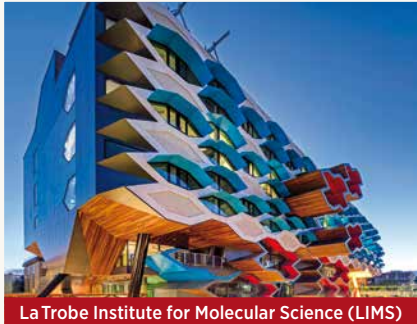


AGRIBIO INTERNATIONAL GRADUATE PROGRAM



Research at La Trobe University



La Trobe Institute for Molecular Science (LIMS)



AgriBio, Centre for AgriBioscience



The Agora, Melbourne Campus main hub

La Trobe University is among the top 100 universities in the world under the age of 50 (Times Higher Education Rankings 2013), one of Australia's research leaders and the largest provider of higher education to regional Victoria. In almost 50 years more than 160,000 students from all walks of life have graduated from La Trobe University.

La Trobe is recognised nationally and internationally for delivering high-quality teaching and research. In the 2012 Excellence in Research for Australia (ERA) assessment, the La Trobe was ranked at world standard or above in 15 fields of research. In Agricultural Sciences (Plant, Soil and Veterinary Science) La Trobe was ranked above or well above world standard.



Interior of the AgriBio building

Our commitment to expanding our research facilities and our ongoing focus on sustainability and social responsibility, underscores our reputation for creating opportunities for all who can benefit from higher education.

Our success is driven by people who are committed to making a difference. Our teaching and research address

some of the most pressing issues of our time; our public intellectuals are among the most engaged in the nation; and our alumni are some of the most influential people their generations have produced.

AGRIBIO INTERNATIONAL GRADUATE PROGRAM

The Centre for AgriBioscience (AgriBio) represent a 300 million dollar investment that brings together government, university and biotech companies in one environment to develop and drive innovative research in agricultural science, to maintain and increase agricultural production to meet the increasing demands for food with a growing world population.



Professor Jim Whelan

AgriBio aims to help meet this demand in an environmentally sustainable and ethical manner. The research carried out in AgriBio and with collaborators will underpin food production and safety standards in the coming decades.

As part of its commitment to AgriBio, La Trobe University has established a Graduate

research program in AgriBioscience. In addition to the normal research training that is obtained during graduate research studies, the program will provide students with skills that will equip them to work in a variety of employment environments once completed.

Agriculture is a multi-disciplinary science, incorporating research in the laboratory, to work on the land, to marketing and putting food on the dining table. Students undertaking the AgriBio graduate program will be exposed to these areas so that from this experience they can choose their interests and where they wish to make a contribution in future.

In this booklet you will find information on the AgriBio research laboratories and some of the research projects hosted by the program. This is not an exhaustive list and you are encouraged to contact the AgriBio staff as indicated. We are very happy to be contacted and to provide you with more specific information.

Entry into the AgriBio International Graduate program can be funded through a number of scholarship schemes. La Trobe University offers a number of scholarships dedicated to the AgriBio international graduate program.

In addition, scholarships for international students may be available through the Australian International Post-graduate awards program, Endeavour, and through a variety of bi-lateral scholarship schemes with various countries (e.g. Chinese Scholarship Council) to study at La Trobe or in Australia.

If you require any further information please contact me: at J.Whelan@latrobe.edu.au.

Professor Jim Whelan

Co-Director AgriBio



Professor Michael F. Clarke

La Trobe University is committed to making a difference and addressing the big issues that matter to the world.

The University is focusing on five cross-disciplinary Research Focus Areas (RFAs), bringing together top researchers to address issues affecting the future of our national and global

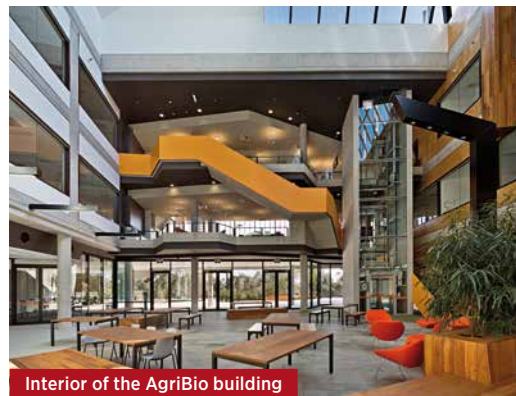
community. La Trobe is investing \$3.75m over 5 years to each of the RFAs. Securing Food, Water and the Environment is one area selected for investment.

It aims to engage partners and to foster cross disciplinary research to find solutions that address the global challenge of securing food, water and environmental integrity on a planet that needs to support 9 billion people in 2050.

This will include issues such as; food security; drought, land degradation and desertification; climate change; water scarcity; marine fish stock depletion; irretrievable loss of biodiversity; biofuel expansion; stressed and dysfunctional ecosystems; agricultural and food supply chain losses and waste.

Professor Michael F. Clarke

Director Securing Food, Water and the Environment.



Interior of the AgriBio building

AGRIBIO INTERNATIONAL GRADUATE PROGRAM

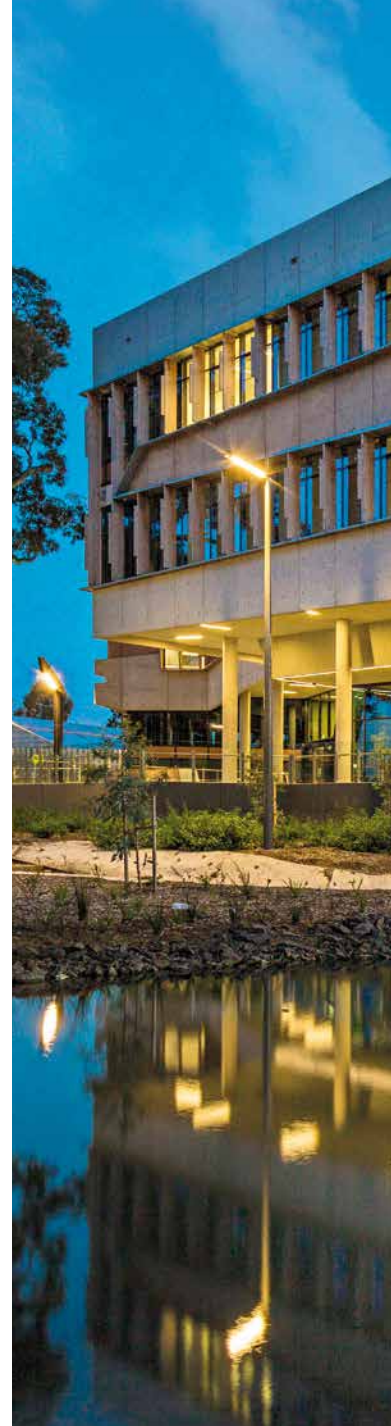


The AgriBio international graduate program is specifically designed for international students to enter an Australian graduate research program either directly from their honors degree program (4 year course) or masters program.

The student will immediately enter a world-class research environment, starting research with their supervisor of choice. In addition to this one-on-one research-training program, the following enrichment modules will be offered in this graduate research program.

YEAR I

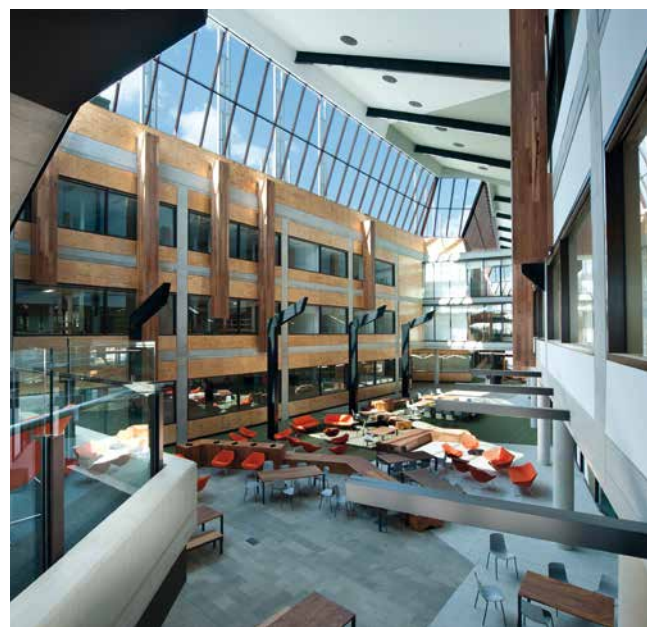
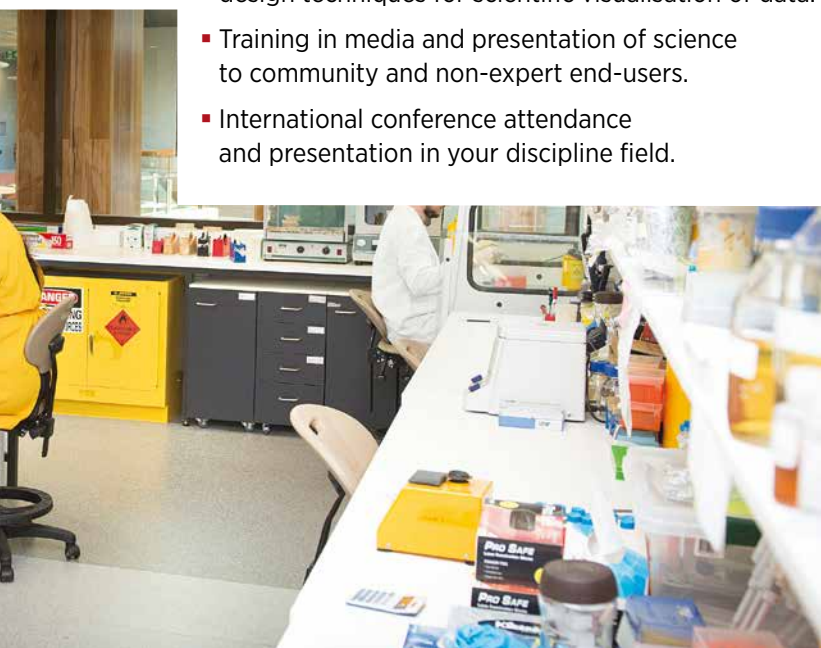
- 10 week English course designed to sharpen both oral and written English skills.
- Research seminar and poster presentation to train and develop skills in scientific presentation.





