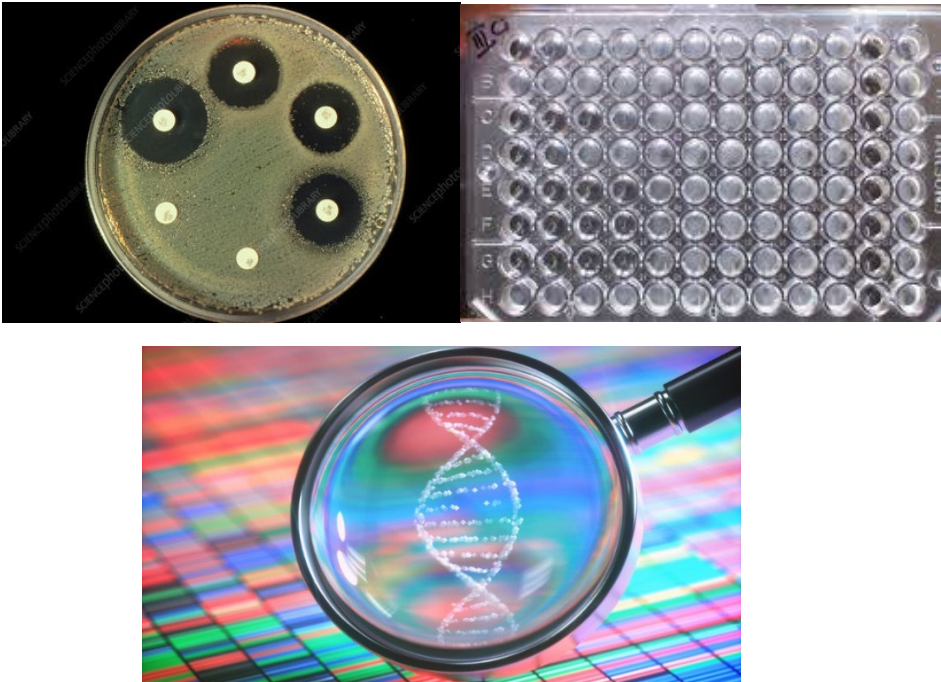


<p><b>CAS 19 Project</b></p> <p><i>Dr Lida Omaleki</i></p> <p><i>Dr Conny Turni</i></p> <p><i>Dr. Noman Naseem</i></p>	<p><b><u>19) CRISPER-CAS system in bacterial pathogen diagnosis and typing</u></b></p> <p>Chicken is the most consumed meat in Australia. Fowl cholera caused by <i>P. multocida</i> is 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.</p>  <p>Free range layer chickens</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Dr Lida Omaleki, l.omalaki@uq.edu.au</li> <li>• Associate Advisor: Dr Conny Turni, c.turni1@uq.edu.au</li> <li>• Associate Advisor: Dr. Noman Naseem: m.naseem@uq.edu.au</li> </ul>
<p>Location</p>	<p>EcoSciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/2477">https://researchers.uq.edu.au/researcher/2477</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Microbiology</p>

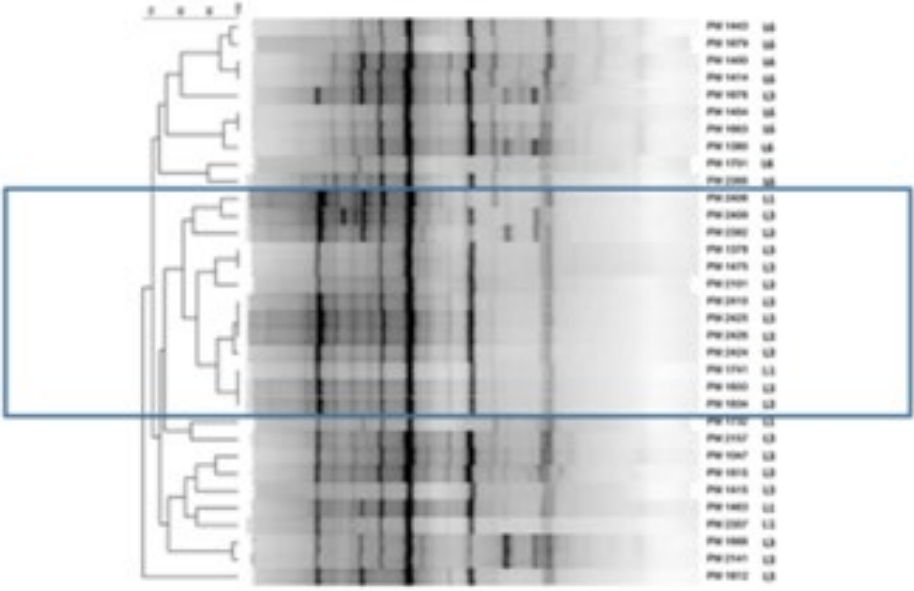


<p><b>CAS 20 Project</b></p> <p><i>Dr Conny Turni</i></p> <p><i>Dr Lida Omaleki</i></p>	<p><b><u>20) Pangenome analysis of avian <i>Pasteurella multocida</i></u></b></p> <p><i>Pasteurella multocida</i> is the cause of fowl cholera, an economically important disease that has re-emerged in both meat chickens 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.</p> <div data-bbox="360 734 805 1019" data-label="Image"></div> <div data-bbox="805 840 1356 1019" data-label="Figure"></div> <p>Fowl cholera outbreak in meat chickens      Whole genome analysis</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Dr Lida Omaleki, l.omal eki@uq.edu.au</li> <li>• Associate Advisor: Dr Conny Turni, c.turni1@uq.edu.au</li> <li>• Associate Advisor: Dr. Noman Naseem: m.naseem@uq.edu.au</li> </ul>
<p>Location</p>	<p>EcoSciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/2477">https://researchers.uq.edu.au/researcher/2477</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Microbiology</p>



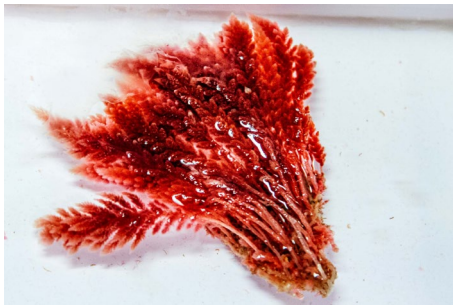
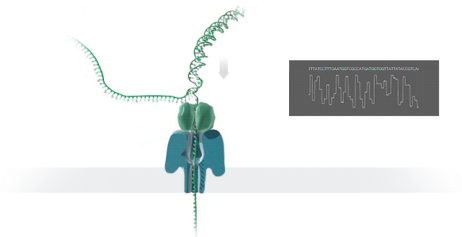
<p><b>CAS 21 Project</b></p> <p><i>Dr Lida Omaleki</i></p> <p><i>Dr Conny Turni</i></p>	<p><b><u>21) Phenotypic and genotypic aspects of antimicrobial resistance in porcine <i>Pasteurella multocida</i></u></b></p> <p><i>Pasteurella multocida</i> is associated with porcine respiratory disease complex, 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.</p> <div data-bbox="362 947 1307 1626">  </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Dr Lida Omaleki, l.omal eki@uq.edu.au</li> <li>• Associate Advisor: Dr Conny Turni, c.turni1@uq.edu.au</li> <li>• Associate Advisor: Dr. Noman Naseem: m.naseem@uq.edu.au</li> </ul>
<p>Location</p>	<p>EcoSciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/2477">https://researchers.uq.edu.au/researcher/2477</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Microbiology</p>



<p><b>CAS 22 Project</b></p> <p><i>Dr Conny Turni</i></p> <p><i>Dr Lida Omaleki</i></p>	<p><b><u>22) Is <i>Pasteurella multocida</i> the primary pathogen in outbreaks of swine diseases?</u></b></p> <p><i>Pasteurella multocida</i> 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 <i>P. multocida</i> 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 <i>P. multocida</i>. Thus, it was hypothesized that the virulence factor profiles of these <i>P. multocida</i> isolates might be different from those considered secondary pathogens. The objective of this study is to compare the virulence factors profile of porcine <i>P. multocida</i> isolates from disease outbreaks where the organism appears to be the primary pathogen with isolates from disease outbreaks where no primary role of <i>P. multocida</i> 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.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Conny Turni</b>, c.turni1@uq.edu.au +61 7 344 32463</li> <li>• Associate Advisor: <b>Dr Lida Omaleki</b>, l.omaleki@uq.edu.au +61 7 344 32576</li> </ul>
<p>Location</p>	<p>EcoSciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/2477">https://researchers.uq.edu.au/researcher/2477</a></p>





Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Microbiology
<p><b>CAS 23 Project</b></p> <p><i>Prof Ben Hayes</i></p> <p><i>Dr Loan Nguyen</i></p> <p><i>Dr Elizabeth Ross</i></p>	<p><b>23) <u>Discovering methane reducing pathways in seaweed</u></b></p> <p>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 (<i>Asparagopsis taxiformis</i>) 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.</p> <div style="display: flex; justify-content: space-around; align-items: center;">   </div>
Advisor(s) contact	<ul style="list-style-type: none"> <li>• <b>Prof Ben Hayes</b>, b.hayes@uq.edu.au +61 7 334 62173</li> <li>• Associate Advisor: Dr Loan Nguyen, <a href="mailto:t.nguyen3@uq.edu.au">t.nguyen3@uq.edu.au</a> +61 7 334 62179</li> <li>• Associate Advisor: Dr Elizabeth Ross, <a href="mailto:e.ross@uq.edu.au">e.ross@uq.edu.au</a> +61 7 334 62162</li> </ul>
Location	Queensland Alliance for Agriculture and Food Innovation, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/profile/1059/ben-hayes">https://qaafi.uq.edu.au/profile/1059/ben-hayes</a>
Useful majors	<p>Please select from:</p> <p>Biochemistry &amp; Molecular Biology / Bioinformatics / Computational Science / Genetics</p>

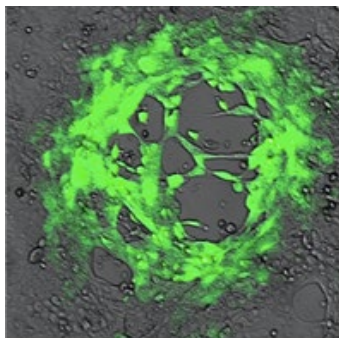
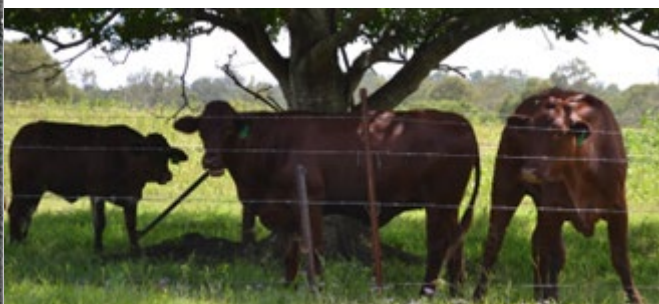


<p><b>CAS 24 Project</b></p> <p><i>Dr Ali Raza</i></p> <p><i>Professor Ala Tabor</i></p>	<p><b>24) Title – Understanding host biology to cattle tick infestation</b></p> <p>The cattle tick, <i>Rhipicephalus microplus</i>, and the diseases it transmits lead to massive economic losses to cattle industries 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.</p> <p>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.</p> <p>The student will gain skills in Mass Spectrometry, Data analysis with variety of software and various online database resources for functional annotation of the proteins.</p> <div data-bbox="357 1122 528 1301"> </div> <div data-bbox="564 1122 855 1317"> </div> <div data-bbox="890 1070 1050 1279"> </div> <div data-bbox="1091 1070 1337 1265"> </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Ali Raza</b>, <a href="mailto:a.raza@uq.edu.au">a.raza@uq.edu.au</a> +61 7 334 62317</li> <li>• Associate Advisor: Professor Ala Tabor, <a href="mailto:a.tabor@uq.edu.au">a.tabor@uq.edu.au</a> +61 7 334 62176</li> </ul>
<p>Location</p>	<p>QBP, Building 80, St Lucia campus</p>
<p>Webpage</p>	<p><a href="#">Dr Ali Raza - UQ Researchers</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Biotechnology</p>



<p><b>CAS 25 to 29 Projects</b></p> <p><i>Prof Tim Mahony</i></p>	<p><b><u>25) The application of gene editing to improve animal resistance to infections</u></b></p> <p>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.</p> <p><b><u>26) Construction of bovine herpesvirus 5 infectious clone</u></b></p> <p>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.</p> <p><b><u>27) Characterisation of bovine herpesvirus 2 genome</u></b></p> <p>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.</p> <p><b><u>28) The application of synthetic biology to large DNA viral genomes</u></b></p> <p>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.</p> <p><b><u>29) The development of strand-specific sequencing methodologies double-stranded DNA viral genomes</u></b></p> <p>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,</p>
---	---

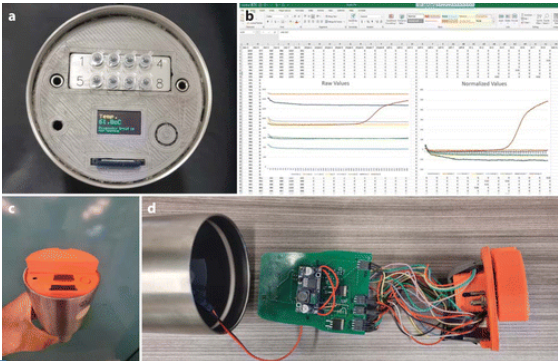



	<p>variants with increased capacity to cause disease have emerged. The molecular basis underpinning the emergence of these virulent subtypes/genotypes for several herpesviruses of importance to veterinary medicine remains poorly understood. This project will utilise Oxford Nanopore sequencing technology to develop strategies to enable the strand-specific sequencing of herpesvirus genomes. The availability of strand-specific sequence data will be used to determine if the emergence of new genotypes of herpesviruses is a result of spontaneous mutation or the selection of existing genetic diversity within a viral isolate. This new knowledge will improve our understanding of this important virus family.</p> <div style="display: flex; justify-content: space-around;">   </div> <p>Candidates with their own project ideas that fit within the research activities described on Prof Mahony's profile page are encouraged to contact him.</p>
Advisor/s Contact	<b>Prof Tim Mahony</b> , <a href="mailto:t.mahony@uq.edu.au">t.mahony@uq.edu.au</a> x66505
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://qaafi.uq.edu.au/profile/486/timothy-mahony">https://qaafi.uq.edu.au/profile/486/timothy-mahony</a>