YEARS 2 AND 3

- Dedicated courses in systems biology, lecture and workshop based to ensure training in all emerging technologies.
- Dedicated training in issues of intellectual property and commercialisation of scientific discoveries.
- Training in marketing and economics of agriculture.
- Training in writing scientific manuscripts.
- Training in multi-media forums and in graphical design techniques for scientific visualisation of data.
- Training in media and presentation of science to community and non-expert end-users.
- International conference attendance and presentation in your discipline field.



YEAR 4

- Training in grant application on how to obtain research and fellowship funding.
- Career advice and development of a web based scientific profile and web page.



HOST-PATHOGEN INTERACTIONS

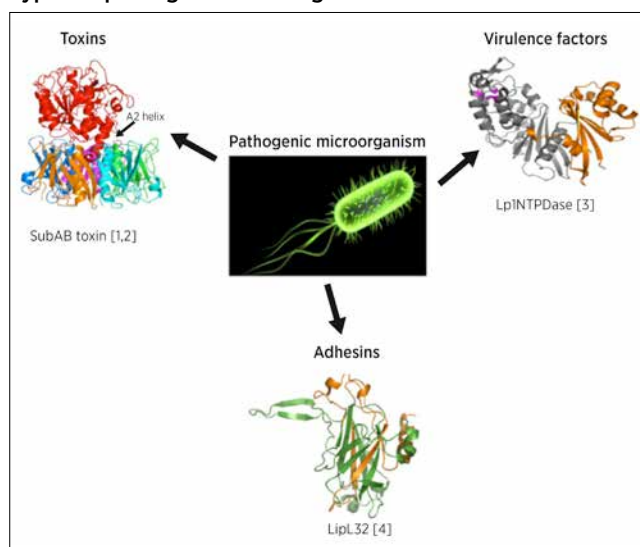
Due to the increase in the world's population, we now face mounting challenges in food production. One of the main challenges to increasing secure food production is that many parasitic and bacterial diseases have a destructive long-term impact on animal and human health.

Pathogenic bacteria and parasites have an arsenal of surface and secreted proteins to allow them to conquer the many unique niches they occupy throughout the course of infection. These proteins have varied functions such as adhesins for attachment to cells, toxins and virulence factors that manipulate or corrupt both host immune responses and cellular functions.

We use a combination of biochemistry, biophysical and X-ray crystallography approaches to determine the molecular role of these proteins in bacterial and parasitic pathogenesis. This will not only unravel key aspects of microbial pathology, but will also provide a range of novel antimicrobial drug targets.

These studies will form the basis of further studies to capitalize on the wealth of bacterial and parasitic genomic data. The encoded proteins from such genomes provide an invaluable resource for the systematic examination of bacterial physiology, host-pathogen interactions and microbial pathogenesis.

Types of pathogenic microorganisms



REFERENCES

- Paton, A.P., et al., (2006), AB5 subtilase cytotoxin inactivates the endoplasmic reticulum chaperone BiP, *Nature*, 433, 548-552
- Byres, E., et al., (2008), Incorporation of a non-human glycan mediates human susceptibility to a bacterial toxin., *Nature*, 456, 648-652
- Vivian, J.P., et al., (2010), Crystal structure of a *Legionella pneumophila* ecto-triphosphate diphosphohydrolase, a structure and functional homologue of the eukaryotic NTPDases., *Structure*, 18, 228-238
- Vivian, J.P., (2009), Crystal structure of LipL32, the most abundant surface protein of pathogenic *Leptospira* spp., *J. Mol. Biol.*, 387, 1229-1238





THESE STUDIES WILL FORM BASIS OF FURTHER STUDIES TO CAPITALISE ON THE WEALTH OF BACTERIAL AND PARASITIC GENOMIC DATA.

RESEARCH PROJECT

Structure and function of novel AB5 toxins produced by pathogenic bacteria

AB5 toxins are an important family of toxins that cause massive global morbidity and mortality, accounting for over 1-2 million deaths each year, particularly amongst children in developing countries.

AB5 toxins exert their effects in a two-step process:

- I. binding of the pentameric B subunit to specific glycan receptors on the target cell surface;
- II. internalisation of the AB5 toxin, followed by A subunit-mediated inhibition or corruption of essential host functions.

The above AB5 toxins ultimately act on cytosolic targets, and so must be internalised, transported to the appropriate site and translocated across the respective organelle membrane.

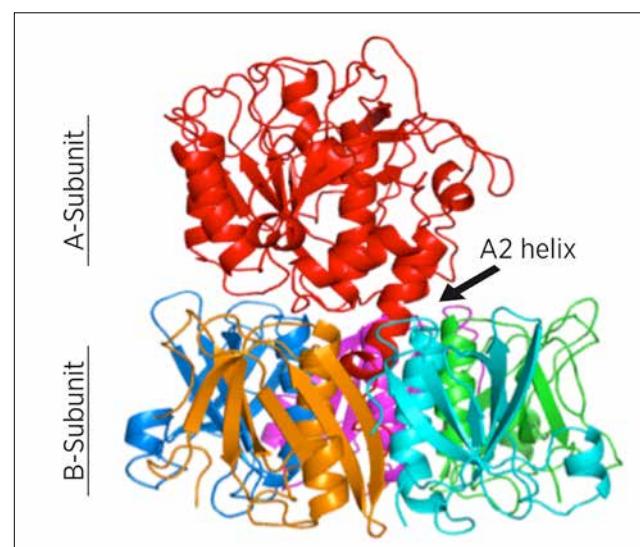
The AB5 toxins from each sub-family possess unique properties that arise from differing catalytic activities of the A subunit and/or differing receptor specificities of the B subunit.

CURRENT PROJECTS

- Understanding the structure and function of several novel AB5 toxins
- Investigating the evolution of AB5 toxins

Further reading: Beddoe et al, (2010), Trends Biochem Sci., 35, 411-18

Structure of the novel AB5 toxin – SubAB



SEED BIOLOGY AND BIOTECHNOLOGY

My lab uses genetic and molecular approaches to study aspects of plant development and physiology using the model plant *Arabidopsis thaliana*, but also have interests in testing the conservation of gene function in other plants.

Our current work is aimed at understanding two important aspects of plant development – flowering time and responses to abiotic stresses. We are particularly interested in using the natural variation present between different varieties (ecotypes or accessions) of a species to identify genes that regulate particular characteristics.

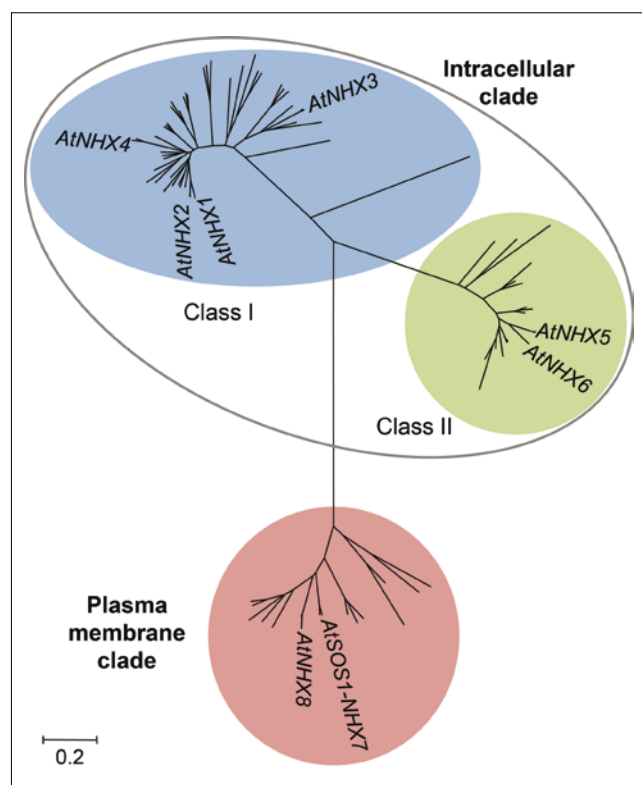
These methods initially use genetic approaches (mapping of segregating traits) to determine how many genes are responsible for a particular trait, and molecular techniques to clone the genes. Additional work uses genetic screens and novel mutants to uncover new genes in flowering time and salt signaling pathways.

A major area of interest in the lab is the regulation of ion homeostasis by a family of intracellular Na^+/H^+ antiporters in the model plant *Arabidopsis*. Overexpression of many of these family members leads to increased salt tolerance, but the mechanisms for this resistance is poorly understood.

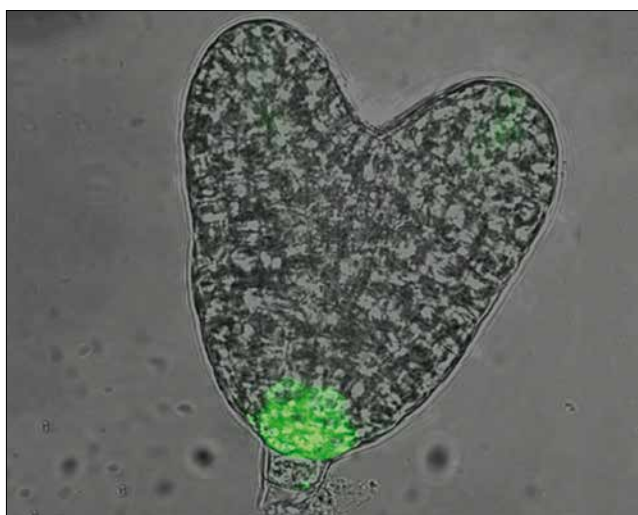
We have recently shown that two of these antiporters are required for normal plant development and appear to have roles in intracellular protein trafficking.

These antiporters regulate the pH of intracellular compartments, and influence ion sensitivity and protein trafficking by interacting with specific components of the protein trafficking, sorting and recycling machinery.

We have recently shown that these antiporters affect the processing and accumulation of seed storage proteins and other vacuole localized proteins.



Heart-shaped embryo



REFERENCES

- Ford, B.A., Ernest J.E. and Gendall A.R.(2012) Identification and characterization of orthologs of *AtNHX5* and *AtNHX6* in *Brassica napus*. *Frontiers in Plant Science* 3, 208.
- Seedat, N., Dinsdale A, Ong, E.K, Gendall, A.R. (2013). Acceleration of flowering in *Arabidopsis thaliana* by Cape Verde Islands alleles of *FLOWERING H* is dependent on the floral promoter *FD*. *Journal of Experimental Botany* 64, 2767-78.



OUR CURRENT WORK IS AIMED AT UNDERSTANDING TWO IMPORTANT ASPECTS OF PLANT DEVELOPMENT – FLOWERING TIME AND RESPONSES TO ABIOTIC STRESSES.

RESEARCH PROJECT

Seed Storage Protein Synthesis and Mobilisation

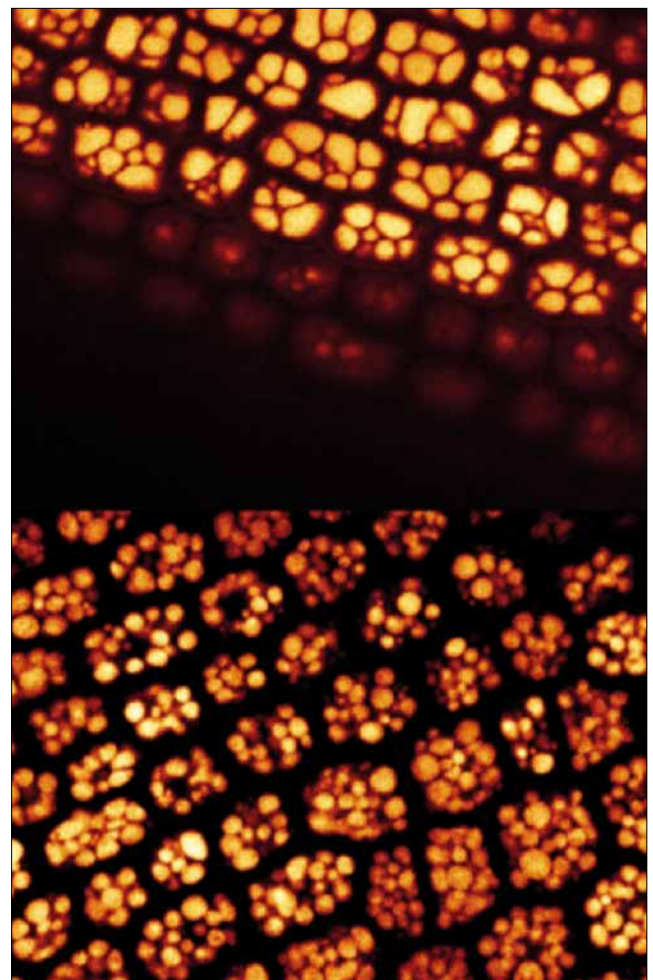
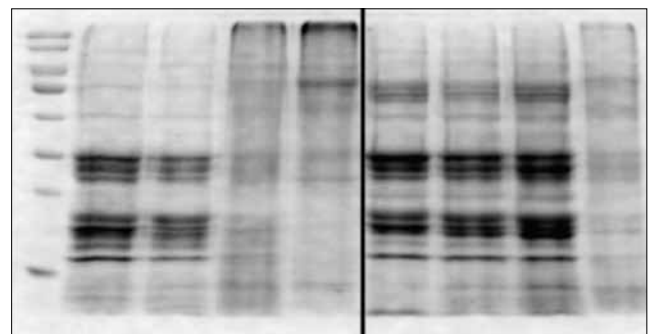
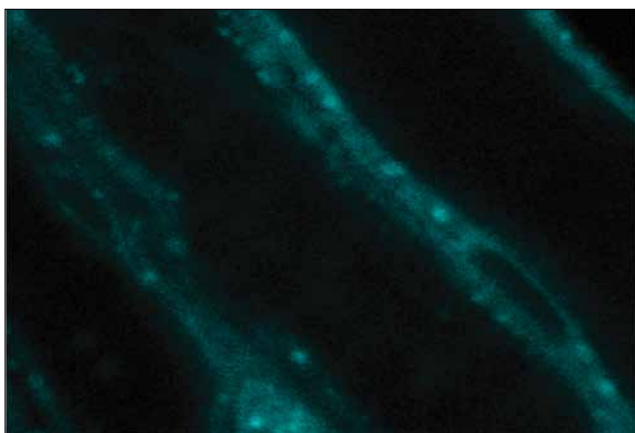
Seed storage proteins accumulate in the seeds of all major food crops. In many plant species, the amount and quality of seed proteins is a critical determinant of their nutritional properties.

The synthesis during embryo development, and the subsequent mobilisation (breakdown) of these nitrogen rich proteins during germination is crucial for seedling establishment.

This project will investigate the mechanism of seed storage protein biosynthesis and mobilisation during germination in a relative of the Brassica oilseeds species, and determine if altering the normal biosynthesis of seed storage proteins leads to changes in protein content and improved nutritional properties.

It will use a combination of sub-cellular fractionation to separate protein storage vacuoles, and proteomics to identify proteins that are mis-localised and/or mis-processed in mutants with trafficking and processing defects, or in plants that overexpress components of the sorting machinery.

Plasma membrane



NEMATODE FUNCTIONAL AND POPULATION GENOMICS

Research in the Grant lab is focused on two major areas related to parasitic nematodes. The first of these is the application of population genomic technologies to analysis of parasitic nematode population biology, especially to the evolution and spread of drug resistance.

Most of this work targets human filarial parasites, with opportunities also to extend these technologies to the helminths parasites of livestock. The second area of interest in the Grant lab is the evolution of parasitism as a life history strategy in nematodes, particularly using the possum parasitic nematode *Parastrongyloides trichosuri* (a parasite of the Australian brushtail possum).

DRUG RESISTANCE

Bioinformatic analysis of next generation sequence data from *Onchocerca volvulus* (the causative organism of river blindness), and development of genotyping assays for drug resistance based on those data,

Investigation of *Cercopithifilaria johnstoni*, a parasite of Australian bush rats, as a novel rodent model for river blindness. This project will require some field work

Genetic analysis of drug resistances in the sheep parasite *Teladorsagia circumcincta*. Resistances in other veterinary parasites may also be of interest if suitable parasites strains are available.

Models of drug resistance in *C. elegans*, including the assessment of candidate resistance genes from parasitic species in transgenic *C. elegans*.

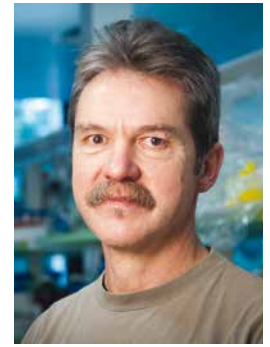
There is a strong emphasis on bioinformatics analysis of next generation sequence data in most of these projects.