<p><b>CAS 30 Project</b></p> <p><i>Dr Noman Naseem</i></p>	<p><b>30) <u>Development of Isothermal LAMP Assay for Point of Management (POM) Detection of Swine Colibacillosis</u></b></p> <p><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</p>
--	--






	<p>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).</p>  <p>BentoLab Device – our remote lab for on farm testing</p>  <p>Diagnostic Droid by Botella Lab</p>
<b>Advisor(s) contact</b>	<ul style="list-style-type: none"> <li>• Dr Noman Naseem (<a href="mailto:m.naseem@uq.edu.au">m.naseem@uq.edu.au</a>)</li> <li>• Associate Advisor - Dr Conny Turni</li> <li>• Dr Lida Omaleki</li> </ul> <p><b>Location:</b> EcoSciences Precinct, Dutton Park</p>
<b>Webpage</b>	<a href="https://qaafi.uq.edu.au/profile/5083/noman-naseem">https://qaafi.uq.edu.au/profile/5083/noman-naseem</a>
<b>Useful majors</b>	Biochemistry & Molecular Biology / Bioinformatics / Microbiology

<p><b>CAS 31 Project</b></p> <p><i>Dr Noman Naseem</i></p>	<p><b>31) Development of Isothermal LAMP Assay for Point of Management (POM) Detection of Swine Colibacillosis</b></p> <p><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).</p> <div data-bbox="395 1055 767 1317"> </div> <p>BentoLab Device – our remote lab for on farm testing</p> <div data-bbox="815 965 1374 1323"> </div> <p>Diagnostic Droid by Botella Lab</p>
<p><b>Advisor(s) contact</b></p>	<ul style="list-style-type: none"> <li>• Dr Noman Naseem (<a href="mailto:m.naseem@uq.edu.au">m.naseem@uq.edu.au</a>)</li> <li>• Associate Advisor - Dr Conny Turni</li> <li>• Dr Lida Omaleki</li> </ul> <p><b>Location:</b> EcoSciences Precinct, Dutton Park</p>
<p><b>Webpage</b></p>	<p><a href="https://qaafi.uq.edu.au/profile/5083/noman-naseem">https://qaafi.uq.edu.au/profile/5083/noman-naseem</a></p>
<p><b>Useful majors</b></p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Microbiology</p>

<p><b>CAS 32 Project</b></p>	<p><b>32) <u>Determining bioactive release rates for slow degrading biocomposites for methane mitigation in cattle</u></b></p> <p>This industry-focused Honours project will focus on chemical analysis of bioactive in both biopolymer composites and in solution to determine release rates in different situations and over time. Biopolymer 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 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.</p> <p>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.</p> <div data-bbox="470 1019 1305 1272"> </div> <p>Created with BioRender.com</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Natasha Hungerford</b>, <a href="mailto:n.hungerford@uq.edu.au">n.hungerford@uq.edu.au</a> +61 7 344 32473</li> <li>• <b>Prof Mary Fletcher</b>, <a href="mailto:mary.fletcher@uq.edu.au">mary.fletcher@uq.edu.au</a> +61 7 344 32479</li> </ul>
<p>Location</p>	<p>Health and Food Sciences Precinct, Coopers Plains</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/20086">https://researchers.uq.edu.au/researcher/20086</a></p> <p><a href="http://researchers.uq.edu.au/researcher/235">http://researchers.uq.edu.au/researcher/235</a></p>
<p>Useful majors</p>	<p>Chemical Sciences / Chemistry / Biochemistry &amp; Molecular Biology</p>




# Centre for Nutrition and Food Sciences Projects

<p><b>CNAFS 1 Project</b></p> <p><i>A/Prof Yasmina Sultanbawa</i></p> <p><i>Dr Anh Phan</i></p>	<p><b>1) <u>Nutritional and bioactive properties of Australian boab (<i>Adansonia gregorii</i>): an emerging functional food ingredient</u></b></p> <p>Boab (<i>Adansonia gregorii</i>) 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 (<i>Adansonia digitata</i>) 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.</p> <p>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.</p> 
<p>Advisor(s)</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Yasmina Sultanbawa</b>, <a href="mailto:y.sultanbawa@uq.edu.au">y.sultanbawa@uq.edu.au</a> +61 7 344 32471</li> <li>• <b>Dr Anh Phan</b>, <a href="mailto:a.phan1@uq.edu.au">a.phan1@uq.edu.au</a> +61 7 344 32476</li> </ul>
<p>Location</p>	<p>Elkhorn Building, Long Pocket Campus</p>
<p>Webpage</p>	<p><a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a>; <a href="http://www.uniquelyaustralianfoods.org">www.uniquelyaustralianfoods.org</a></p>
<p>Useful majors</p>	<p>Biochemistry, Chemistry, Microbiology, Agriculture, Food Science</p>






<p><b>CNAFS 2 Project</b></p> <p><i>A/Prof Yasmina Sultanbawa</i></p> <p><i>Dr Oladapo Olukomaiya</i></p>	<p><b>2) <u>Bioprocessing of seaweed into protein-enriched food product: effect of solid-state fermentation on the physicochemical, functional properties and extraction of bioactive compounds</u></b></p> <p>Seaweed is a high-yield crop, with productivity levels as high as a dense terrestrial vegetation. It is the largest aquaculture crop in the world with more than 25 million tonnes of seaweed produced per annum, which is steadily increasing at a rate of 8% per year and represents a \$US7 billion-dollar aquaculture industry. Seaweed can have versatility and diversity in its use. In addition to seaweed being an important food source for a growing human population, there is also a massive scope to increase the commercial side of the industry and to create optimistic environmental change at a grand scale. Some studies have reported on the potential of seaweed, including its chemical composition, functionality, and effectiveness in reducing methane emission in cattle. However, it is still unknown how solid-state fermented seaweed can mitigate climate change's ongoing problems and support the concept of a circular economy, as well as how this relates to the development of novel value-added products. This project aims to explore the effect of solid-state fermentation on the physicochemical, functional properties and extraction of bioactive compounds. Outcomes will help bridge the current knowledge gaps.</p> 
<p>Advisor(s)</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Yasmina Sultanbawa</b>, <a href="mailto:y.sultanbawa@uq.edu.au">y.sultanbawa@uq.edu.au</a> +61 7 344 32471</li> <li>• <b>Dr Oladapo Olukomaiya</b>, <a href="mailto:uqooluko@uq.edu.au">uqooluko@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Elkhorn Building, Long Pocket Campus</p>
<p>Webpage</p>	<p><a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a></p> <p><a href="http://www.uniquelyaustralianfoods.org">www.uniquelyaustralianfoods.org</a></p>
<p>Useful majors</p>	<p>Chemistry, Microbiology, Food Science</p>




<p><b>CNAFS 3 Project</b></p> <p><i>A/Prof Heather Smyth</i></p>	<p><b>3) <u>Food applications of native plant foods and ingredients</u></b></p> <p>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.</p> <p>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.</p> <div data-bbox="395 837 928 1191" data-label="Image"> </div> <div data-bbox="938 786 1356 1191" data-label="Image"> </div>
<p>Advisor(s)</p>	<p><b>A/Prof Heather Smyth</b>, <a href="mailto:h.smyth@uq.edu.au">h.smyth@uq.edu.au</a> +61 7 344 32469</p>
<p>Location</p>	<p>Elkhorn Building, Long Pocket Campus</p>
<p>Webpage</p>	<p><a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a> <a href="http://www.uniquelyaustralianfoods.org">www.uniquelyaustralianfoods.org</a></p>
<p>Useful majors</p>	<p>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:</p> <p>Biochemistry &amp; Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Microbiology / Agriculture / Food Science</p>




<b>CNAFS 4 Project</b>  <i>A/Prof Heather Smyth</i>	<p><b>4) <u>Impact of processing on honey quality</u></b></p> <p>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.</p> <p>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.</p> 
Advisor(s)	<b>A/Prof Heather Smyth</b> , <a href="mailto:h.smyth@uq.edu.au">h.smyth@uq.edu.au</a> +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
Webpage	<a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a> <a href="http://www.uniquelyaustralianfoods.org">www.uniquelyaustralianfoods.org</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Microbiology / Agriculture / Food Science / Entomology




<p><b>CNAFS 5 Project</b></p> <p><i>A/Prof Heather Smyth</i></p> <p><i>Dr Thoa Nguyen</i></p>	<p><b>5) <u>Flavour chemistry of tropical fruits</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p> 
<p>Advisor(s)</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Heather Smyth</b>, <a href="mailto:h.smyth@uq.edu.au">h.smyth@uq.edu.au</a> +61 7 344 32469</li> <li>• <b>Dr Thoa Nguyen</b>, <a href="mailto:thoa.nguyen@uq.edu.au">thoa.nguyen@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Elkhorn Building, Long Pocket Campus</p>
<p>Webpage</p>	<p><a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Computational Science / Food Science / Psychology</p>





<b>CNAFS 6 Project</b>  <i>A/Prof Heather Smyth</i>	<p><b>6) <u>Individual human variation and sensory experience</u></b></p> <p>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.</p> <p>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.</p> 
Advisor(s)	<b>A/Prof Heather Smyth</b> , <a href="mailto:h.smyth@uq.edu.au">h.smyth@uq.edu.au</a> +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
Webpage	<a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a>
Useful majors	<p>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:</p> <p>Biochemistry &amp; Molecular Biology / Bioinformatics / Chemical Sciences / Chemistry / Chemical Engineering / Agriculture / Food Science / Psychology</p>




<b>CNAFS 7 Project</b>  <i>A/Prof Heather Smyth</i>	<p><b>7) <u>Plant protein – towards better tasting meatless burgers</u></b></p> <p>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 been 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.</p> <p>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.</p> 
Advisor(s)	<b>A/Prof Heather Smyth</b> , <a href="mailto:h.smyth@uq.edu.au">h.smyth@uq.edu.au</a> +61 7 344 32469
Location	Elkhorn Building, Long Pocket Campus
Webpage	<a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a>
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Chemical Engineering / Agriculture / Food Science / Psychology



<p><b>CNAFS 8 Project</b></p> <p><i>Dr Tim O'Hare</i></p>	<p><b>8) <u>The effect of popping on carotenoid content in zeaxanthin-biofortified popcorn</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p> <p>The student will work as part of a larger team in QAAFI working on the Naturally Nutritious project.</p> <div data-bbox="360 1088 683 1330"></div> <div data-bbox="695 1088 1018 1330"></div> <div data-bbox="1023 1077 1377 1330"> <p>Chemical structures of Zeaxanthin, beta-Cryptoxanthin, and beta-Carotene are shown. Zeaxanthin is a xanthophyll carotenoid with two hydroxyl groups. beta-Cryptoxanthin is a xanthophyll carotenoid with one hydroxyl group. beta-Carotene is a tetraterpene carotenoid with no hydroxyl groups.</p> </div>
<p>Advisor(s)</p>	<p><b>Dr Tim O'Hare</b>, <a href="mailto:t.ohare@uq.edu.au">t.ohare@uq.edu.au</a> +61 7 535 15068</p>
<p>Location</p>	<p>Health and Food Sciences Precinct, Coopers Plains</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/459/tim-ohare">https://qaafi.uq.edu.au/profile/459/tim-ohare</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Chemistry / Agriculture / Horticulture / Food Science</p>



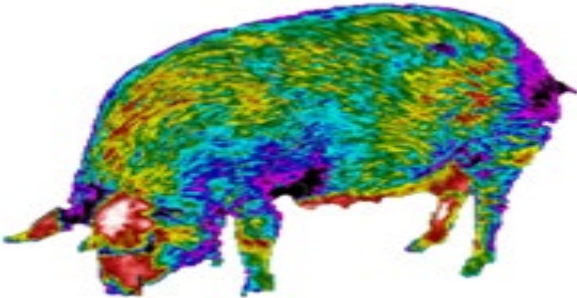
<b>CNAFS 9 Project</b>  <i>Dr Tim O'Hare</i>	<p><b>9) <u>Fresh and cooked purple sweetcorn aroma, chemical components and influence on flavour volatiles</u></b></p> <p>Sweetcorn aromas are volatile compounds which can be detected in fresh and cooked sweetcorn. Aroma compounds play an important role in 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.</p> <p>The aim of this study is to determine novel volatile compounds in purple sweetcorn (a new sweetcorn established by Tim O'Hare's research group), compared to commercial yellow sweetcorn using GC-MS. The student will work as part of a larger team in QAAFI working on Naturally Nutritious project.</p> <div data-bbox="416 842 1318 1245">Three ears of sweetcorn are shown. On the left, two ears of purple sweetcorn are displayed vertically, showing their deep purple kernels. On the right, three ears of yellow sweetcorn are shown, with their bright yellow kernels and green husks clearly visible.</div>
Advisor(s)	<b>Dr Tim O'Hare</b> , <a href="mailto:t.ohare@uq.edu.au">t.ohare@uq.edu.au</a> +61 7 535 15068
Location	Health and Food Sciences Precinct, Coopers Plains
Webpage	<a href="https://qaafi.uq.edu.au/profile/459/tim-ohare">https://qaafi.uq.edu.au/profile/459/tim-ohare</a>
Useful majors	Biochemistry & Molecular Biology / Chemistry / Agriculture / Horticulture / Food Science






<p><b>CNAFS 10 Project</b></p> <p><i>Dr Michael Netzel</i></p> <p><i>Dr Olivia Wright</i></p> <p><i>Dr Hung Trieu Hong</i></p> <p><i>Prof Yasmina Sultanbawa</i></p>	<p><b>10) <u>Exploring the nutritional value of Saltbush, an Australian indigenous edible Halophyte</u></b></p> <p>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 (<i>Atriplex</i> 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.</p> <div data-bbox="657 996 1112 1368" data-label="Image"></div> <p style="text-align: center;">Saltbush (<i>Atriplex</i> sp.)</p>
<p>Advisor(s)</p>	<ul style="list-style-type: none"> <li>• <b>Dr Michael Netzel</b>, <a href="mailto:m.netzel@uq.edu.au">m.netzel@uq.edu.au</a> M: 0400 887 072</li> <li>• <b>Dr Olivia Wright</b>, <a href="mailto:o.wright@uq.edu.au">o.wright@uq.edu.au</a> +61 7 336 56116</li> <li>• <b>Dr Hung Trieu Hong</b>, <a href="mailto:h.trieu@uq.edu.au">h.trieu@uq.edu.au</a></li> <li>• <b>Prof Yasmina Sultanbawa</b>, <a href="mailto:y.sultanbawa@uq.edu.au">y.sultanbawa@uq.edu.au</a> +61 7 344 32471</li> </ul>
<p>Location</p>	<p>Health and Food Sciences Precinct, Coopers Plains</p>
<p>Webpage</p>	<p><a href="http://www.qaafi.uq.edu.au">www.qaafi.uq.edu.au</a>; <a href="http://www.uniquelyaustralianfoods.org">www.uniquelyaustralianfoods.org</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Chemical Sciences / Chemistry / Agriculture / Food Science</p>