PARASITE EVOLUTION

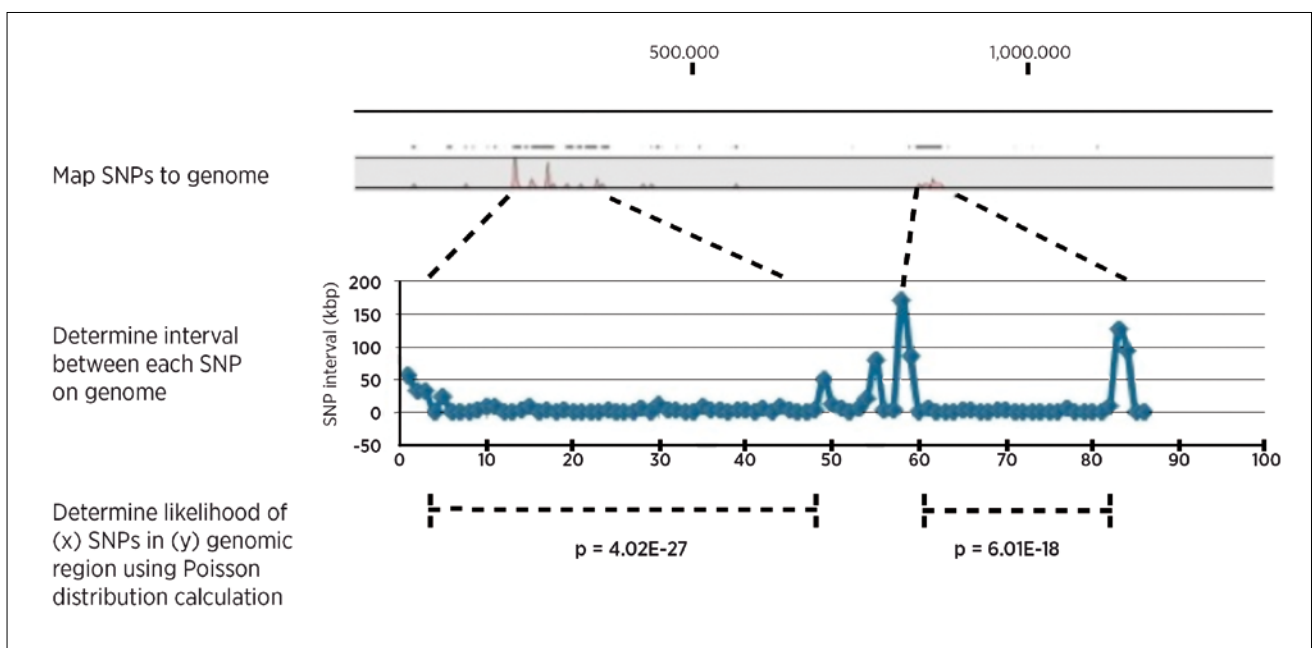
The current focus of this work is the analysis of next generation sequencing data to develop genotyping markers for gene mapping in *Parastrongyloides trichosuri*. The main techniques are some simple bioinformatics, worm culture, PCR and sequencing. In addition, some help with maintaining parasite cultures may be required, including collecting samples of parasite material from captive brush tail possums.

REFERENCES

- Crook, M. Grant, K. & Grant W. N. 2010, Failure of *Parastongyloides trichosuri* daf-7 to complement a *Caenorhabditis elegans* daf-7 (e1372) mutant: implications for the evolution of parasitism. *International Journal for Parasitology*, 40, 1675-83 (Epub 2010 Jul 29).
- Doyle, S.r., Chan, C.k., Grant, W.n. (2011). Enhanced annealing of mismatched oligonucleotides using a novel melt-curve assay allows efficient in vitro discrimination and restriction of a single nucleotide polymorphism. *BMC Biotechnology*, 11: 83. DOI:10.1186/1472-6750-11-83
- Stasiuk, S., Scott, M. And Grant, W. N. (2012) Developmental plasticity and the evolution of parasitism in an unusual nematode, *Parastrongyloides trichosuri*. *Evo Devo*, 3: 1
- Ma, G., Rahman, M. M., Grant, W., Schmidt, O And Asgari, S. (2012) Insect tolerance to the crystal toxins Cry1Ac and Cry2Ab is mediated by the binding of monomeric toxin to lipophorin glycolipids causing oligomerization and sequestration reactions. *Developmental and Comparative Immunology*, 37: 184 – 192
- Peeters, L., Janssen, T., De Haes, W., Beets, I., Meelkop, E., Grant, W. And Schoofs, L. (2012) A pharmacological study of NLP-12 neuropeptide signalling in free-living and parasitic nematodes. *Peptides*, 34: 82 – 87.
- Boatin, B. A., Basanez, M. - G, Prichard, R. K., Awadzi, K., Barakat, R. M., Garcia, H. H., .Grant, W. N. & Lustigman, S. (2012). A research agenda for helminth diseases of humans: Towards control and elimination. *PLoS Neglected Tropical Diseases*, 6(4)
- Lustigman, S., Geldhof, P., Grant, W. N., Osei-Atweneboana, M. Y., Sripa, B., & Basanez, M. -G, Prichard, R. K. (2012). A research agenda for helminth diseases of humans: Basic research and enabling technologies to support control and elimination of helminthiasis. *PLoS Neglected Tropical Diseases*, 6(4)



THERE IS A STRONG EMPHASIS ON BIOINFORMATICS ANALYSIS OF NEXT GENERATION SEQUENCE DATA IN MOST OF THESE PROJECTS.



- Lustigman, S., Prichard, R. K., Gazzinelli, A., Grant, W. N., Boatin, B. A., McCarthy, J. S., & Basanez, M. - G. (2012). A research agenda for helminth diseases of humans: The problem of helminthiasis. *PLoS Neglected Tropical Diseases*, 6(4)
- Crook, M. & Grant, W. N. (2013) Dominant negative mutations of *Caenorhabditis elegans* daf-7 confer a novel developmental phenotype. *Dev. Dynamics*, 242(6): 654-664,
- Doyle, S.r., Naga R. P. Kasinadhuni, Chan, C.k., & Grant, W.n. (2013) Evidence of evolutionary constraints on the sequence composition of mitochondrial matrix targeting sequences. *PLoS One* 10.1371/journal.pone.0067938
- Kulkarni, A., Dyka, A., Nemetschke, L., Grant, W. N. And Streit, A. (2013) *Parastrongyloides trichosuri* suggests that XX/XO sex 1 determination is ancestral in Strongyloidea (Nematoda). *Parasitology* (in press).



GENE NETWORKS, TAPETAL AND SEED COAT DEVELOPMENT

We study the gene networks regulating anther and seed coat development and controlling response to heat stress. We employ cutting-edge technologies to identify and characterize the components in these networks. The new technologies developed in these studies are being used to improve grain quality and yields.

The anther tapetum (tp) provides nutrients, proteins, lipids and polysaccharides to pollen. Tapetum undergoes programmed cell death (PCD) in late anther stages, which is essential for its functions. Tapetal PCD is highly sensitive to heat stress in several major crops. Substantial losses in grain yield occur as a consequence of heat stress.

We have identified a transcription factor gene MYB80 which is involved in regulating tapetal development and PCD. The expression of the MYB80 gene is restricted to the anther tapetum and the microspores (Figure).

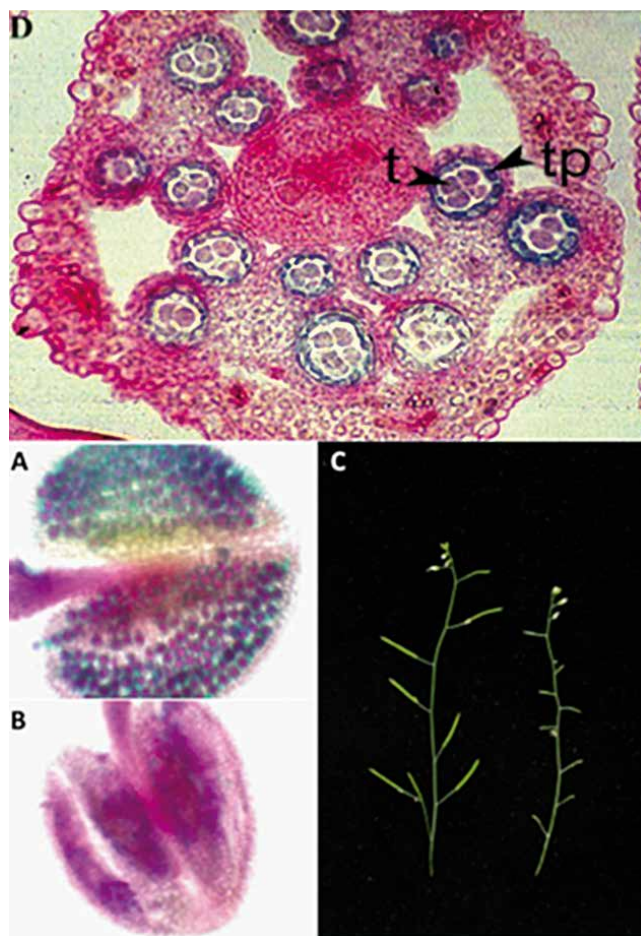
Male sterility and silique abortion occur when the MYB80 gene is disrupted. One of the MYB80 target gene is UNDEAD coding for an aspartic protease, which is involved in the timing of tapetal PCD.

Hybrid varieties are known to exhibit increased yields and improved tolerance to stresses and diseases. Hybrid seed production requires the induction and then the reversal of male sterility.

We have developed a reversible male sterility system using MYB80 for hybrid seed production. MYB80 homologues occur in flowering plants and hence our patented technology can be applied in many major crop plants.

Seed coat development plays a fundamental role in seed dormancy, germination and protection. We have identified the MYB5/TTG1 network which when inhibited causes disruption in mucilage (pectin) and tannin synthesis. The myb5 and ttg1 mutants exhibit increased seed oil contents.

Many MYB5/TTG1 target genes which are involved in these metabolic pathways have been identified and their roles in seed coat development will be examined. The MYB5/TTG1 network may be modified to achieve higher seed oil contents in oilseed crops.



A. Alexander's staining of a wild-type Arabidopsis anther
B. Alexander's staining of a myb80 mutant anther
C. Elongated siliques in a wild-type Arabidopsis inflorescence (left) and aborted siliques in a myb80 mutant inflorescence (right)
D. Expression of MYB80 promoter/GUS in tapetum (tp) and microspores (t, tetrads)

Dr Song Li
E s.li@latrobe.edu.au



Professor Roger Parish
E r.parish@latrobe.edu.au



WE HAVE IDENTIFIED A TRANSCRIPTION FACTOR GENE MYB80 WHICH IS INVOLVED IN REGULATING TAPETAL DEVELOPMENT AND PCD.

RESEARCH PROJECT

The genes and pathways regulated by MYB80 involved in pollen development and the effects of heat stress on tapetal PCD in Arabidopsis and wheat

The MYB80-regulated network consists of many pathways including tapetal PCD, breakdown of the callose wall surrounding tetrads and the synthesis of pollen exine wall. Whilst we have identified several MYB80 target genes, the identity and functions of the network components are still largely unknown. The project aims to identify and study the network components regulated by MYB80.

Heat stress is a key abiotic stress influencing wheat yield in Australia. Global warming is projected to increase the average temperature and the frequency of heat events and the consequent reductions in yield will seriously undermine global food security.

In many self-pollinating crops such as wheat, heat stress at the time of pollen development results in pollen sterility and a severe reduction in grain number. Heat stress affects tapetal development and the timing of tapetal PCD, making it occur prematurely and thereby causing pollen abortion and sterility. The objective of this project is to ascertain to what extent heat stress interferes with tapetal development and PCD in Arabidopsis and wheat, and to study the effect of heat stress on MYB80 gene network.

Methods

Laser capture microscopy, RNA-seq, chromatin immunoprecipitation, electrophoretic mobility shift assay, qRT-PCR, analysis of T-DNA insertion mutants, plasmid construction and plant transformation.



RECENT PUBLICATIONS

- Parish, R.W., Phan, H.A., Iacuone, S. and Li, S.F. (2012) Tapetal development and abiotic stress: a centre of vulnerability. *Functional Plant Biology* 39: 553–559.
- Phan, H.A., Li, S.F. and Parish, R.W. (2012) MYB80, a regulator of tapetal and pollen development, is functionally conserved in crops. *Plant Molecular Biol.* 78:171–83.
- Phan, H.A., Iacuone, S., Li, S.F. and Parish, R.W. (2011). The MYB80 transcription factor is required for pollen development and the regulation of tapetal programmed cell death in *Arabidopsis thaliana*. *The Plant Cell* 23: 2209–2224.
- Parish, R.W. and Li, S.F. (2010). Death of a tapetum: A programme of developmental altruism. *Plant Sci.* 178: 73–89.
- Li, S.F., Milliken, O.N., Pham, H., Seyit, R., Napoli, R., Preston, J., Koltunow, A.M. and Parish, R.W. (2009) The Arabidopsis MYB5 transcription factor regulates mucilage synthesis, seed coat development, and trichome morphogenesis. *The Plant Cell*, 21, 72–89.
- Li, S.F., Iacuone, S. and Parish, R.W. (2007). Suppression and restoration of male fertility using a transcription factor. *Plant Biotech. J.* 5: 297–312.

THE INTERACTIONS OF PATHOGENIC FUNGI AND PLANTS

Dr Plummer's research work within the CRC Plant Biosecurity is to investigate mechanisms for accurate and unambiguous identification of pathogens, using comparative genomics. This work is a collaborative effort between Dr Plummer's lab and researchers within DEPI Victoria and Plant and Food Research, NZ and various other international groups.

Currently, fungicides are used to prevent losses due to fungal diseases. It is anticipated that these diseases will become more economically important as fungicides are phased out (due to health risks and fungicide resistance) or as pathogens adapt to overcome these chemicals.

The main goal of Kim's research is to understand the mechanisms involved in interactions between fungal pathogens and their plant hosts.

The ultimate aim will be to identify and isolate the genes involved in these interactions with a view to improving the plant's natural resistance barriers to diseases and pests. The focus of this research is the molecular basis of plant-pathogen interactions and development of white rot (*Sclerotinia sclerotiorum*), apple scab disease (*Venturia inaequalis*) and pear scab (*V. pirina*) (utilizing genomics, proteomics and cytological techniques).

The main goal of this research is to understand the mechanisms involved in interactions between fungal pathogens and their hosts with a view to isolating the genes determining the interactions. Key developmental stages are being identified as targets for control.

The long-term aim is to develop strategies for sustainable plant disease control. The focus is on the identification of genes involved in the interaction of the fungal pathogens with their host. They are specifically identifying factors that are involved in pathogenicity, host recognition and host resistance responses.

This work is in collaboration with researchers at University of Florida, USA, Lincoln University, NZ, Plant & Food Research. The long-term focus is on the development of strategies for sustainable plant disease resistance.

RESEARCH PROJECT

Identifying and characterizing effectors involved in host specificity.

Effectors are generally proteins that pathogens secrete to enable them to infect plants. Plants in turn can adapt to be able to recognize these proteins and react with a defense response to the would-be invading pathogen. We are using comparative proteomics, transcriptomics and genomics to identify effectors produced by various fungal pathogens in the genus *Venturia* (cause of scab diseases in apples and pears). The project will identify and characterise specific candidate effectors and will include a variety of lab work and bioinformatics (computer work). We have sequenced races of the various scab fungi to enable this work to be conducted. A range of approaches will be used including genome wide association studies, RNAseq analyses and protein bioassays on resistant hosts.

PAPERS RELEVANT TO THE PROJECT

- Vincent G.M. Bus, Erik H.A. Rikkerink, Valérie Caffier, Charles-Eric Durel, and Kim M. Plummer. (2011) Revision of the Nomenclature of the Differential Host-Pathogen Interactions of *Venturia inaequalis* and *Malus*. Annual Review of Phytopathology Volume 49:391-413.
- Joanna K. Bowen, Carl H. Mesarich, Vincent G. M. Bus, Robert M. Beresford, Kim M. Plummer and Matthew D. Templeton (2011) *Venturia inaequalis*: the causal agent of apple scab. Molecular Plant Pathology 12(2):105
- Fitzgerald, A.M., van Kan, J.A.L., Plummer, K.M. (2004) Simultaneous silencing of multiple genes in the apple scab fungus, *Venturia inaequalis*, by expression of chimeric inverted repeats. Fungal Genetics and Biology 41 (10): 963-971
- Win, J, Greenwood, D.R. and Plummer, K.M. (2003) Characterisation of a protein from *Venturia inaequalis* that induces necrosis in *Malus* carrying the *Vm* resistance gene. Physiological and Molecular Plant Pathology 62 (4): 193-202.



THE FOCUS IS ON THE IDENTIFICATION OF GENES INVOLVED IN THE INTERACTION OF THE FUNGAL PATHOGENS WITH THEIR HOST.

VENTURIA SPP: HOST AND CV SPECIFICITY	
Pathogen	Host
Venturia inaequalis	Apple <i>Malus</i> spp.
	<i>Malus X domestica</i>
	<i>Pyracantha</i>
	<i>Eriobotrya</i> (loquat)
Venturia pirina	European pear
	<i>Pyrus communis</i>
Venturia nashicola	Asian pear
	<i>Pyrus pyrifolia</i>
	<i>Pyrus ussuriensis</i>
	<i>Pyrus bretschneideri</i>



MOLECULAR PARASITOLOGY LABORATORY

Food Security is a key global issue with nearly 700 million of the world's poor dependent on livestock for their survival. Over 2 billion cattle and sheep represent a critical and often sole source of economic security for people in the developing world, as well as being major components of agricultural production systems in developed countries such as Australia.

Successful livestock management in developing countries is a critical link between animal health and human health, and between livestock livelihood and emergence from poverty. Parasites such as liver flukes (*Fasciola hepatica*, *F. gigantica*) cause major disease in animals and humans throughout the world but drug resistance threatens fluke control. Fasciolosis affects all agriculturally important ruminants and its wide dispersal makes this one of the major parasitic diseases, causing global losses at over US\$3 billion/year. Liver fluke is prevalent in tropical regions of Asia and Africa where it is considered the single most important helminth infection of cattle and buffaloes which provide 80% of the draught power for crop cultivation.

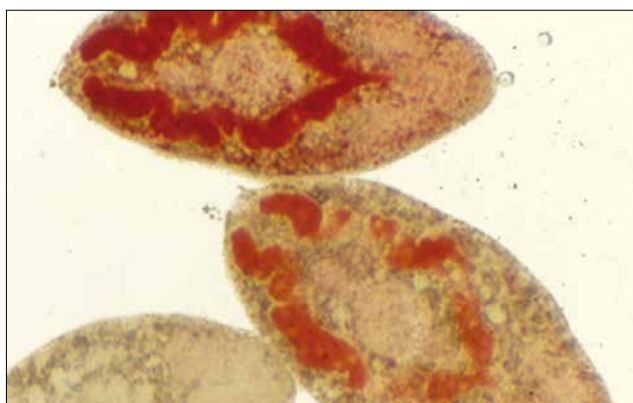
The control of these parasites requires research into new drugs and vaccines. My group is focused on developing fluke vaccines using biochemical, immunological and molecular research. As part of an Australian Research Council Linkage Grant, our laboratory is discovering, characterizing and evaluating new vaccine antigens for livestock. We are also defining the prevalence and distribution of drug resistant flukes in dairy and cattle herds in Australia in order to inform the industry of the scale of the problem.