<p><b>CNAFS 11 Project</b></p> <p><i>Dr Marta Navarro</i></p> <p><i>Prof Eugeni Roura</i></p>	<p><b>11) <u>Metabolic resilience to heat stress in lactating sows</u></b></p> <p>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.</p> 
<p>Advisor(s)</p>	<ul style="list-style-type: none"> <li>• <b>Dr Marta Navarro</b>, <a href="mailto:m.navarrogomez@uq.edu.au">m.navarrogomez@uq.edu.au</a> 0458 999 192</li> <li>• <b>Prof Eugeni Roura</b>, <a href="mailto:e.roura@uq.edu.au">e.roura@uq.edu.au</a> +61 7 336 52526</li> </ul>
<p>Location</p>	<p>St Lucia or Gatton campus</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/26066">https://researchers.uq.edu.au/researcher/26066</a></p> <p><a href="https://qaafi.uq.edu.au/profile/429/eugeni-roura">https://qaafi.uq.edu.au/profile/429/eugeni-roura</a></p>
<p>Useful majors</p>	<p>Animal or Veterinary Sciences/ Nutrition / Biomedical Science / Computational Science / Microbiology</p>



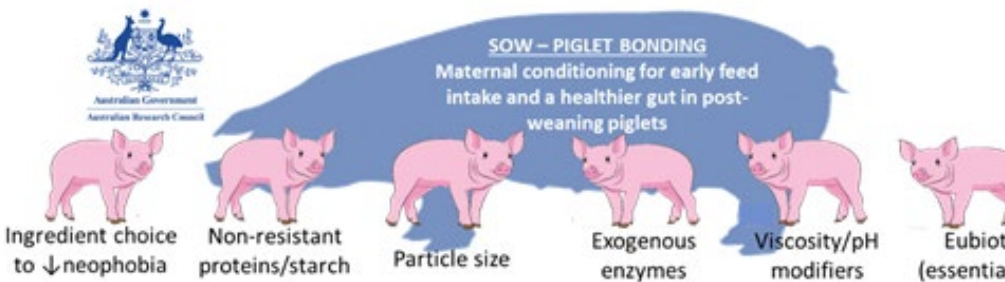
<p><b>CNAFS 12 Project</b></p> <p><i>Dr Shahram Niknafs</i></p> <p><i>Prof Eugeni Roura</i></p>	<p><b>12) <u>Peri-hatching programs that naturally improve chicken gut health</u></b></p> <p>Chicken's gastrointestinal tract undergoes significant physiological changes during the first days after hatch, 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.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Shahram Niknafs</b>, s.niknafs@uq.edu.au 0468 691 705</li> <li>• <b>Prof Eugeni Roura</b>, <a href="mailto:e.roura@uq.edu.au">e.roura@uq.edu.au</a> +61 7 336 52526</li> </ul>
<p>Location</p>	<p>St Lucia or Gatton campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/429/eugeni-roura">https://qaafi.uq.edu.au/profile/429/eugeni-roura</a></p> <p><a href="http://researchers.uq.edu.au/researcher/24913">http://researchers.uq.edu.au/researcher/24913</a></p>
<p>Useful majors</p>	<p>Animal or Veterinary Sciences/ Nutrition / Biomedical Science / Computational Science / Microbiology</p>



<p><b>CNAFS 13 Project</b></p> <p><i>Dr Shahram Niknafs</i></p> <p><i>Prof Eugeni Roura</i></p>	<p><b>13) Dietary fibre involvement in gut-brain dialogues</b></p> <p>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.</p> <div data-bbox="395 958 805 1265"> </div> <div data-bbox="826 817 1385 1265"> </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Shahram Niknafs</b>, s.niknafs@uq.edu.au 0468 691 705</li> <li>• <b>Prof Eugeni Roura</b>, e.roura@uq.edu.au, +61 7 336 52526</li> </ul>
<p>Location</p>	<p>St Lucia or Gatton campuses</p>
<p>Webpage</p>	<p><a href="http://researchers.uq.edu.au/researcher/24913">http://researchers.uq.edu.au/researcher/24913</a></p> <p><a href="https://qaafi.uq.edu.au/profile/429/eugeni-roura">https://qaafi.uq.edu.au/profile/429/eugeni-roura</a></p>
<p>Useful majors</p>	<p>Animal or Veterinary Sciences/ Nutrition / Biochemistry &amp; Molecular Biology / Bioinformatics / Biomedical Science/ Genetics / Microbiology</p>





<p><b>CNAFS 14 Project</b></p> <p><i>Dr Marta Navarro</i></p> <p><i>Prof Eugeni Roura</i></p>	<p><b>14) <u>How to make antibiotics in pig feed redundant, naturally</u></b></p> <p>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.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Marta Navarro</b>, <a href="mailto:m.navarrogomez@uq.edu.au">m.navarrogomez@uq.edu.au</a> 0458999192</li> <li>• <b>Prof Eugeni Roura</b>, <a href="mailto:e.roura@uq.edu.au">e.roura@uq.edu.au</a> +61 7 336 52526</li> </ul>
<p>Location</p>	<p>St Lucia or Gatton campus</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/26066">https://researchers.uq.edu.au/researcher/26066</a></p> <p><a href="https://qaafi.uq.edu.au/profile/429/eugeni-roura">https://qaafi.uq.edu.au/profile/429/eugeni-roura</a></p>
<p>Useful majors</p>	<p>Animal or Veterinary Sciences/ Nutrition/ Biochemistry &amp; Molecular Biology / Biomedical Sciences/ Immunology/ Microbiology</p>



<b>CNAFS 15 Project</b>  <i>A/Prof Daniel Cozzolino</i>  <i>Prof Louw Hoffman</i>	<b>15) <u>Non-invasive and non-destructive analytical methods for food evaluation</u></b>  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	<ul style="list-style-type: none"><li>• <b>A/Prof Daniel Cozzolino</b>, <a href="mailto:d.cozzolino@uq.edu.au">d.cozzolino@uq.edu.au</a> +61 7 336 52144</li><li>• Associate Advisors: Prof Louw Hoffman, <a href="mailto:louwrens.hoffman@uq.edu.au">louwrens.hoffman@uq.edu.au</a> +61 7 344 32602</li></ul>
Location	St Lucia Campus or Gatton Campus
Webpage	<a href="https://qaafi.uq.edu.au/profile/6668/daniel-cozzolino">https://qaafi.uq.edu.au/profile/6668/daniel-cozzolino</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics / Biomedical Science / Biophysics / Chemical Sciences / Chemistry / Computational Science / Genetics / Microbiology




<p><b>CNAFS 16 Project</b></p> <p><i>A/Prof Daniel Cozzolino</i></p> <p><i>Prof Louw Hoffman</i></p>	<p><b>16) <u>Sensors and math to assure value and provenance in the food chain</u></b></p> <p>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.</p> <p>The aim of this project is to develop protocols and test analytical methods based in vibrational spectroscopy sensors combined with multivariate data analysis to trace and authenticate the value and provenance of foods of economic importance in order to ensure the integrity of the food value chain.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Daniel Cozzolino</b>, <a href="mailto:d.cozzolino@uq.edu.au">d.cozzolino@uq.edu.au</a> +61 7 336 52144</li> <li>• Associate Advisors: Prof Louw Hoffman, <a href="mailto:louwrens.hoffman@uq.edu.au">louwrens.hoffman@uq.edu.au</a> +61 7 344 32602</li> </ul>
<p>Location</p>	<p>St Lucia Campus or Gatton Campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/6668/daniel-cozzolino">https://qaafi.uq.edu.au/profile/6668/daniel-cozzolino</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Biomedical Science / Biophysics / Chemical Sciences / Chemistry / Computational Science / Genetics / Microbiology</p>



<p><b>CNAFS 17 Project</b></p> <p><i>Prof Louw Hoffman</i></p> <p><i>Prof Eugeni Roura</i></p> <p><i>A/Prof Daniel Cozzolino</i></p>	<p><b>17) <u>Is chicken breast becoming spaghetti meat?</u></b></p> <p>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.</p> <p>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.</p> <div data-bbox="638 1030 1112 1462" data-label="Image"> </div> <p>Figure 1 A chicken breast showing the woody breast syndrome.</p>
<p>Advisor(s)</p>	<ul style="list-style-type: none"> <li>• <b>Prof Louw Hoffman</b>, <a href="mailto:Louwrens.hoffman@uq.edu.au">Louwrens.hoffman@uq.edu.au</a> +61 7 344 32602</li> <li>• Associate Advisors: Prof Eugeni Roura, <a href="mailto:e.roura@uq.edu.au">e.roura@uq.edu.au</a> +61 7 336 52526</li> <li>• Associate Advisors: A/Prof Daniel Cozzolino, <a href="mailto:d.cozzolino@uq.edu.au">d.cozzolino@uq.edu.au</a> +61 7 336 52144</li> </ul>
<p>Location</p>	<p>St Lucia or Gatton campus</p>
<p>Webpage</p>	<p><a href="https://qaaifi.uq.edu.au/profile/4974/louw-hoffman">https://qaaifi.uq.edu.au/profile/4974/louw-hoffman</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Chemical Sciences / Chemistry / Microbiology / Agriculture / Animal Science</p>




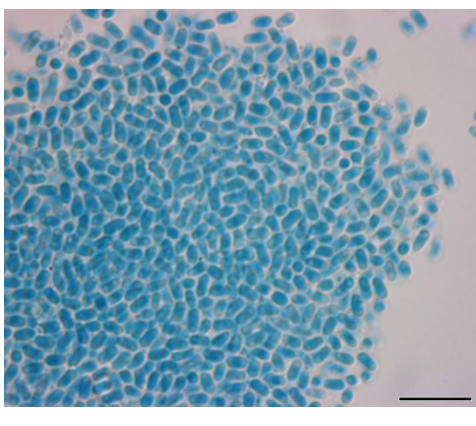
<b>CNAFS 18 Project</b>  <i>Prof Louw Hoffman</i>  <i>Dr Deirdre Mikkelsen</i>	<p><b>18) <u>Black soldier fly fit for nutrition</u></b></p> <p>Most of Australia's 7 million tons of waste come from post-consumer waste streams with most of it is going to landfill. With the global drive to up-stream this 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.</p> <p>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.</p>  <p>Figure 1 Black soldier fly larvae at point of harvest.</p>
Advisor(s)	<ul style="list-style-type: none"><li>• <b>Prof Louw Hoffman</b>, <a href="mailto:Louwrens.hoffman@uq.edu.au">Louwrens.hoffman@uq.edu.au</a> +61 7 344 32602</li><li>• Associate Advisors: Dr Deirdre Mikkelsen, <a href="mailto:d.mikkelsen@uq.edu.au">d.mikkelsen@uq.edu.au</a> +61 7 334 69642</li></ul>
Location	St Lucia or Gatton campus
Webpage	<a href="https://qaafi.uq.edu.au/profile/4974/louw-hoffman">https://qaafi.uq.edu.au/profile/4974/louw-hoffman</a>
Useful majors	Biochemistry & Molecular Biology / Chemical Sciences / Chemistry / Microbiology





# Centre for Horticultural Science Projects

<p><b>CHS 1 Project</b></p> <p><i>Dr Lilia Costa Carvalhais</i></p> <p><i>Prof Andre Drenth</i></p> <p><i>Dr Alistair McTaggart</i></p> <p><i>Dr Vivian Rincon-Florez</i></p>	<p><b>1) <u>Sex in banana fungi</u></b></p> <p>Bananas are the fourth most important food crop worldwide, surpassed only by crops such as rice, maize and wheat. The production, consumption and trade can be greatly affected by pests and mainly fungal diseases such as Sigatoka leaf spot and Fusarium wilt. The spread of the Fusarium wilt race 1 in the last century led to the replacement of Gros Michel by Cavendish variety, which is resistant to this particular race. However, new pathogens strains are constantly emerging, such as the tropical race 4 (TR4) which has been devastating banana plantations after invasion. The origins of diversity in fungal pathogens usually stem from sexual reproduction and the objective of the project you will be involved in is to gain knowledge concerning the genetic mechanisms that create diversity in <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> and <i>Pseudocercospora musae</i>, the causal agents of Fusarium wilt and yellow Sigatoka, respectively. The specific aims of this study are: 1) to obtain cultures and DNA from banana fungal pathogens, 2) to screen isolates of banana fungal pathogens for the presence of mating type sequences, 3) evaluate whether mating type genes are transcribed during vegetative growth.</p> <div>   </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Lilia Costa Carvalhais</b>, <a href="mailto:l.carvalhais@uq.edu.au">l.carvalhais@uq.edu.au</a> 0426 197 372</li> <li>• Associate Advisor: Prof Andre Drenth, <a href="mailto:a.drenth@uq.edu.au">a.drenth@uq.edu.au</a> +61 7 344 32460</li> <li>• Associate Advisor: Dr Alistair McTaggart, <a href="mailto:a.mctaggart@uq.edu.au">a.mctaggart@uq.edu.au</a></li> <li>• Associate Advisor: Dr Vivian Rincon-Florez, <a href="mailto:v.rinconflorez@uq.edu.au">v.rinconflorez@uq.edu.au</a> x32454</li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/3177/lilia-costa-carvalhais">https://qaafi.uq.edu.au/profile/3177/lilia-costa-carvalhais</a></p>
<p>Useful majors</p>	<p>Microbiology/Genetics</p>