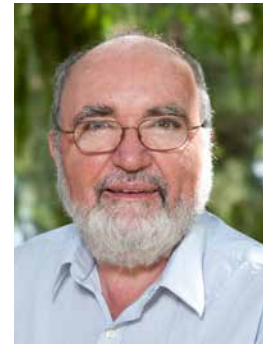
RESEARCH AREAS

- Biochemical, proteomic and functional analysis of liver fluke tegument proteins
- Evaluation of tegument proteins as vaccine candidates in livestock
- Analysis of antigens recognized by immune responses in sheep and cattle associated with resistance to liver fluke to identify novel candidate vaccine targets
- Developing methods for in vitro culture of liver fluke life stages for transcriptome and proteomic studies
- Understanding the distribution of drug resistant liver flukes in Australia

REFERENCES FROM MY LABORATORY

- Piedrafita, D. et al. Improving animal and human health through understanding liver fluke immunology. *Parasite Immunology* 32: 572-581 (2010)
- Wilson, R.A. et al. Exploring the *Fasciola hepatica* tegument proteome. *Int J Parasitology* 41: 1347-1359 (2011)
- Spithill, T.W. et al. Prospects for immunoprophylaxis against *Fasciola hepatica* (Liver Fluke). In: *Parasitic Helminths: Targets, Screens, Drugs, and Vaccines*, First Edition. (Edited by C.R. Caffrey), Wiley-VCH Verlag GmbH & Co. KGaA (2012)
- Brockwell, Y.M. et al. Confirmation of *Fasciola hepatica* resistant to Triclabendazole in naturally infected Australian beef and dairy cattle. *Int J Drugs Drug Res* 4: 48-54 (2014)





THIS RESEARCH WILL INVOLVE TECHNIQUES IN PARASITE BIOLOGY, RNA SEQ ANALYSIS, PROTEOMIC ANALYSIS, IN VITRO CULTURE AND HOST INFECTION.

RESEARCH AREA

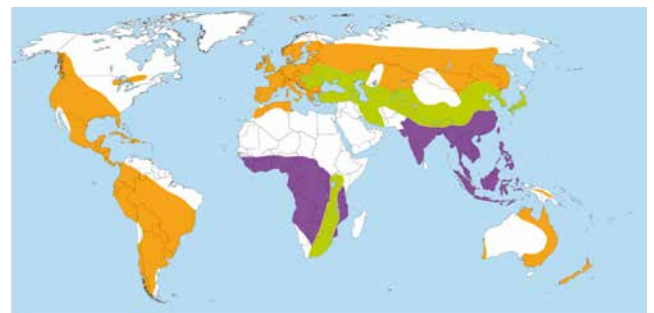
Identifying and characterizing membrane proteins important for tegument function in *F. hepatica*

- Our laboratory is interested to determine the kinetics of expression of tegument membrane proteins during fluke development and to study the effect of protein knock-down on fluke biology. This project will use in vitro culture techniques we have discovered to allow the fluke to develop from the juvenile stage to the immature liver stage.
- We will characterise gene and protein expression profiles in the developing flukes to define which tegument proteins are switched on at different stages in the life cycle in the host.
- Using RNAi techniques, we will evaluate how knock-down of different proteins influence the parasite's behavior in vitro and in vivo.
- We will evaluate how tegument proteins associate with each other to create the overall tegument structure
- These studies will help define the functional role of various tegument proteins in fluke development and the ability of the parasite to infect the host. These studies will allow us to prioritise certain tegument proteins as drug or vaccine targets.

This research will involve techniques in parasite biology, RNA seq analysis, proteomic analysis, in vitro culture and host infection.

The image (left above) shows the juvenile liver fluke which is the target of our vaccine control program. The image (left below) shows the Juvenile Fasciola parasites.

The image (above right) shows buffalo in Nanning, China, which are a natural host for liver fluke and a key target for a fluke vaccine. The world map (right centre) shows the wide global distribution of liver flukes indicating the importance of this parasite in livestock production systems in developing and developed countries. The flow chart (below right) shows one of our strategies for fluke vaccine development.



STEP 1

Identify parasite stage that is target of immunity
Define immune mechanism in sheep/cattle that kills this stage
Hypothesis: the mechanism in sheep is likely to exist in cattle

STEP 2

Identify antigen targets of the immune mechanism
Hypothesis: these antigens are vaccine targets

STEP 3

Design recombinant vaccine to target antigen(s)
Hypothesis: we can design a vaccine formulation to harness the immune mechanism

SOIL-PLANT INTERACTIONS

Soil degradation and nutrient deficiency in agro-ecosystems are widely-recognised problems and major limiting factors for sustainable food production under current climate change.

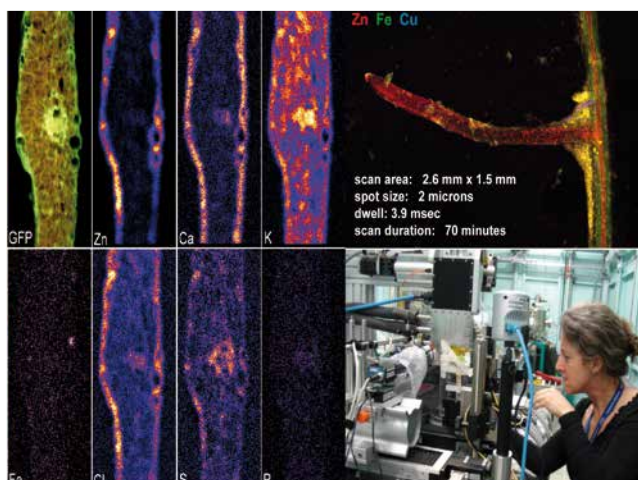
Research in this group focuses on soil and nutrient management and soil-plant interactions (including rhizosphere biochemistry) and impacts of elevated CO₂ and farming practice on soil processes and carbon sequestration. Interdisciplinary and multi-institutional research is a feature in these key research areas. Major contributions of the group include:

- understanding nutrient acquisition by plants and transformation in agroecosystems,
- understanding causes of subsoil acidification,
- elucidating impacts of elevated CO₂ on nutrient cycles (particularly C, N and P), and;
- developing new management options to ameliorate subsoil constraints.

This research group is financially supported by Australian Research Council (ARC), Grains Research and Development Corporation (GRDC) and other funding bodies, and collaborates extensively with other organisations in Victoria, nationally and internationally.

latrobe.edu.au/agriculture/research/specialisations/plant-soil-science

Using mPIXE and synchrotron to determine localization and speciation of metals in plant tissues.



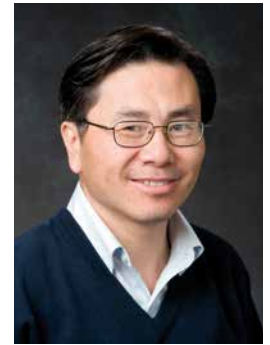
RESEARCH PROJECT I

Impact of elevated CO₂ on crop growth and soil nutrient dynamics

Climate change is expected to have a major impact on food production. Although increases in atmospheric CO₂ are predicted to initially increase plant productivity, achieving these productivity benefits is expected to be limited by water and/or nutrient deficiencies. Australian grain production systems are characterized by low rainfall and infertile soils and there is considerable uncertainty about the applicability of overseas data to predict how these systems will respond to elevated CO₂.

This project utilizes the Free Air CO₂ Enrichment (SoilFACE) array and stable isotope techniques to examine how the interactions between elevated CO₂, water supply and soil physiochemical properties affect above- and below-ground biomass distribution, N₂ fixation and litter quality (C:N:P) and chemical and microbial processes regulating the subsequent cycling of C, N and P in a cereal-legume rotation. We have shown that elevated CO₂ increased P and N uptake and nodule number in legumes.

Elevated CO₂ also enhances microbial P and hence P immobilization in the rhizosphere. The project aims to fill significant knowledge gaps that currently limit the reliability of process-based models to accurately predict the impact of future climates on the productivity and sustainability of Australian grain systems.



Professor Caixian Tang
E c.tang@latrobe.edu.au

PHOSPHORUS FERTILIZERS PLAY AN IMPORTANT ROLE IN SUSTAINING CROP YIELDS IN MODERN FARMING SYSTEMS.