<p><b>CHS 2 Project</b></p> <p><i>Dr Louisa Parkinson</i></p> <p><i>Prof Roger Shivas</i></p> <p><i>A/Prof Andrew Geering</i></p>	<p><b>2) <u>Phylogeny and taxonomy of Claviceps associated with ergot of native grasses in Australia</u></b></p> <p>Ergot is a disease of some cultivated and wild grasses caused by species of the ascomycete <i>Claviceps</i>. In Australia, ergot is an economically important disease of some grain crops, e.g. sorghum, and is a problem in some native Australian grasses, e.g. <i>Paspalum</i>. The fungus is also known to produce alkaloids that are hallucinogenic to humans and toxic to grazing livestock. Worldwide there are approximately 60 species of <i>Claviceps</i> known, including about 14 Australian species. A collection of 31 <i>Claviceps</i> isolates from native Australian grasses held in the Queensland Plant Pathology Herbarium (BRIP) requires taxonomic identification and phylogenetic revision. Novel species of <i>Claviceps</i> may result from this study and these will require formal taxonomic description. The aim of this Honours project is to identify the <i>Claviceps</i> isolates held in BRIP to species-level with multigene phylogenetic analyses and to formally classify and describe new taxa. The project methods will develop skills in microbiology (isolation and culture of isolates); morphology (descriptions of new taxa), molecular biology (fungal DNA extractions, PCR); phylogenetics and bioinformatics (analysis of DNA sequences); and plant pathology (fungus-host interactions).</p> <div style="display: flex; justify-content: space-around; align-items: flex-end;"> <div data-bbox="438 1003 759 1426">  <p>Claviceps purpurea on barley (<i>Hordeum vulgare</i>). Scale Bar = 1 cm</p> </div> <div data-bbox="834 1003 1311 1426">  <p>Conidia of <i>Claviceps purpurea</i> on perennial ryegrass (<i>Lolium perenne</i>). Scale bar = 20 µm.</p> </div> </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Louisa Parkinson</b>, <a href="mailto:l.parkinson@uq.edu.au">l.parkinson@uq.edu.au</a> +61 7 344 32457</li> <li>• Associate Advisor: Prof Roger Shivas, (DAF Biosecurity; USQ) <a href="mailto:r.shivas@uq.edu.au">r.shivas@uq.edu.au</a></li> <li>• Associate Advisor: A/Prof Andrew Geering, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, 41 Boggo Road, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/">https://qaafi.uq.edu.au/</a></p>
<p>Useful majors</p>	<p>Molecular Biology, Bioinformatics, Microbiology, Plant Pathology</p>



<p><b>CHS 3 Project</b></p> <p><i>Dr Louisa Parkinson</i></p> <p><i>A/Prof Andrew Geering</i></p> <p><i>A/Prof Elizabeth Dann</i></p>	<p><b>3) <u>Investigation of biosecurity threats to the Australian avocado industry</u></b></p> <p>Avocado is a billion-dollar industry and is threatened by exotic and emerging pests and diseases, which could hinder production and impact Australia's ability to enter global markets. Plant biosecurity and pathology diagnostics contributes towards food security and protecting agricultural crops by enabling the capacity for quickly identifying and responding to incursions.</p> <p>Although a primary pathogen of potato, Potato Spindle Tuber Viroid (PSTVd) is a biosecurity threat to avocados and has been reported to infect avocados in several locations in Peru, where potatoes are grown as a staple crop. In Australia, PSTVd outbreaks have been reported in commercial tomato glasshouse facilities, and have been successfully eradicated. However the ability of Australian PSTVd isolates to cause disease in avocado has not been tested.</p> <p>Branch dieback of avocado trees is an emerging problem in Queensland, and is associated with tree-boring ambrosia beetles, <i>Euwallacea perbrevis</i> (formerly <i>E. fornicatus</i>), known in Australia as the Tea Shot Hole Borer (TSHB). The beetles carry <i>Fusarium</i> fungal symbionts in their mouth parts, which they deposit into the heartwood of tree branches for the beetles and larvae to feed; the fungus causes branch dieback. The <i>Fusarium</i> symbionts in Australia represent new species within the Ambrosia <i>Fusarium</i> Clade (AFC) of the <i>Fusarium</i> genus, and the pathogenicity of these species are yet to be demonstrated. Other ornamental and horticultural trees in Queensland, such as tuckeroo (<i>Cupaniopsis anacardioides</i>), have also been reported with branch dieback associated with TSHB. The ability of AFC species affecting tuckeroo to cause disease in avocados (and vice versa) has not been tested; an investigation of cross-pathogenicity may shed light on the potential host range of the beetles and <i>Fusarium</i> symbionts. A molecular diagnostic test for detecting <i>Fusarium</i> species within the AFC clade would be useful in confirming diagnoses of Ambrosia beetle-vectored branch dieback horticultural and ornamental trees in Australia. Moreover a test for quick molecular identification of TSHB (<i>Euwallacea perbrevis</i>) is yet to be developed. Molecular identification of beetles is often done with morphology or sequencing of the cytochrome c oxidase subunit 1 (CO1) gene. A qPCR molecular test for TSHB based on the CO1 gene would be useful in aiding quick identification of beetle specimens from symptomatic trees.</p> <p>This Honours project aims to (i) test Australian PSTVd isolates for pathogenicity on avocado in glasshouse pathogenicity experiments (ii) test the ability of <i>Fusarium</i> AFC isolates from tuckeroo and avocado to cause disease on both hosts in glasshouse pathogenicity experiments; (iii) and develop a real time qPCR diagnostic test for identifying <i>Fusarium</i> AFC species or TSHB using available gene sequence data. The project methods will develop skills in microbiology through culturing of isolates; molecular biology through molecular diagnostic design and optimization of qPCR assays; bioinformatics through analyses of gene sequence data and primer design; and plant pathology through fungus-host interactions investigated in glasshouse pathogenicity experiments.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Louisa Parkinson</b>, <a href="mailto:l.parkinson@uq.edu.au">l.parkinson@uq.edu.au</a> +61 7 344 32457</li> <li>• Associate Advisor: A/Prof Andrew Geering, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> </ul>



	<ul style="list-style-type: none"> <li>Associate Advisor: A/Prof Elizabeth Dann, <a href="mailto:e.dann@uq.edu.au">e.dann@uq.edu.au</a> +61 7 344 32455</li> </ul>
Location	Ecosciences Precinct, 41 Boggo Road, Dutton Park
Webpage	<a href="https://qaafi.uq.edu.au/">https://qaafi.uq.edu.au/</a>
Useful majors	Molecular Biology, Bioinformatics, Microbiology, Plant Pathology


<p><b>CHS 4 Project</b></p> <p><i>Prof Neena Mitter</i></p> <p><i>Dr Karishma Mody</i></p>	<p><b>4) <u>Topical application of RNAi for management of Fire Ants</u></b></p> <p>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.</p> <p>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.</p> <div data-bbox="454 1075 1295 1335" data-label="Image"> </div> <p>Students in both Themes can learn valuable techniques in cloning, PCR, qRT-PCR, 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.</p>
Advisor(s) contact	<ul style="list-style-type: none"> <li><b>Prof Neena Mitter</b>, <a href="mailto:n.mitter@uq.edu.au">n.mitter@uq.edu.au</a> +61 7 334 66513</li> <li>Associate Advisor: Dr Karishma Mody, <a href="mailto:k.mody@uq.edu.au">k.mody@uq.edu.au</a> +61 7 334 62318</li> </ul>
Location	QBP, Building 80, St Lucia campus
Webpage	<a href="https://researchers.uq.edu.au/researcher/1427">https://researchers.uq.edu.au/researcher/1427</a>
Useful majors	Biochemistry & Molecular Biology / Bioinformatics




<p><b>CHS 5 Project</b></p> <p><i>Dr Karishma Mody</i></p> <p><i>Prof Neena Mitter</i></p> <p><i>Prof Tim Mahony</i></p>	<p><b>5) <u>Clay innovation: sustainable alternative to pesticides for protecting Queensland's livestock</u></b></p> <p>Sheep flystrike and lice-infestation are the top two diseases economically affecting the Queensland's sheep and wool industry. <i>L. cuprina</i> (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.</p> <p>Current control measures and limitations:</p> <ul style="list-style-type: none"> <li>• Resistance build up to the existing chemicals</li> <li>• Mulesing sheep</li> <li>• Withholding periods for live exports</li> <li>• Longer slaughter intervals impacting trade</li> </ul> <p><b><u>RNAi delivery using Clay nanoparticles – Innovative Solution</u></b></p> <div data-bbox="635 1014 1082 1330" data-label="Image"> </div> <p>The current project is aimed at investigating RNA interference (RNAi) as a tool to manage sheep blowfly and lice-infestation. In this project, the RNAi platform will be further explored to develop novel targets to control both blowfly and lice. Students in both Themes can learn valuable techniques in cloning, PCR, qRT-PCR, 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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Karishma Mody</b>, k.mody@uq.edu.au +61 7 334 62318</li> <li>• Associate Advisor: Prof Neena Mitter, <a href="mailto:n.mitter@uq.edu.au">n.mitter@uq.edu.au</a> +61 7 334 66513</li> <li>• Associate Advisor: Prof Tim Mahony, t.mahony@uq.edu.au +61 7 334 66505</li> </ul>
<p>Location</p>	<p>QBP, Building 80, St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/23229">https://researchers.uq.edu.au/researcher/23229</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics</p>



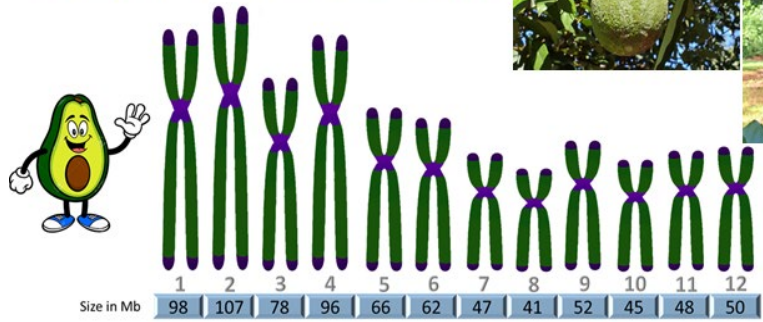



<p><b>CHS 6 Project</b></p> <p><i>Dr Chris O'Brien</i></p> <p><i>Dr Alice Hayward</i></p> <p><i>Prof Neena Mitter</i></p>	<p><b>6) <u>From Freezer to Field - Cryostasis for Conservation!</u></b></p> <p>Plants possess the incredible ability of cell totipotency, with each cell having potential to generate 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.</p> <p><b>Three Projects are available in this space!</b></p> <ol style="list-style-type: none"> <li>1. Development of a cryopreservation regeneration media for different avocado cultivars.</li> <li>2. Cryopreservation of critically endangered native myrtaceae species</li> <li>3. Cryopreservation of critically endangered <i>Macadamia janseni</i></li> </ol> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Dr Chris O'Brien, <a href="mailto:c.obrien4@uq.edu.au">c.obrien4@uq.edu.au</a></li> <li>• Dr Alice Hayward, <a href="mailto:a.hayward@uq.edu.au">a.hayward@uq.edu.au</a></li> <li>• Dr Albert Wong, <a href="mailto:albertchernsun.wong@uq.edu.au">albertchernsun.wong@uq.edu.au</a></li> <li>• Prof Neena Mitter, <a href="mailto:n.mitter@uq.edu.au">n.mitter@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>QBP, Building 80 Level 3 South, St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/honours">https://qaafi.uq.edu.au/honours</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Plant Biology/ Botany/ Horticulture / Conservation</p>




<p><b>CHS 7 Project</b></p> <p><i>Dr Alice Hayward</i></p> <p><i>Prof Neena Mitter</i></p> <p><i>Dr Jayeni Hiti-Bandaralage</i></p>	<p><b>7) <u>Novel Tissue Culture Tools for Ginger Breeding</u></b></p> <p>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 <b>sustainable, cost-effective and climate-secure</b> way to produce plants.</p> <p>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.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Alice Hayward</b>, <a href="mailto:a.hayward@uq.edu.au">a.hayward@uq.edu.au</a></li> <li>• <b>Dr Jayeni Hiti-Bandaralage</b>, <a href="mailto:j.hitibandalarage@uq.edu.au">j.hitibandalarage@uq.edu.au</a></li> <li>• <b>Prof Neena Mitter</b>, <a href="mailto:n.mitter@uq.edu.au">n.mitter@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>QBP, Building 80 Level 3 South, St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/honours">https://qaafi.uq.edu.au/honours</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Plant Biology/ Botany / Microbiology/ Horticulture</p>



<p><b>CHS 8 Project</b></p> <p><i>Dr Alice Hayward</i></p> <p><i>Mr Stephen Fletcher</i></p> <p><i>Prof Neena Mitter</i></p>	<p><b>8) <u>Genomics and DNA Markers for Australian Avocado</u></b></p> <p>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.</p> <div><table><tr><th></th><th>1</th><th>2</th><th>3</th><th>4</th><th>5</th><th>6</th><th>7</th><th>8</th><th>9</th><th>10</th><th>11</th><th>12</th></tr><tr><td>Size in Mb</td><td>98</td><td>107</td><td>78</td><td>96</td><td>66</td><td>62</td><td>47</td><td>41</td><td>52</td><td>45</td><td>48</td><td>50</td></tr></table></div>		1	2	3	4	5	6	7	8	9	10	11	12	Size in Mb	98	107	78	96	66	62	47	41	52	45	48	50
	1	2	3	4	5	6	7	8	9	10	11	12															
Size in Mb	98	107	78	96	66	62	47	41	52	45	48	50															
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"><li>• <b>Dr Alice Hayward</b>, <a href="mailto:a.hayward@uq.edu.au">a.hayward@uq.edu.au</a></li><li>• <b>Mr Stephen Fletcher</b>, <a href="mailto:s.fletcher@uq.edu.au">s.fletcher@uq.edu.au</a></li><li>• <b>Prof Neena Mitter</b>, <a href="mailto:n.mitter@uq.edu.au">n.mitter@uq.edu.au</a></li></ul>																										
<p>Location</p>	<p>QBP, Building 80 Level 3 South, St Lucia campus</p>																										
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/honours">https://qaafi.uq.edu.au/honours</a></p>																										
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Plant Biology/ Horticulture/ Genetics/ Bioinformatics</p>																										



<p><b>CHS 9 Project</b></p> <p><i>A/Prof Femi Akinsanmi</i></p> <p><i>Dr Vivian Rincon-Florez,</i></p>	<p><b>9) <u>Agroecological Crop Protection</u></b></p> <p>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.</p> <p>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:</p> <ol style="list-style-type: none"> <li>1. <b>Pathogen biology:</b> Characterization of the biology of causal agents of major foliar and soilborne diseases</li> <li>2. <b>Molecular epidemiology:</b> Spatial and temporal analysis of dynamics of fungal pathogens in agricultural ecosystems</li> <li>3. <b>Sustainable solutions:</b> Develop new alternative solutions to synthetic chemical pesticides to manage fungal diseases in horticultural crops</li> </ol> <p>Scholars will join the pathology team and have opportunity to contribute to publications arisen from the research.</p> <div data-bbox="392 1048 1362 1514">  </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Femi Akinsanmi</b>, <a href="mailto:o.akersanmi@uq.edu.au">o.akersanmi@uq.edu.au</a> +61 7 344 32453</li> <li>• <b>Dr Vivian Rincon-Florez</b>, <a href="mailto:v.rinconflorez@uq.edu.au">v.rinconflorez@uq.edu.au</a> Tel: +61 (0)7 3443 2762</li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, 41 Boggo Road, Dutton Park (10-min walk from St Lucia campus)</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/186/femi-akersanmi">https://qaafi.uq.edu.au/profile/186/femi-akersanmi</a></p>
<p>Useful majors</p>	<p>Agriculture / Biotechnology / Molecular Biology / Microbiology</p>