RESEARCH PROJECT 2

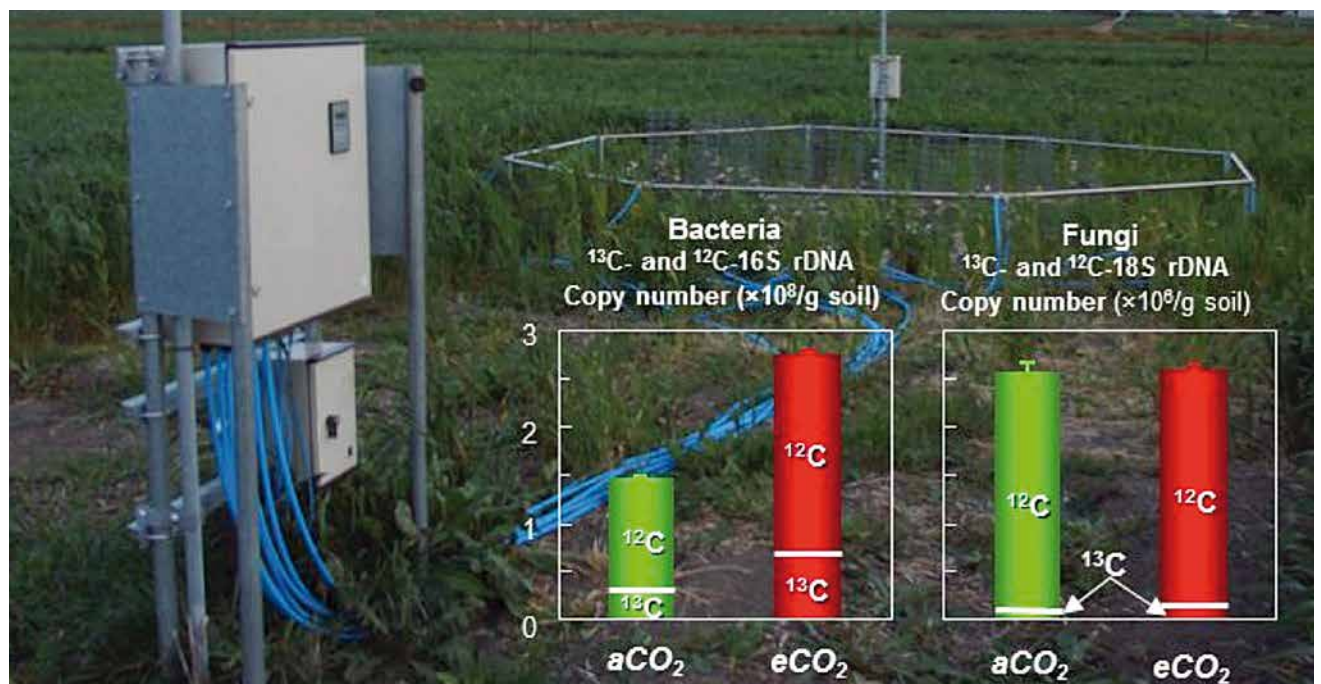
Rhizosphere processes and phosphorus acquisition

Phosphorus fertilizers play an important role in sustaining crop yields in modern farming systems. Each year, Australian farmers use about 450,000 tonnes of phosphorus in the form of phosphate fertilizer at an estimated cost of 1.4 billion dollars; a cost that will increase as global phosphorus reserves diminish. Remarkably only 10-30% of the phosphorus fertilizers farmers apply is absorbed by crops, leading to an accumulation of unused phosphorus remaining in the cropping soil.

This project will investigate the biochemistry and microbiology at the soil-plant interface, including the impact of soil type, farming practice and climate (water and CO₂ concentration), to understand how to enhance the absorption of phosphorus by crops. By identifying high-yielding crops that can access and absorb phosphorus from unavailable pools in soil, we will reduce P fertiliser use and improve P-use efficiency.



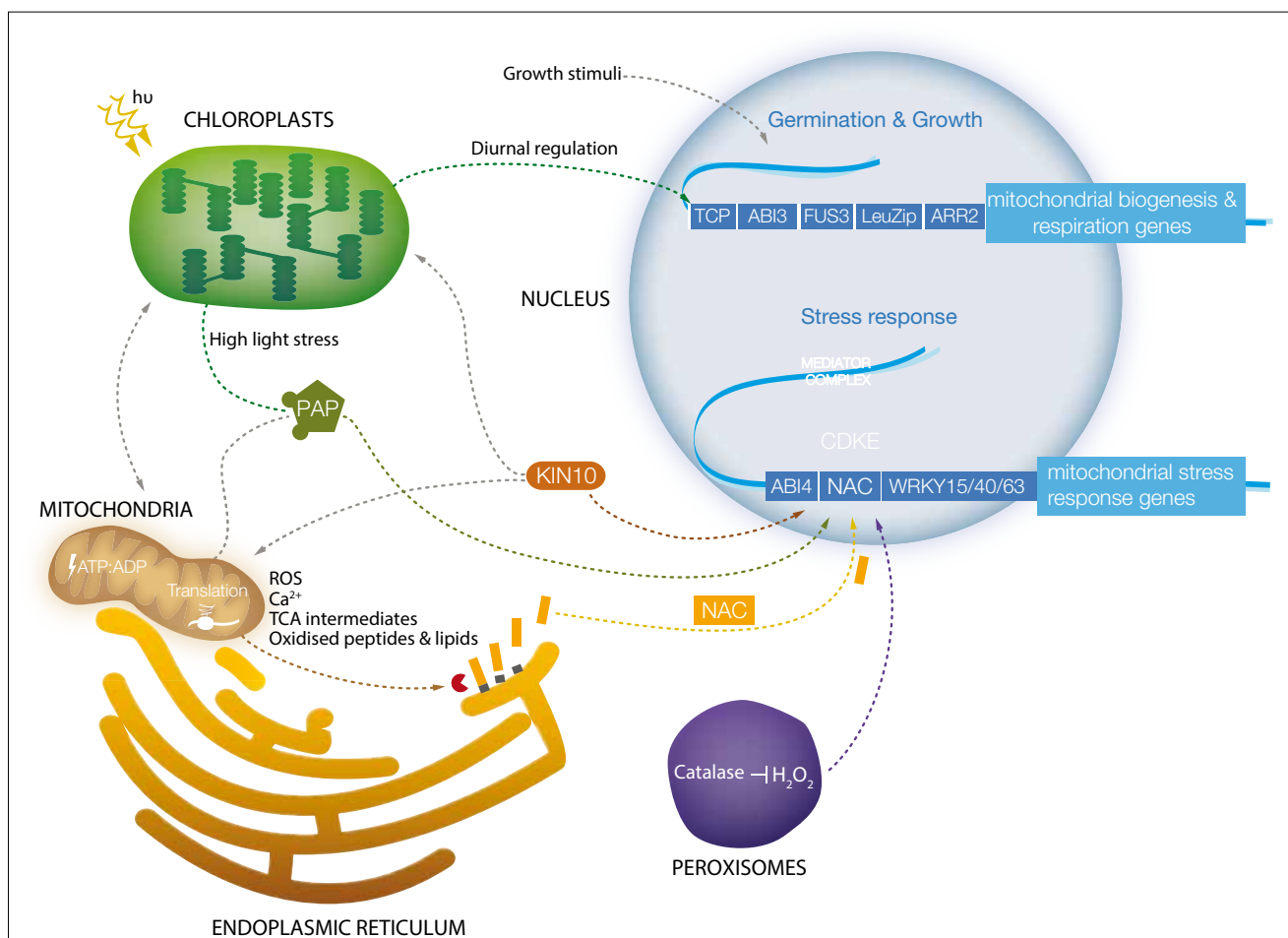
Experimental set-up to study rhizosphere priming.



SoilFACE facility at Victorian Department of Environment and Primary Industries to study the effect of elevated CO₂ on below-ground processes (in collaboration with Professor Roger Armstrong)

PLANT ENERGY BIOLOGY

All food comes directly or indirectly from plants in the form of molecules such as sugars, amino acids, proteins, starch, oils and cellulose. The bio-synthesis of these compounds occurs during plant growth and development, and can be viewed as a complex engineering project where water, CO₂ and sunlight, with macro- and micro-nutrients are converted into food.



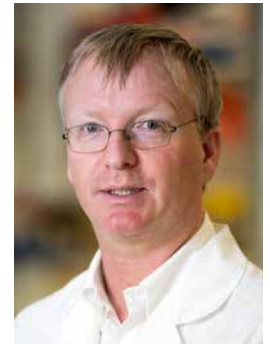
Plants fix 100 gigatonnes of carbon a year, 10 times the carbon that is used by humans. If viewed as a engineering project this process can be changes at optimized at a variety of levels to improve efficiency and alter the outputs (and inputs) to meet the growing demands for food production. As part of an Australian Research Council Centre of Excellence in Plant Energy Biology (www.plantenergy.edu.au), our laboratory is involved in trying to engineer more efficient process in plants for specific industry purposes.

In our laboratory we work on two aspect of plant energy biology, on mitochondria the powerhouse of cells and on phosphate acquisition – phosphate being the universal energy currency of cells.

REFERENCES

- Ng et al (2014). Anterograde and retrograde regulation of nuclear genes encoding mitochondrial proteins during growth, development and stress. *Molecular Plant* 7:
- Ng et al (2013). A membrane bound NAC transcription factor, ANAC017, mediates mitochondrial retrograde signaling in Arabidopsis. *Plant Cell* 25: 3450-3471
- Millar et al (2011). Organisation and regulation of mitochondrial respiration in plants. *Annu Rev Plant Biol* 67: 79-104

Professor Jim Whelan
E. J.Whelan@latrobe.edu.au



WE WORK ON TWO ASPECTS OF PLANT ENERGY BIOLOGY, ON MITOCHONDRIA THE POWERHOUSE OF CELLS AND ON PHOSPHATE ACQUISITION.