<p><b>CHS 10 Project</b></p> <p><i>Dr Inigo Auzmendi</i></p> <p><i>Dr Emma Carrie</i></p>	<p><b>10) <u>Simulating fruit tree growth and development</u></b></p> <p>Functional-structural plant models <a href="#">simulate</a> 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.</p> <p>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.</p> <p>The project focuses on one of <a href="#">four areas</a>: 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.</p> <p>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.</p> <div data-bbox="379 1205 900 1545" data-label="Image"></div> <div data-bbox="933 981 1366 1545" data-label="Image"></div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Inigo Auzmendi</b>, <a href="mailto:i.auzmendi@uq.edu.au">i.auzmendi@uq.edu.au</a> +61 7 344 32702</li> <li>• Associate Advisor: Dr Emma Carrie, <a href="mailto:e.carrie@uq.edu.au">e.carrie@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/762/inigo-auzmendi">https://qaafi.uq.edu.au/profile/762/inigo-auzmendi</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Biophysics / Computational Science / Plant Science / Horticulture</p>






<p><b>CHS 11 Project</b></p> <p><i>Dr Craig Hardner</i></p> <p><i>Dr Elizabeth Ross</i></p> <p><i>Dr Robyn Cave</i></p> <p><i>Dr Mulsuew Fikere</i></p>	<p><b>11) <u>Genomics of horticultural tree crops</u></b></p>  <p>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</p> <ul style="list-style-type: none"> <li>• Robustness of Japanese genomic prediction models for mandarin fruit quality in Australian germplasm</li> <li>• Chromosome structural variation in citrus using nanopore technology</li> <li>• Global prediction of sweetness in peach</li> <li>• Selection for timing of fruit maturity for adaption of cherry to changing environment</li> </ul> <p>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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Craig Hardner</b>, <a href="mailto:craig.hardner@uq.edu.au">craig.hardner@uq.edu.au</a> +61 7 334 69465</li> <li>• Potential Associate Advisor: Dr Elizabeth Ross, <a href="mailto:e.ross@uq.edu.au">e.ross@uq.edu.au</a> +61 7 334 62162</li> <li>• Potential Associate Advisor: Dr Robyn Cave, <a href="mailto:r.cave@uq.edu.au">r.cave@uq.edu.au</a> +61 7 546 01 240</li> <li>• Potential Associate Advisor: Dr Mulsuew Fikere</li> </ul>
<p>Location</p>	<p>St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/1973">https://researchers.uq.edu.au/researcher/1973</a></p>
<p>Useful majors</p>	<p>Genetics, Bioinformatics, (Agriculture, Horticulture, Plant breeding)</p>






<p><b>CHS 12 Project</b></p> <p><i>Dr Craig Hardner</i></p> <p><i>Dr Vivi Arief</i></p> <p><i>Dr Robyn Cave</i></p> <p><i>Prof Bruce Topp</i></p> <p><i>Shane Mulo</i></p>	<p><b>12) <u>Optimising horticultural tree crops breeding</u></b></p> <p>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</p> <ul style="list-style-type: none"> <li>• Bio-economic models for trait evaluation in macadamia or coffee</li> <li>• Modelling apple, macadamia, mango breeding strategies</li> </ul> <p>Student will collaborate with local and international research groups. Student will develop skills in systems modelling, economics, plant breeding, quantitative genetics, and scientific writing. All projects are aimed at producing manuscripts for submission to peer-reviewed journals.</p>
Advisor(s) contact	<ul style="list-style-type: none"> <li>• <b>Dr Craig Hardner</b>, <a href="mailto:craig.hardner@uq.edu.au">craig.hardner@uq.edu.au</a> +61 7 334 69465</li> <li>• Potential Associate Advisor: Dr Vivi Arief</li> <li>• Potential Associate Advisor: Dr Robyn Cave, <a href="mailto:r.cave@uq.edu.au">r.cave@uq.edu.au</a> +61 7 546 01 240</li> <li>• Potential Associate Advisor: Prof Bruce Topp, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> <li>• Potential Associate Advisor: Shane Mulo (QDAF)</li> </ul>
Location	St Lucia campus
Webpage	<a href="https://researchers.uq.edu.au/researcher/1973">https://researchers.uq.edu.au/researcher/1973</a>
Useful majors	Genetics, Plant breeding, Agricultural economics


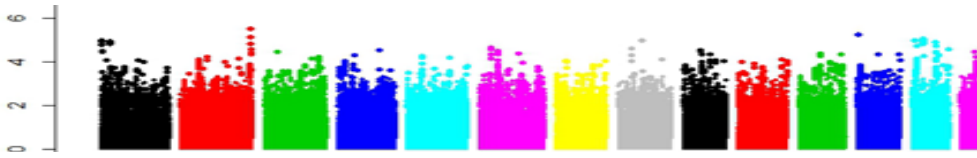


<b>CHS 13 Project</b>  <i>Dr Craig Hardner</i>	<b>13) <u>Genomic platform for understanding the population genetics of pre-colonisation distribution of Bunya pine</u></b>  <p>Bunya pine is a special Queensland forest tree. While widespread prior to European colonisation, the only remnant large population occurs in Bunya mountains with isolated individual trees distributed throughout SEQ Queensland.</p> <p>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.</p> 
Advisor(s) contact	<ul style="list-style-type: none"><li>• <b>Dr Craig Hardner</b>, craig.hardner@uq.edu.au +61 7 334 69465</li><li>• Potential Associate Advisors: To be advised</li></ul>
Location	St Lucia campus
Webpage	<a href="https://researchers.uq.edu.au/researcher/1973">https://researchers.uq.edu.au/researcher/1973</a>
Useful majors	Genetics, Bioinformatics, Social history




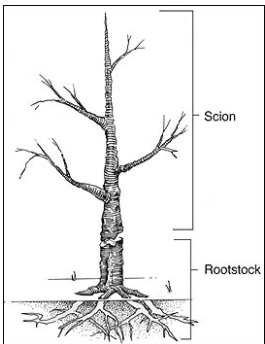

<p><b>CHS 14 Project</b></p> <p><i>Dr Craig Hardner</i></p> <p><i>A/Prof Mark Dieters</i></p> <p><i>Dr Vivi Arief</i></p>	<p><b>14) <u>General recursive equations for estimating relationship coefficients in auto-polyploid organisms</u></b></p> <div data-bbox="363 409 1249 638">    </div> <p>The aim of 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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Craig Hardner</b>, <a href="mailto:craig.hardner@uq.edu.au">craig.hardner@uq.edu.au</a> +61 7 334 69465</li> <li>• Potential Associate Advisor: A/Prof Mark Dieters, <a href="mailto:m.dieters@uq.edu.au">m.dieters@uq.edu.au</a> x 57410</li> <li>• Potential Associate Advisor: Dr Vivi Arief</li> </ul>
<p>Location</p>	<p>St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/1973">https://researchers.uq.edu.au/researcher/1973</a></p>
<p>Useful majors</p>	<p>Quantitative genetics, statistics, poly-ploid genetics</p>




<p><b>CHS 15 Project</b></p> <p><i>Dr Mobashwer Alam</i></p> <p><i>Prof Bruce Topp</i></p>	<p><b>15) <u>Molecular investigation on the phenotypic variability in flowering time in macadamia</u></b></p> <p>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 macadamia 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 collection of wild genetic resources. Identified markers can be used in future marker assisted selection of breeding progeny.</p>  
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Mobashwer Alam</b>, <a href="mailto:m.alam@uq.edu.au">m.alam@uq.edu.au</a> 0753 811 371</li> <li>• Associate Advisor: Prof Bruce Topp, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> </ul>
<p>Location</p>	<p>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)</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/13285">https://researchers.uq.edu.au/researcher/13285</a></p> <p><a href="https://researchers.uq.edu.au/researcher/2467">https://researchers.uq.edu.au/researcher/2467</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology</p>



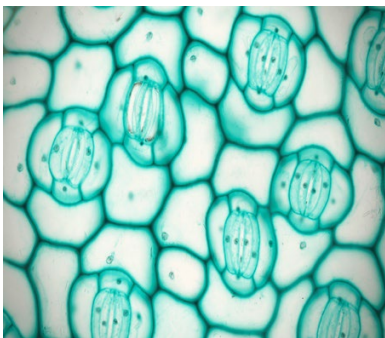

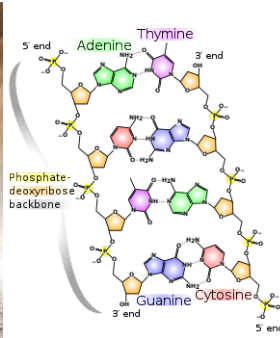


<p><b>CHS 16 Project</b></p> <p><i>Dr Mobashwer Alam</i></p> <p><i>Prof Bruce Topp</i></p>	<p><b>16) <u>Investigating macadamia rootstock genetics on the variability in scion architecture and branching.</u></b></p> <p>The management of excessive vigour through pruning and hedging is a major expense in 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.</p> <div style="display: flex; justify-content: space-around; align-items: center;">    </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Mobashwer Alam</b>, <a href="mailto:m.alam@uq.edu.au">m.alam@uq.edu.au</a> 0753 811 371</li> <li>• Associate Advisor: Prof Bruce Topp, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> </ul>
<p>Location</p>	<p>Maroochy Research Facility, 47 Mayers Rd, Nambour (Student can be based at St Lucia, but needs to travel to Nambour for data/sample collection)</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/13285">https://researchers.uq.edu.au/researcher/13285</a></p> <p><a href="https://researchers.uq.edu.au/researcher/2467">https://researchers.uq.edu.au/researcher/2467</a></p>
<p>Useful majors</p>	<p>Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology</p>






<p><b>CHS 17 Project</b></p> <p><i>Dr Mobashwer Alam</i></p> <p><i>Prof Bruce Topp</i></p>	<p><b>17) <u>Molecular investigation to determine species composition and extent of genetic base of Australian elite selections of Macadamia</u></b></p> <p>Macadamia is an Australian native crop and is highly valued for its kernel. Using the available cultivars as parents, Australian national macadamia breeding program generated &gt;15,000 breeding progeny and selected 53 elites through first and generation of progeny evaluation. Most of the parents of these selections belong to <i>Macadamia integrifolia</i> or <i>M. tetraphylla</i> or their hybrids. Although pedigree information of the 53 selections is available, species identity is still unexplored.</p> <p>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.</p> <div data-bbox="376 813 1378 1164">  </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Mobashwer Alam</b>, <a href="mailto:m.alam@uq.edu.au">m.alam@uq.edu.au</a> 0753 811 371</li> <li>• Associate Advisors: Prof Bruce Topp, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> </ul>
<p>Location</p>	<p>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)</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/13285">https://researchers.uq.edu.au/researcher/13285</a></p> <p><a href="https://researchers.uq.edu.au/researcher/2467">https://researchers.uq.edu.au/researcher/2467</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology</p>




<p><b>CHS 18 Project</b></p> <p><i>Dr Mobashwer Alam</i></p> <p><i>Prof Bruce Topp</i></p>	<p><b>18) <u>Investigating genetic architecture of stomatal traits to exploit in climate change adaptation</u></b></p> <p>To cope with global climate change, one of the key focuses of the plant breeding program is to develop climate-smart varieties with efficient water use and photosynthesis. Finding out heritable and simple traits associated with less water loss and high photosynthesis can help breeders to select drought and high temperature tolerant elite cultivars. Stomatal pores on the leaf epidermis are the windows of water loss through transpiration and CO<sub>2</sub> uptake for photosynthesis. By altering the stomatal size and density, it can be possible to optimize the amount of CO<sub>2</sub> 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.</p> <div data-bbox="376 837 1382 1173">    </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Mobashwer Alam</b>, <a href="mailto:m.alam@uq.edu.au">m.alam@uq.edu.au</a> 0753 811 371</li> <li>• Associate Advisor: Prof Bruce Topp, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> </ul>
<p>Location</p>	<p>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)</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/13285">https://researchers.uq.edu.au/researcher/13285</a></p> <p><a href="https://researchers.uq.edu.au/researcher/2467">https://researchers.uq.edu.au/researcher/2467</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology</p>



<p><b>CHS 19 Project</b></p> <p><i>Prof Bruce Topp</i></p> <p><i>Prof Jose Chaparro</i></p> <p><i>Dr Mobashwer Alam</i></p>	<p><b>19) Investigating genetic diversity in feral peach</b></p> <p>Feralisation is a complex process that involves domestic populations reverting to wild phenotypes. In the absence of human interruption, feral plants may show adaptation to new environments and display characteristics of their wild ancestors. We have collected 30 accessions of feral peach from Queensland and New South Wales which have been propagated and planted at Stanthorpe. This project will investigate the genetic and morphological variation in these feral accessions and compare them to commercial cultivars. Flowering, fruiting and vegetative growth traits will be measured. SSR markers will be used to study genetic diversity.</p> <p>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.</p> <div>    </div>
Advisor(s) contact	<ul style="list-style-type: none"> <li>• <b>Prof Bruce Topp</b>, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> <li>• Associate Advisor: Prof Jose Chaparro</li> <li>• Associate Advisor: Dr Mobashwer Alam, <a href="mailto:m.alam@uq.edu.au">m.alam@uq.edu.au</a> 0753 811 371</li> </ul>
Location	Nambour at the Maroochy Research Facility (Student will need to travel to Stanthorpe for data/sample collection)
Webpage	<a href="https://researchers.uq.edu.au/researcher/2467">https://researchers.uq.edu.au/researcher/2467</a> <a href="https://hos.ifas.ufl.edu/people/on-campus-faculty/jose-x-chaparro/">https://hos.ifas.ufl.edu/people/on-campus-faculty/jose-x-chaparro/</a> <a href="https://researchers.uq.edu.au/researcher/13285">https://researchers.uq.edu.au/researcher/13285</a>
Useful majors	Biochemistry & Molecular Biology / Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology






<p><b>CHS 20 Project</b></p> <p><i>Prof Bruce Topp</i></p> <p><i>Prof Jose Chaparro</i></p> <p><i>Dr Mobashwer Alam</i></p>	<p><b>20) <u>Investigating rootstock effect on scion vigour, flowering, and fruiting in low chill peach</u></b></p> <p>Rootstocks play a vital role on the performance of horticultural crops. As a part of a dual plant system, rootstocks translocate water and nutrients to the above ground scion and thereby, regulate resource supply for growth and development of vegetative and reproductive parts. In several tree crops, rootstocks have been widely used to manage the size and vigour of the scion. Although extensive studies have been conducted previously in peach, but the investigation on low-chill rootstock effect on low chill peach cultivars is limited. In this project, the scholar will collect data on growth, flowering and fruit quality traits of 3 low-chill scion cultivars grafted onto 7 different low chill rootstocks. Statistical analysis will be conducted to identify best vigour managing rootstocks.</p> <div data-bbox="389 696 1366 1039">  </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Prof Bruce Topp</b>, <a href="mailto:b.topp@uq.edu.au">b.topp@uq.edu.au</a> +61 7 538 11373</li> <li>• Associate Advisor: Prof Jose Chaparro</li> <li>• Associate Advisor: Dr Mobashwer Alam, <a href="mailto:m.alam@uq.edu.au">m.alam@uq.edu.au</a> 0753 811 371</li> </ul>
<p>Location</p>	<p>Nambour at the Maroochy Research Facility (Student may need to travel to Stanthorpe for data/sample collection)</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/2467">https://researchers.uq.edu.au/researcher/2467</a></p> <p><a href="https://hos.ifas.ufl.edu/people/on-campus-faculty/jose-x-chaparro/">https://hos.ifas.ufl.edu/people/on-campus-faculty/jose-x-chaparro/</a></p> <p><a href="https://researchers.uq.edu.au/researcher/13285">https://researchers.uq.edu.au/researcher/13285</a></p>
<p>Useful majors</p>	<p>Genetics / Agriculture/ Botany/ Plant Breeding /Environmental Science/ Ecology</p>





<p><b>CHS 21 Project</b></p> <p><i>A/Prof Andrew Geering</i></p> <p><i>A/Prof John Thomas</i></p> <p><i>Dr Kathy Crew</i></p>	<p><b>21) 3-D imaging of badnaviral replication structures</b></p> <p>Badnaviruses are some of the most common viral pathogens in the tropics and infect a range of economically important plants such as banana, citrus, cacao, sugarcane and yam. Very little information is available on the replication strategies they use but an important advance has been made by our group with the discovery of replication structures (viroplasms) in the cytoplasm of infected cells. This project, a collaboration between QAAFI and the Centre for Electron Microscopy and Microanalysis, will utilize cryosectioning and transmission electron microscopy to image multiple layers of an infected cell, which will then be integrated using software to construct a 3-D image of the cell including the replication structures. Methods will then be developed to fluorescently label the replication structures, with the ultimate aim of dissecting out these structures using laser technology for analysis of protein and nucleic acid composition.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Andrew Geering</b>, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> <li>• Associate Advisor: A/Prof John Thomas, <a href="mailto:j.thomas2@uq.edu.au">j.thomas2@uq.edu.au</a> +61 7 325 54393 +61 7 344 32461</li> <li>• Associate Advisor: Dr Kathy Crew, <a href="mailto:kathleen.crew@uq.edu.au">kathleen.crew@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Centre for Electron Microscopy and Microanalysis, Ecosciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/81/andrew-geering">https://qaafi.uq.edu.au/profile/81/andrew-geering</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Microbiology</p>



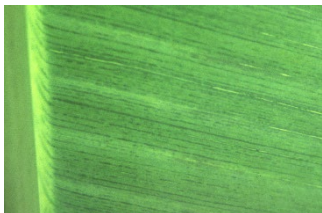

<p><b>CHS 22 Project</b></p> <p><i>A/Prof Andrew Geering</i></p> <p><i>A/Prof John Thomas</i></p> <p><i>Dr Kathy Crew</i></p>	<p><b>22) <u>Population genetics of Alternanthera mosaic virus and development of an infectious clone</u></b></p> <p>Alternanthera mosaic virus (AltMV) was discovered in Australia but is thought to have been introduced into Australia in the early 20<sup>th</sup> Century in fodder shipments from the USA. In this project, research will be done to investigate sequence variation of this virus in Australia and to compare with isolates of the virus from the USA and Europe. AltMV shows great potential to be used as a gene expression vector and as a first step towards this goal, an infectious clone of the virus will be prepared. Full length genome constructs will need to be prepared and linked to a transcription promoter to allow infection of plants by mechanical transmission of the plasmid constructs.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Andrew Geering</b>, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> <li>• Associate Advisor: A/Prof John Thomas, <a href="mailto:j.thomas2@uq.edu.au">j.thomas2@uq.edu.au</a> +61 7 325 54393 +61 7 344 32461</li> <li>• Associate Advisor: Dr Kathy Crew, <a href="mailto:kathleen.crew@uq.edu.au">kathleen.crew@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/81/andrew-geering">https://qaafi.uq.edu.au/profile/81/andrew-geering</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Microbiology</p>



<p><b>CHS 23 Project</b></p> <p>A/Prof Andrew Geering</p> <p>A/Prof John Thomas</p> <p>Dr Nga Tran</p>	<p><b>23) <u>Epidemiology of a new nepovirus associated with buffalo grass yellows</u></b></p> <p>Buffalo grass (<i>Stenotaphrum secundatum</i>) is the most valuable turfgrass species in Australia, and is also an important pasture species. Over the last few years, turf farmers along the eastern seaboard of Australia have been affected by an enigmatic disease called buffalo grass yellowing. High throughput sequencing was done to identify viruses infecting the diseased plants, and a new nepovirus was discovered and shown to be widely distributed in Australia. Virtually nothing is known about the biology of this virus, including its host range, impact on growth of buffalo grass, and mode of transmission. In this project, a broad diversity of experimental work (laboratory, glasshouse and field) will be done to provide a better understanding of the epidemiology of this virus. It is also hypothesised that the nepovirus synergistically interacts with other buffalo grass viruses to cause a worse disease than either virus would alone, and experiments will be done to test this hypothesis.</p> 
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• A/Prof Andrew Geering, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> <li>• Associate Advisor: A/Prof John Thomas, <a href="mailto:j.thomas2@uq.edu.au">j.thomas2@uq.edu.au</a> +61 7 325 54393 +61 7 344 32461</li> <li>• Associate Advisor: Dr Nga Tran, <a href="mailto:n.tran3@uq.edu.au">n.tran3@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/81/andrew-geering">https://qaafi.uq.edu.au/profile/81/andrew-geering</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Microbiology</p>





<p><b>CHS 24 Project</b></p> <p><i>A/Prof John Thomas</i></p> <p><i>A/Prof Andrew Geering</i></p> <p><i>Dr Kathy Crew</i></p> <p><i>Dr Megan Vance</i></p> <p><i>Mr Ric Webb</i></p>	<p><b>24) <u>Cytopathology and sites of replication of banana bunchy top virus</u></b></p> <p>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.</p> <div>   </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof John Thomas</b>, <a href="mailto:j.thomas2@uq.edu.au">j.thomas2@uq.edu.au</a>, +61 7 325 54393 +61 7 344 32461</li> <li>• Associate Advisor: A/Prof Andrew Geering, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> <li>• Associate Advisor: Dr Kathy Crew, <a href="mailto:kathleen.crew@uq.edu.au">kathleen.crew@uq.edu.au</a></li> <li>• Associate Advisor: Dr Megan Vance, <a href="mailto:m.vance@uq.edu.au">m.vance@uq.edu.au</a> +61 7 344 32456</li> <li>• Associate Advisor: Mr Ric Webb, <a href="mailto:r.webb@uq.edu.au">r.webb@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/228/john-thomas">https://qaafi.uq.edu.au/profile/228/john-thomas</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Microbiology</p>



<p><b>CHS 25 Project</b></p> <p><i>Dr Louisa Parkinson</i></p> <p><i>A/Prof Andrew Geering</i></p>	<p><b>25) <u>Developing molecular diagnostic tests for rapid detection of Phytophthora and Phytophthium spp. causing root rot of avocado</u></b></p> <p>Phytophthora root rot (PRR) of avocado is the most important soilborne disease of orchard avocado trees, estimating an annual \$17 million loss to the Australian avocado industry. The primary cause of PRR is oomycete, <i>Phytophthora cinnamomi</i>, a fungal-like microorganism. However numerous other species have been increasingly isolated from symptomatic roots and also demonstrated to cause PRR, including <i>P. multivora</i>, <i>P. niederhauserii</i>, <i>P. nicotianae</i>, <i>P. palmivora</i> and <i>Phytophthium vexans</i>. Testing for PRR typically involves baiting and isolating the pathogen from root and soil samples, however such methods render it difficult to distinguish between oomycete species based on oomycete morphology alone. Rapid molecular diagnostic tests such as loop-mediated isothermal amplification (LAMP) assays can enable fast, sensitive and specific detection of PRR-causing oomycetes in symptomatic roots. This research project aims to develop rapid LAMP diagnostic tests for the detection of <i>P. cinnamomi</i>, <i>P. multivora</i>, <i>P. niederhauserii</i> and <i>Pp. vexans</i> in avocado roots. Project activities will include using bioinformatics software for analysing the phylogeny of Phytophthora and Phytophthium to select candidate genes as a backbone for the LAMP assay; analysing gene sequence data for the design of species-specific LAMP primers; testing and optimising the assay in laboratory conditions followed by validation with inoculated avocado roots and lupin baits. The Honours research candidate will develop skills in bioinformatics, plant pathology, molecular biology and molecular diagnostic design and development.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Louisa Parkinson</b>, <a href="mailto:l.parkinson@uq.edu.au">l.parkinson@uq.edu.au</a> +61 7 344 32457</li> <li>• Associate Advisor: A/Prof Andrew Geering, <a href="mailto:a.geering@uq.edu.au">a.geering@uq.edu.au</a> +61 7 344 32459</li> </ul>
<p>Location</p>	<p>Ecosciences Precinct, 41 Boggo Road, Dutton Park</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/">https://qaafi.uq.edu.au/</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Bioinformatics / Microbiology / Plant Pathology</p>







<p><b>CHS 26-27 Project</b></p> <p><i>A/Prof Craig Hardner</i></p>	<p><b><u>26) New technologies for efficient genomic prediction in horticultural tree crops</u></b></p> <p>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.</p> <p><b>27)</b></p> <p>Nanopore is a new low cost whole-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.</p> <p>A \$5,000 scholarship will be offered for a high-quality student to undertake either of these projects.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Craig Hardner</b>, <a href="mailto:craig.hardner@uq.edu.au">craig.hardner@uq.edu.au</a> +61 7 334 69465</li> </ul>
<p>Location</p>	<p>St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/48/craig-hardner">https://qaafi.uq.edu.au/profile/48/craig-hardner</a></p>
<p>Useful majors</p>	<p>Plant biology, genetics, molecular genetics, bioinformatics</p>

<p><b>CHS 28 project</b></p> <p><i>Dr Albert Wong</i></p> <p>&amp;</p> <p><i>Dr Alice Hayward</i></p>	<p><b><u>28) Molecular Physiology of Root Formation in Macadamia</u></b></p> <p>Adventitious root (AR) formation is critical for the efficient propagation of elite 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</p>
---	---



	<p>design future experiments to evaluate gene expression profiles. If time permits, the student can learn to design CRISPR/Cas9 gene editing constructs</p> 
Advisor(s) contact	<ul style="list-style-type: none"> <li>• <b>Dr Albert Wong</b>, <a href="mailto:albertchernsun.wong@uq.edu.au">albertchernsun.wong@uq.edu.au</a></li> <li>• <b>Dr Alice Hayward</b>, <a href="mailto:a.hayward@uq.edu.au">a.hayward@uq.edu.au</a></li> </ul>
Location	UQ Long Pocket (10 min from St Lucia), Building 1024
Webpage	<a href="https://qaafi.uq.edu.au/honours">https://qaafi.uq.edu.au/honours</a>
Useful majors	Biochemistry & Molecular Biology / Plant Biology/ Horticulture/ Genetics/ Bioinformatics


<p><b>CHS 29 project</b></p> <p>Dr Anne Sawyer</p> <p>Prof Neena Mitter</p> <p>Prof Elizabeth Aitken</p>	<p><b><u>29) RNA-based fungicides for ginger</u></b></p> <p>The soilborne diseases <i>Pythium</i> Soft Rot (PSR) and <i>Fusarium</i> yellows caused by <i>Pythium</i> sp. and <i>Fusarium oxysporum</i> f.sp. <i>zingiberi</i> (<i>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.</p> <p>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™ to control plant viruses and insect pests.</p> 
--	---





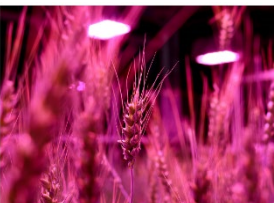

Advisor(s) contact	<ul style="list-style-type: none"><li>• Dr Anne Sawyer, <a href="mailto:a.sawyer@uq.edu.au">a.sawyer@uq.edu.au</a>, 3346 2295</li><li>• Associate Advisor: Prof Neena Mitter, <a href="mailto:n.mitter@uq.edu.au">n.mitter@uq.edu.au</a>, 3346 6513</li><li>• Associate Advisor: Prof Elizabeth Aitken, <a href="mailto:e.aitken@uq.edu.au">e.aitken@uq.edu.au</a>, 33654775</li></ul>
Location	<u>Location:</u> Queensland Bioscience Precinct, St Lucia
Webpage	<a href="#">Dr Anne Sawyer - UQ Researchers</a>  <a href="#">Queensland Alliance for Agriculture and Food Innovation - University of Queensland (uq.edu.au)</a>
Useful majors	Plant Science / Biochemistry & Molecular Biology / Bioinformatics / Genetics / Microbiology