RESEARCH PROJECT

Identifying and characterizing pathways to improve phosphate acquisition and use in plants.

The diagram at right displays the various aspects of phosphate metabolism that are being studied in our laboratory in order to produce plants that can acquire and use phosphate most efficiently.

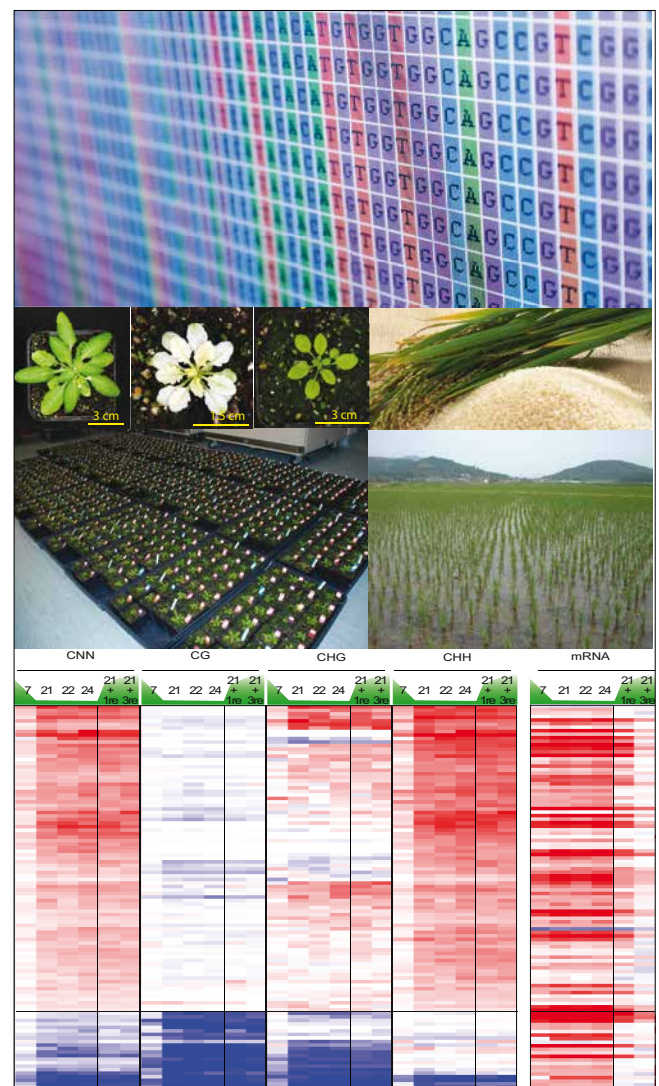
The research carried out uses both forward and reverse genetics, transcript profiling, epigenome characterisation and biochemistry and physiology of phosphate acquisition of Pi transport to identify steps in phosphate metabolism that can be targeted to optimise plant growth and production.

Examples of research projects available in this area include:

Use cell specific transcriptome profiling (RNA-Seq) to identify the cell specific nature of phosphate metabolism in plant cells. This will identify which cells do what under different Pi nutrient regimes and identify what needs to be improved and where it needs to be improved.

This project will involve a variety of cutting edge techniques such as obtaining cell specific profiles of transcripts, epigenomes, metabolites and cell specific modification to improve whole plant growth.

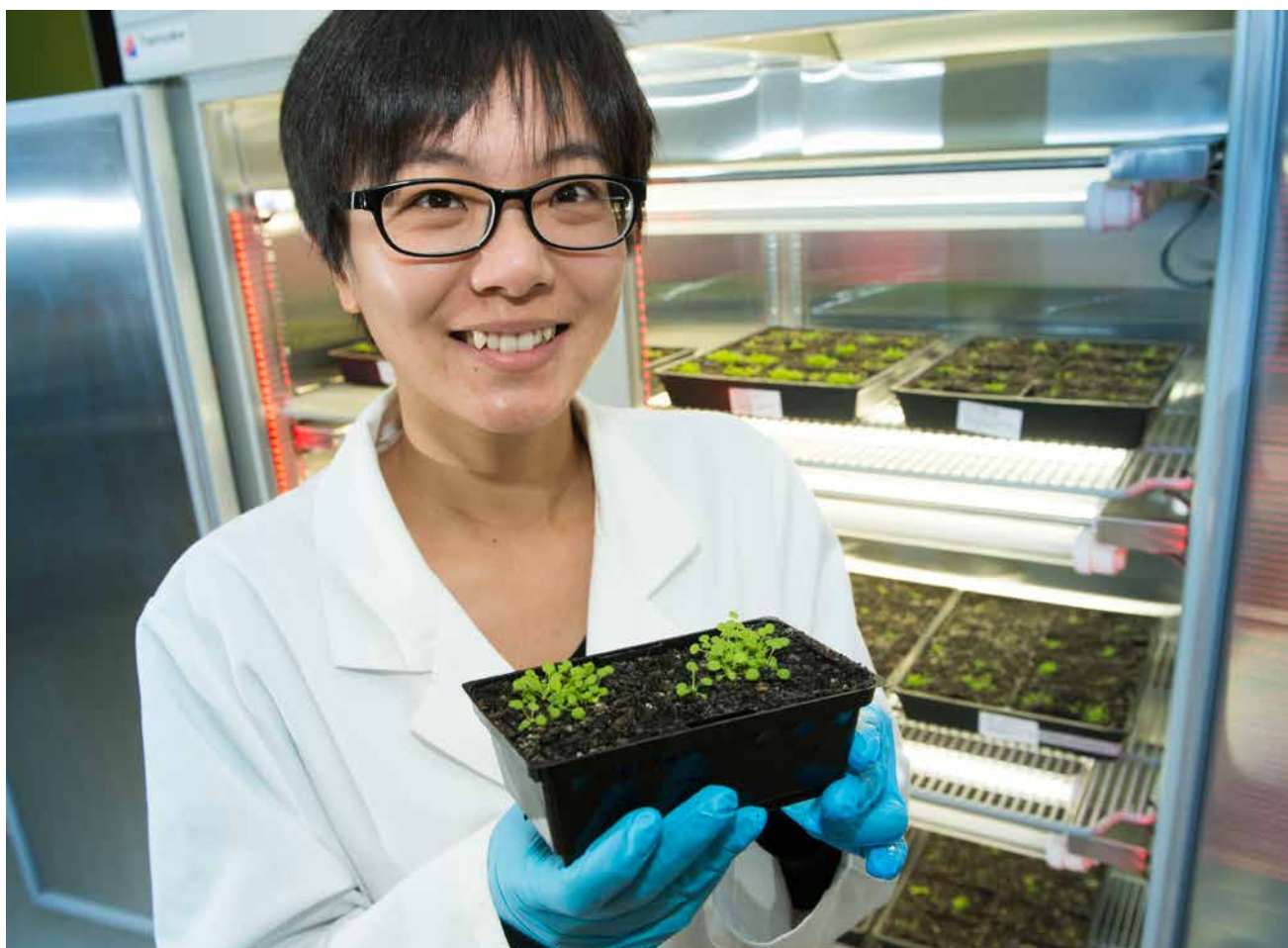
Forward genetics is a powerful tool to identify novel regulators of cellular processes. While forward genetics has been possible for many decades, the ability to identify the causative mutations was often time consuming, taking up to several years to identify. The advent of Next-generation sequencing allows high through-put forward genetic screening, with the ability to identify novel mutations in months rather than years.



AGRIBIO CHINA PHD SCHOLARSHIP SCHEME

La Trobe University offers a number of scholarships dedicated to the Agribio International Graduate Program. The process for application and approval of these scholarships is as follows:

1. Pre-selection of applicants will be based on information provided using the attached form (pre-application form) that requests details about academic background and performance.
2. Applicants should list up to three potential supervisors and projects that interest them.
3. The form and any accompanying material should be sent by email to: J.Whelan@latrobe.edu.au
4. The successful applicants will be selected by a panel of academics from AgriBio, Centre for AgriBioscience. Successful applicants will be informed via email.
5. Please send your pre-application by:
 - 31 August 2014 for commencement February 2015
 - 31 January 2015 for commencement June 2015
6. La Trobe International, which manages applications for graduate research programs, will send the successful applicant a form to formally enrol in the research higher degree program at La Trobe University. The applicant will receive guidance in what information is required to enrol.
7. The applicant will receive a formal offer of candidature at the University and offer of a scholarship, with details of the value and terms of the scholarship, which will include a tax-free living allowance and fee waiver.



PRE-APPLICATION FORM

La Trobe University and China PhD Scholarship

Please provide information as listed below in a single PDF file before the selection dates to:
J.Whelan@latrobe.edu.au

Name:

Sex:

Address:

Telephone:

Email:

Date of birth

Nationality:

Academic background:

Degree:

GPA:

Standardised test scores (If available):

TOEFL:

IELTS:

GRE:

Date of graduation:

Awards/prizes:

Describe your research experience/specialised training: (attach up to one page)

Describe your research interests and the area you would like to concentrate on for your PhD.
(attach up to one page)

List potential supervisor for your PhD studies in AgriBio, centre for Agribioscience at La Trobe University from
information booklet (You should have contacted this person and discussed project(s). Attach information)