# Centre for Crop Science Projects

<p><b>CCS 1 Project</b></p> <p><i>Prof Daniel Rodriguez</i></p> <p><i>Dr Dongxue Zhao</i></p> <p><i>Dr Peter deVoil</i></p>	<p><b>1) Title: Proximal sensing of soil water for root phenotyping</b></p> <p>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.</p> <div data-bbox="375 875 828 1211">  </div> <p>DualEM 21S being used to survey root activity in a sorghum crop, at UQ's Gatton Campus.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Prof Daniel Rodriguez</b>, <a href="mailto:d.rodriguez@uq.edu.au">d.rodriguez@uq.edu.au</a> +61 7 535 15091</li> <li>• <b>Dr Dongxue Zhao</b>, <a href="mailto:dongxue.zhao@uq.edu.au">dongxue.zhao@uq.edu.au</a></li> <li>• <b>Dr Peter deVoil</b>, <a href="mailto:p.devoil@uq.edu.au">p.devoil@uq.edu.au</a> +61 7 535 15087</li> </ul>
<p>Location</p>	<p>Gatton or St Lucia Campus</p>
<p>Webpage</p>	<p><a href="https://www.qld-fsr.info/">https://www.qld-fsr.info/</a></p>
<p>Useful majors</p>	<p>Please select from:</p> <p>Bioinformatics / Biophysics / Computational Science / Agronomy</p>




<p><b>CCS 2 Project</b></p> <p><i>A/Prof Lee Hickey</i></p> <p><i>Dr Millicent Smith</i></p> <p><i>Prof Graeme Hammer</i></p>	<p><b>2) <u>Need for speed: growing plants fast to feed the world</u></b></p> <div data-bbox="379 331 654 481">  </div> <p>We need more robust and productive crops to feed the world, but developing new crop varieties is slow using traditional plant breeding approaches.</p> <div data-bbox="379 481 654 750">  </div> <p>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.</p> <div data-bbox="379 828 654 1030">  </div> <p>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.</p> <div data-bbox="379 1041 654 1288">  </div> <p>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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Lee Hickey</b>, <a href="mailto:l.hickey@uq.edu.au">l.hickey@uq.edu.au</a> +61 408 210 286</li> <li>• Associate Advisor: Dr Millicent Smith, <a href="mailto:millicent.smith@uq.edu.au">millicent.smith@uq.edu.au</a></li> <li>• Associate Advisor: Prof Graeme Hammer, <a href="mailto:g.hammer@uq.edu.au">g.hammer@uq.edu.au</a> +61 7 334 69463</li> </ul>
<p>Location</p>	<p>St Lucia or Gatton campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/108/lee-hickey">https://qaafi.uq.edu.au/profile/108/lee-hickey</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Genetics / Plant Science</p>




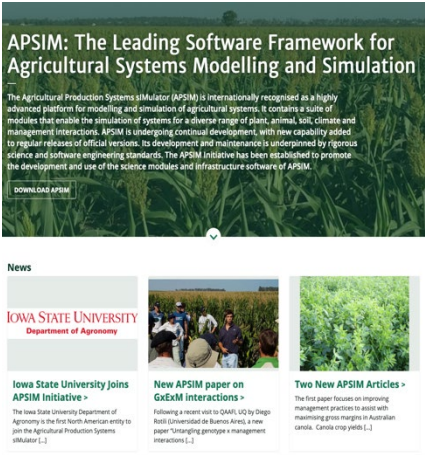


<p><b>CCS 3 Project</b></p> <p><i>A/Prof Bhagirath Chauhan</i></p> <p><i>Dr Bradley Campbell</i></p> <p><i>Dr Guoquan Liu</i></p>	<p><b><u>3) Developing Herbicide Resistant Pigeonpea and Mung Bean</u></b></p> <p>Pigeonpea and Mung Bean have great potential as legume rotation crops in cereal farming systems 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 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.</p> <p>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.</p> <p>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.</p> <div data-bbox="395 1064 911 1339"> </div> <div data-bbox="963 1079 1358 1332"> <p><b>EMS</b></p> <p><b>Mutagenesis</b></p> </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Professor Bhagirath Chauhan; <a href="mailto:b.chauhan@uq.edu.au">b.chauhan@uq.edu.au</a> ; +61 7 535 15092</li> <li>• Associate Advisors: Dr Bradley Campbell ; <a href="mailto:b.campbell2@uq.edu.au">b.campbell2@uq.edu.au</a> &amp;</li> <li>• Dr Guoquan Liu; <a href="mailto:g.liu2@uq.edu.au">g.liu2@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Lab based work will be conducted at St Lucia (UQ), while field based work will be conducted at Gatton.</p>
<p>Webpage</p>	<p><a href="https://researchers.uq.edu.au/researcher/10189">https://researchers.uq.edu.au/researcher/10189</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology, Genetics</p>



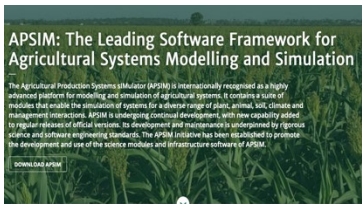
<p><b>CCS 4 Project</b></p> <p><i>Prof Daniel Rodriguez</i></p> <p><i>Dr Fer Dreccer</i></p> <p><i>Dr Jeremy Whish</i></p>	<p><b><u>4) Matching adapted chickpea genotypes with soil and climate to maximise yield and profit: Field experimentation</u></b></p> <p>Pulses can increase profits, diversify income 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.</p> <p>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.</p> <p>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 (<a href="http://www.apsim.info">www.apsim.info</a>).</p> <div data-bbox="400 1079 1323 1520">  </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Prof Daniel Rodriguez, <a href="mailto:d.rodriguez@uq.edu.au">d.rodriguez@uq.edu.au</a> +61 7 535 15091</li> <li>• Dr Fer Dreccer (CSIRO),</li> <li>• Dr Jeremy Whish (CSIRO),</li> </ul>
<p>Location</p>	<p>Gatton campus</p>
<p>Webpage</p>	<p><a href="https://www.qld-fsr.info/">https://www.qld-fsr.info/</a></p> <p><a href="https://qaafi.uq.edu.au/profile/471/daniel-rodriguez">https://qaafi.uq.edu.au/profile/471/daniel-rodriguez</a></p>
<p>Useful majors</p>	<p>Agriculture, crop physiology, agronomy</p>



<p><b>CCS 5 Project</b></p> <p><i>Prof Daniel Rodriguez</i></p> <p><i>Dr Peter deVoi</i></p> <p><i>Dr Jeremy Whish</i></p>	<p><b><u>5) Matching adapted pulse genotypes with soil and climate to maximise yield and profit: Cropping systems modelling</u></b></p> <p>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.</p> <p>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 (<a href="http://www.apsim.info">www.apsim.info</a>).</p> <p>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).</p> <div data-bbox="446 1142 794 1601">  </div> <div data-bbox="874 1137 1300 1590">  </div>
<p><b>Advisor(s) contact</b></p>	<ul style="list-style-type: none"> <li>• <b>Prof Daniel Rodriguez</b>, <a href="mailto:d.rodriguez@uq.edu.au">d.rodriguez@uq.edu.au</a> +61 7 535 15091</li> <li>• <b>Dr Peter deVoi</b>, <a href="mailto:p.devoil@uq.edu.au">p.devoil@uq.edu.au</a> +61 7 535 15087</li> <li>• <b>Dr Jeremy Whish</b> (CSIRO)</li> </ul>
<p><b>Location</b></p>	<p>Gatton Campus</p>
<p><b>Webpage</b></p>	<p><a href="https://www.qld-fsr.info/">https://www.qld-fsr.info/</a></p> <p><a href="https://qaafi.uq.edu.au/profile/471/daniel-rodriguez">https://qaafi.uq.edu.au/profile/471/daniel-rodriguez</a></p>



Useful majors	Agriculture, crop physiology, agronomy, systems modelling, IT, software engineering
---------------	---

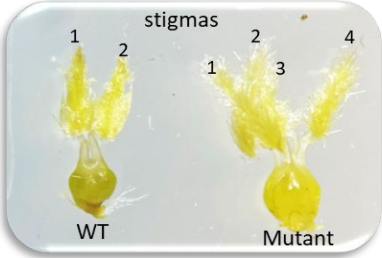


<p><b>CCS 6 Project</b></p> <p><i>Prof Daniel Rodriguez</i></p>	<p><b><u>6) Winter sown sorghum as an adaptation to present and future climates</u></b></p> <p>Water stress and extreme heat at flowering are becoming common abiotic stresses limiting sorghum production across the Northern Grains Region. 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.</p> <p>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 (<a href="http://www.apsim.info">www.apsim.info</a>), and climate projections from a wide range of global circulation models.</p> <p>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.</p> <div style="display: flex; justify-content: space-around; align-items: center;">  <div style="text-align: center;">  <div style="display: flex; justify-content: space-around; margin-top: 10px;"> <div style="text-align: center;"> <p><b>News</b></p> <p><b>IOWA STATE UNIVERSITY</b> Department of Agronomy</p> <p><b>Iowa State University joins APSIM Initiative</b></p> <p>The new Iowa State University Department of Agronomy is the first North American entity to join the Agricultural Production Systems (APSIM) Initiative.</p> </div> <div style="text-align: center;"> <p><b>New APSIM paper on GxE x M interactions</b></p> <p>Following a recent visit to QAAFI, UQ by Drago Basso (Universidade de Buenos Aires), a new paper "Emerging genotype x management interactions".</p> </div> <div style="text-align: center;"> <p><b>Two New APSIM Articles</b></p> <p>The first paper focuses on improving management practices to deal with increasing grain margins in Australian sorghum. Carlos crop yields (1)</p> </div> </div> </div> </div>
Advisor(s) contact	<ul style="list-style-type: none"> <li><b>Prof Daniel Rodriguez</b>, <a href="mailto:d.rodriguez@uq.edu.au">d.rodriguez@uq.edu.au</a> +61 7 535 15091</li> </ul>
Location	Gatton campus
Webpage	<a href="https://www.qld-fsr.info/">https://www.qld-fsr.info/</a> <a href="https://qaafi.uq.edu.au/profile/471/daniel-rodriguez">https://qaafi.uq.edu.au/profile/471/daniel-rodriguez</a>
Useful majors	Agriculture, crop physiology, agronomy, systems modelling, IT, software engineering, climate sciences





<p><b>CCS 7 Project</b></p> <p><i>Dr Karen Massel</i></p> <p><i>Dr Bradley Campbell</i></p>	<p><b><u>7) Revolutionizing Turf Management: Optimizing Gene Editing for Resilient Bermuda Grass</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p> <p>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.</p> <div data-bbox="379 1214 842 1556">  </div> <div data-bbox="858 1214 1375 1556">  </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Dr Karen Massel; <a href="mailto:k.massel@uq.edu.au">k.massel@uq.edu.au</a>; 61+ 420 676 979</li> <li>• Associate Advisors: Dr Bradley Campbell; <a href="mailto:b.campbell2@uq.edu.au">b.campbell2@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>John Hines Building (62); St Lucia Campus (UQ)</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/6037/karen-massel">https://qaafi.uq.edu.au/profile/6037/karen-massel</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Biomedical Science / Genetics / Microbiology</p>



<p>CCS 8 Project</p> <p>Dr Karen Massel</p>	<p><b>8) Fascinating fasciation via gene editing</b></p> <p><b>Background:</b> 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.</p> <p><b>Approach:</b> 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 homodimer, but there is some evidence to suggest it may also be able 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.</p> <div data-bbox="427 1070 1262 1664"> <p style="text-align: center;"><b>Supernumerary floral organs</b></p>  <p style="text-align: center;"><b>Polyembryony</b></p>   </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>Dr Karen Massel <a href="mailto:k.massel@uq.edu.au">k.massel@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Rm 319, John Hines (62), St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/">https://qaafi.uq.edu.au/</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology Genetics / Biotechnology</p>



<p><b>CCS 9 Project</b></p> <p><i>Dr Jack Christopher</i></p> <p><i>Dr Karine Chenu</i></p>	<p><b><u>9) Sustaining food production on the face of climate change through crop root adaptation</u></b></p> <p>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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Jack Christopher</b>, <a href="mailto:j.christopher@uq.edu.au">j.christopher@uq.edu.au</a> +61 7 452 91413</li> <li>• Associate Advisor: Dr Karine Chenu, <a href="mailto:karine.chenu@uq.edu.au">karine.chenu@uq.edu.au</a> +61 7 452 94252 +61 7 535 15084</li> </ul>
<p>Location</p>	<p>Leslie Research Facility, Toowoomba</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/">https://qaafi.uq.edu.au/</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Agriculture</p>



<p><b>CCS 10 Project</b></p> <p><i>Dr Jack Christopher</i></p> <p><i>Dr Yash Dang</i></p>	<p><b><u>10) Increased food production on constrained soils</u></b></p> <p>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.</p> <p>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.</p> <p>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.</p>
Advisor(s) contact	<ul style="list-style-type: none"> <li>• <b>Dr Jack Christopher</b>, <a href="mailto:j.christopher@uq.edu.au">j.christopher@uq.edu.au</a> +61 7 452 91413</li> <li>• Associate Advisor: Dr Yash Dang, SAFS, <a href="mailto:y.dang@uq.edu.au">y.dang@uq.edu.au</a></li> </ul>
Location	Leslie Research Facility, Toowoomba
Webpage	<a href="https://qaafi.uq.edu.au/">https://qaafi.uq.edu.au/</a>
Useful majors	Biochemistry & Molecular Biology / Agriculture



<p><b>CCS 11 Project</b></p> <p><i>A/Prof Andries Potgieter</i></p> <p><i>Dr Yan Zhao</i></p>	<p><b><u>11) Determining soil moisture from high-resolution satellite imagery (Sentinel-2)</u></b></p> <p>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 from this project will benefit growers with informed crop management strategies.</p> <p>Skills in machine learning and remotesensing 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..</p> <div style="display: flex; justify-content: space-around; align-items: flex-end;"> <div data-bbox="357 869 836 1196" data-label="Figure"> </div> <div data-bbox="852 878 1362 1191" data-label="Figure"> </div> </div> <div style="display: flex; justify-content: space-around; margin-top: 10px;"> <p data-bbox="399 1223 775 1294">Moisture related spectral index derived from satellite data</p> <p data-bbox="919 1227 1375 1299">Possible relationships between soil moisture and remotely sensed indices</p> </div>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>A/Prof Andries Potgieter</b>, <a href="mailto:a.potgieter@uq.edu.au">a.potgieter@uq.edu.au</a> +61 7 535 15085</li> <li>• Associate Advisor: Dr Yan Zhao, <a href="mailto:yan.zhao@uq.edu.au">yan.zhao@uq.edu.au</a> +61 7 336 56529</li> </ul>
<p>Location</p>	<p>St Lucia &amp; Gatton (at least 1 day per week using UQ bus service)</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/465/andries-potgieter">https://qaafi.uq.edu.au/profile/465/andries-potgieter</a></p>
<p>Useful majors</p>	<p>Please select from: Statistics / Mathematics / Biophysics / Computational Science</p>

<p><b>CCS 12 Project</b></p> <p><i>Dr Owen Powell</i></p> <p><i>Dr Francois Barbier</i></p> <p><i>Prof Mark Cooper</i></p> <p><i>Prof Christine Beveridge</i></p>	<h2><u>12) Predicting Plant Success - Big Data for Small Plants</u></h2> <div data-bbox="363 338 1382 741"> </div> <p>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.</p> <p>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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Owen Powell</b>, <a href="mailto:o.powell2@uq.edu.au">o.powell2@uq.edu.au</a></li> <li>• Associate Advisor: Dr Francois Barbier, SBS, <a href="mailto:f.barbier@uq.edu.au">f.barbier@uq.edu.au</a></li> <li>• Associate Advisor: Prof Mark Cooper, <a href="mailto:mark.cooper@uq.edu.au">mark.cooper@uq.edu.au</a> +61 7 334 62778</li> <li>• Associate Advisor: Prof Christine Beveridge, SBS, <a href="mailto:c.beveridge@uq.edu.au">c.beveridge@uq.edu.au</a> +61 7 336 57525</li> </ul>
<p>Location</p>	<p>St Lucia campus</p>
<p>Webpage</p>	<p><a href="https://qaafi.uq.edu.au/profile/7515/owen-powell">https://qaafi.uq.edu.au/profile/7515/owen-powell</a></p>
<p>Useful majors</p>	<p>Please select from:</p> <p>Molecular Biology / Genetics/ Computational Science</p>

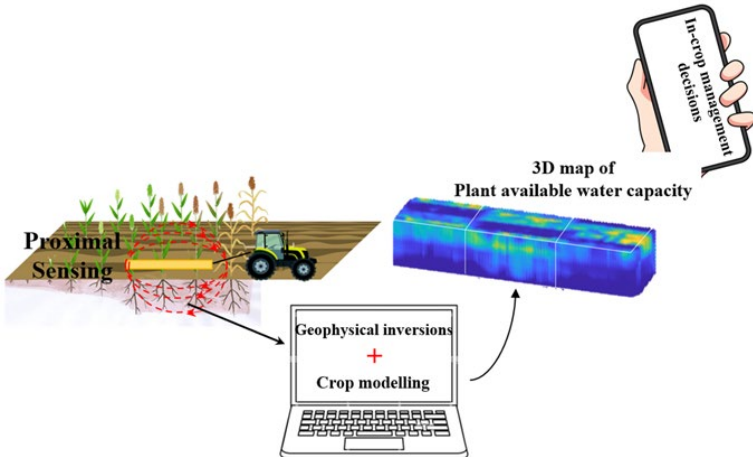




<p><b>CCS 13-18 Project</b></p> <p><i>A/Prof Emma Mace</i></p> <p><i>Prof David Jordan</i></p> <p><i>Ms Geetika Geetika</i></p>	<p><b><u>13) Mapping the genes controlling grain density in sorghum</u></b></p> <p>The density of sorghum grain is an important factor in determining its potential grain yield 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.</p> <p><b><u>14) Genetic diversity of genes involved in pollen fertility restoration in sorghum</u></b></p> <p>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.</p> <p><b><u>15) Genetic diversity of genes involved in lignin biosynthesis in sorghum</u></b></p> <p>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.</p> <p><b><u>16) Correlation of lignin content in midrib versus stem in sorghum</u></b></p> <p>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.</p> <p><b><u>17) Investigating genetic variation in lignin content in sorghum</u></b></p> <p>Lignocellulosic substance's such as lignin, cellulose and hemi-cellulose are components that make up the plant cell wall. Stem strength is comprised of varying amounts of these components. Lignin, is one of the major component of lignocellulosic biomass, and hence, determines the stem strength. Stem strength and likelihood of lodging are negatively associated and genotypes with weaker stem</p>
---	---



	<p>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.</p> <p><b><u>18) Investigating genetic control of Johnsons grass mosaic virus in sorghum</u></b></p> <p>Johnsons grass mosaic virus is a significant disease of sugarcane, sorghum and maize. In this project the student would screen a range of genotypes for resistance to this disease and contribute to mapping and cloning the genes underlying this trait.</p>
Advisor(s) contact	<ul style="list-style-type: none"> <li>• <b>A/Prof Emma Mace</b>, <a href="mailto:emma.mace@uq.edu.au">emma.mace@uq.edu.au</a> +61 7 454 26729, +61 7 336 54368</li> <li>• <b>Prof David Jordan</b>, <a href="mailto:David.jordan@uq.edu.au">David.jordan@uq.edu.au</a> +61 7 454 26722, +61 7 336 54367</li> <li>• <b>Ms Geetika Geetika</b>, <a href="mailto:g.geetika@uq.edu.au">g.geetika@uq.edu.au</a> x54366</li> </ul>
Location	<p>St Lucia or Gatton campus – data collection may occur at Gatton and Warwick.</p> <p>Project 23 could be located at the Bogo road Ecosciences Precinct Brisbane</p>
Webpage	<p><a href="https://qaafi.uq.edu.au/profile/333/emma-mace">https://qaafi.uq.edu.au/profile/333/emma-mace</a></p> <p><a href="https://qaafi.uq.edu.au/profile/222/david-jordan">https://qaafi.uq.edu.au/profile/222/david-jordan</a></p> <p><a href="https://qaafi.uq.edu.au/profile/2088/geetika-geetika">https://qaafi.uq.edu.au/profile/2088/geetika-geetika</a></p>
Useful majors	<p>Agricultural science/ Biochemistry &amp; Molecular Biology / Bioinformatics / Chemical Sciences / Genetics</p>

<p><b>CCS 19 Project</b></p> <p><i>Dr Dongxue Zhao</i></p> <p><i>Prof Daniel Rodriguez</i></p> <p><i>Dr Peter deVoil</i></p>	<p><b><u>19) 3D mapping of plant available water capacity</u></b></p>  <p>The amount of soil water available to crops – 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.</p> <p>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.</p> <p>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.</p> <p>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.</p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• <b>Dr Dongxue Zhao</b> Email: <a href="mailto:dongxue.zhao@uq.edu.au">dongxue.zhao@uq.edu.au</a></li> <li>• <b>Prof Daniel Rodriguez</b> Email: <a href="mailto:d.rodriguez@uq.edu.au">d.rodriguez@uq.edu.au</a></li> <li>• <b>Dr Peter deVoil</b> Email: <a href="mailto:p.devoil@uq.edu.au">p.devoil@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>Gatton or St Lucia Campus</p>
<p>Webpage</p>	<p><a href="https://www.qld-fsr.info/">https://www.qld-fsr.info/</a></p> <p><a href="https://qaafi.uq.edu.au/profile/9642/dongxue-zhao">https://qaafi.uq.edu.au/profile/9642/dongxue-zhao</a></p>
<p>Useful majors</p>	<p>Plant Science / Soil Science / Computational Science / Agronomy</p>

<p><b>CCS 20 Project</b></p> <p><i>Dr Bradley Campbell</i></p> <p><i>Dr Karen Massel</i></p>	<p><b><u>20) Breaking the Barriers: Developing a Protoplast System for Genetic Advancement of Taro and Root Crops</u></b></p> <p>Taro (<i>Colocasia esculenta</i>) is an important root crop cultivated globally for its starchy tuberous roots. It serves as a staple food source for millions of people in developing countries. Despite its significance, the genetic improvement of taro has been limited due to its recalcitrance to genetic transformation. Protoplast development, which involves the removal of the cell wall from plant cells, has been shown to be a promising method for genetic modification in several plant species. The development of an efficient protoplast system for taro can pave the way for genetic improvement of this important crop.</p> <p>Protoplast isolation and culture can provide an alternative platform for gene transfer and editing in taro. Protoplast technology has been used successfully to regenerate several economically important crops, such as rice, wheat, and potato. Developing an efficient protoplast system for taro can facilitate the transfer of desirable traits from related species to taro, leading to improved yield, quality, and resistance to biotic and abiotic stresses.</p> <p>Furthermore, taro can serve as a model for genetic improvement of other root crops, such as cassava, sweet potato, and yam. These crops face similar genetic transformation challenges as taro and would benefit from the development of an efficient protoplast system.</p> <div data-bbox="363 1093 842 1608"> </div> <div data-bbox="858 1093 1385 1451"> </div> <p style="text-align: center;"><b>Protoplast Image</b></p>
<p>Advisor(s) contact</p>	<ul style="list-style-type: none"> <li>• Dr Bradley Campbell; <a href="mailto:b.campbell2@uq.edu.au">b.campbell2@uq.edu.au</a>; 61+ 412 648 391</li> <li>• Associate Advisors: Dr Karen Massel; <a href="mailto:k.massel@uq.edu.au">k.massel@uq.edu.au</a></li> </ul>
<p>Location</p>	<p>John Hines Building (62), St Lucia Campus (UQ)</p>
<p>Webpage</p>	<p><a href="https://www.abc.net.au/gardening/how-to/future-proofing-taro/13881562">https://www.abc.net.au/gardening/how-to/future-proofing-taro/13881562</a></p>
<p>Useful majors</p>	<p>Biochemistry &amp; Molecular Biology / Biomedical Science / Chemical Sciences / Genetics / Microbiology</p>



<p><b>CCS 21 Project</b></p>	<p><b><u>21) What is the value of increased sorghum grain quality to grain growers and cattle producers?</u></b></p>
<p><i>Dr Joseph Eyre</i></p>	<p>Sorghum is one of the most important crops across the semi-arid tropics worldwide 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</p>
<p><i>Dr Karen Harper</i></p>	<p>sustainability. Understanding the genetic and environmental drivers of grain quality 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.</p>
<p><i>A/Pro Daniel Cozzolino</i></p>	<p>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.</p>
	<p>Our previous research showed that new grain sorghums have greater value to livestock per hectare (Digestible Energy [DE], MJ/ha) than industry standard 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.</p>
	<p>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</p>
	<p>Topics for honours project within this program include;</p> <ol style="list-style-type: none"> <li>1- Field crop agronomy – Grain density distribution of waxy, white and red sorghum types and the morphological attributes,</li> </ol>





	<p>2- Cattle nutrition – Effect of sorghum grain density and genotype on in-vitro digestible energy.</p> <p>3- Grain quality analysis - MIR/NIRs methods to quantify grain sorghum quality,</p> <p>4- Crop-physiology – Environmental drivers of grain sorghum quality variability for selected waxy, white and red sorghum types.</p> <p>5- Crop modelling – Simulation modelling sorghum and maize production systems.</p> <p>Scholars will be expected to provide Joseph Eyre <a href="mailto:j.eyre@uq.edu.au">j.eyre@uq.edu.au</a> 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.</p>
Advisor(s) contact	<ul style="list-style-type: none"> <li>• Principle advisor: Dr Joseph Eyre <a href="mailto:j.eyre@uq.edu.au">j.eyre@uq.edu.au</a></li> <li>• Associate Advisors: Dr Karen Harper <a href="mailto:karen.harper@uq.edu.au">karen.harper@uq.edu.au</a> ;</li> <li>• A/Pro Daniel Cozzolino <a href="mailto:d.cozzolino@uq.edu.au">d.cozzolino@uq.edu.au</a></li> </ul>
Location	Gatton and St Lucia Campus
Webpage	
Useful majors	Agronomy / Crop physiology / Biochemistry / Computational Science

<b>CCS 22 Project</b>	<b><u>22) Economic thresholds for managing fall armyworm damage in sorghum and maize</u></b>
<i>Dr Joseph Eyre</i>	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 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.
<i>Melina Miles</i>	
<i>Roslyn Gleadow</i>	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 <https://www.apsim.info/>) 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 <a href="mailto:j.eyre@uq.edu.au">j.eyre@uq.edu.au</a> 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	<ul style="list-style-type: none"> <li>• Principle advisor: Dr Joseph Eyre <a href="mailto:j.eyre@uq.edu.au">j.eyre@uq.edu.au</a></li> <li>• Associate Advisors: Melina Miles <a href="mailto:Melina.Miles@daf.qld.gov.au">Melina.Miles@daf.qld.gov.au</a></li> <li>• Roslyn Gleadow <a href="mailto:ros.gleadow@monash.edu.au">ros.gleadow@monash.edu.au</a></li> </ul>
Location	Gatton Campus
Webpage	
Useful majors	Agronomy / Crop physiology / Biochemistry / Computational Science

<b>CCS 23 Project</b>	<b><u>23) What is the influence of sustainability frameworks on grower/producer decision making?</u></b>
<i>Dr Joseph Eyre</i>	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.
<i>Melina Miles</i>	
<i>Roslyn Gleadow</i>	<p>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.</p> <p>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".</p>



	<p>During the emersion tour the project team will conduct surveys with stakeholders including farmers, community leaders, agri-business and government representatives to;</p> <ul style="list-style-type: none"><li>• Benchmark farmers' current sustainable practices</li><li>• Understand farmers' interpretation of the term 'sustainability'</li><li>• Explore farmers' views on the sustainability of Australian agriculture, both now and in the future</li><li>• Gauge awareness of, and participation in, industry frameworks or schemes that demonstrate sustainability</li><li>• Identify expectations and concerns around premium payments for frameworks or schemes and explore compliance issues</li></ul> <p>Honours scholars will have access to this survey dataset to complete a thesis on topics such as;</p> <ul style="list-style-type: none"><li>- Review of sustainability frameworks and best practice guidelines in mixed-farming systems,</li><li>- What is the influence of industry sustainability frameworks on farmers decision making?</li><li>- What can we learn from farmers learning?</li><li>- What are the bridging points for improving farming practices as well as tailoring sustainability framework for tracking and improving sustainability outcomes.</li></ul> <p>Scholars will be expected to provide Associate Professor Sudhir Yadav <a href="mailto:sudhir.yadav@uq.edu.au">sudhir.yadav@uq.edu.au</a> 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.</p>
Advisor(s) contact	<ul style="list-style-type: none"><li>• Principle advisor: Associate Professor Sudhir Yadav <a href="mailto:sudhir.yadav@uq.edu.au">sudhir.yadav@uq.edu.au</a></li><li>• Associate Advisors: Dr Joseph Eyre <a href="mailto:j.eyre@uq.edu.au">j.eyre@uq.edu.au</a></li></ul>
Location	Remote
Webpage	
Useful majors	Agronomy / Crop physiology / Biochemistry / Computational Science