

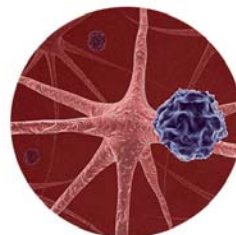


Queensland Institute of
Medical Research

Griffith Medical Research College

2009 Retreat

**28th April 2009
Griffith University
South Bank Campus**



Griffith Medical Research College - 2009 Retreat

South Bank Graduate Centre (2nd Floor above the Ship Inn)

28th April 2009, 9.30am – 5pm

9.00 – 9.30	Participants Arrive
9.30 – 9.50	<u>Welcome and Overview of GMRC</u> Prof. Michael Good (GMRC Director) Prof. Ned Pankhurst (Incoming DVC (Research), GU)
Plenary 1	Plenary Presentation (25 minutes plus 5 minutes questions) Chair: Dr Alex Loukas (QIMR)
9.50 – 10.20	Plenary Speaker – Prof. Alan Mackay-Sim (GU) <i>"Olfactory stem cells"</i>
10.20 – 10.45	Morning Tea
Session 1	Scientific Session (13 minutes plus 2 minutes questions) Chairs: Dr Kelli MacDonald (QIMR) and TBC
10.45 – 11.00	Dr Alejandro Lopez (QIMR/GU) <i>"Breast Cancer Stem Cells as Targets for Immunotherapy"</i>
11.00 - 11.15	Dr Nathan Subramaniam (QIMR) <i>"Novel Insights into Iron Metabolism: The Role of ATM (Ataxia-Telangiectasia-Mutated)"</i>
11.15 - 11.30	A/Prof. Dianne Watters (GU) <i>"A tale of two tumour suppressors"</i>
11.30 – 11.45	Dr Don Gardiner (QIMR) <i>"The aspartyl aminopeptidase of Plasmodium falciparum"</i>
11.45 – 12.00	Prof. Ifor Beacham (GU) <i>"Nasal Associated Lymphoid Tissue (NALT) and Olfactory Epithelium as Portals of Entry for Burkholderia pseudomallei in Murine Melioidosis."</i>
12.00 – 12.15	Dr David McMillan (QIMR) <i>"Bacterial colonisation of intravascular devices"</i>
12.15 – 12.30	Dr Jamie Nourse (QIMR) <i>"EBV microRNA expression in an in-vitro model of B-cell differentiation and lymphomagenesis"</i>
12.30 – 1.30	Lunch

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Session 2	Scientific Session (13 minutes plus 2 minutes questions) Chairs: Dr Dan Wallace (QIMR) and Prof. Claire Rickard (GU)
1.30 - 1.45	Prof. Denise Doolan (QIMR) <i>“Genome Credentialing and Vaccine Development”</i>
1.45 - 2.00	Dr Jose Rey-Ladino (GU) <i>“Discovery of novel T cell antigens from intracellular Chlamydia by using the immunoproteomics”</i>
2.00 - 2.15	Dr Christine Wells (GU) <i>“The genome network of stem cells”</i>
2.15 - 2.30	Dr Derek Richard (QIMR) <i>“From volcanoes to bedside, hssb1 a potential diagnostic/prognostic tool and cancer therapy target”</i>
2.30 - 2.45	Dr Albert Mellick (GMRC Research Fellow; GU) <i>“Bone marrow mediated tumour progression: The Enemy Within.”</i>
2.45 – 3.00	Thanh Tran (GMRC PhD Student – Final Year) <i>“P. falciparum histone deacetylases as new antimalarial drug targets”</i>
3.00 – 3.15	Dr Suyinn Chong (QIMR) <i>“Maternal ethanol consumption alters the epigenotype and phenotype of offspring in a mouse model”</i>
3.15 – 3.45	Afternoon Tea
Plenary 2	Plenary Presentation (2) (25 minutes plus 5 minutes questions) Chair: Prof. Lyn Griffiths
3.45-4.15	Plenary Speaker – Dr Naomi Wray (QIMR) <i>“From genome-wide association studies to genetic risk prediction”</i>
Session 3	Core Facilities/Major Technology Platforms/Joint Initiatives Chair: Prof. Andreas Suhrbier
4.15 – 4.25	Dr David Camp (GU) (10 min) <i>“The QCL - a major technology platform to support biomedical research”</i>
4.25 – 4.35	Prof. Emma Whitelaw (QIMR) (10 min) <i>“New technical capabilities at QIMR”</i>
4.35 – 4.50	Prof. Brian Kay (QIMR) (15 min) <i>“Joint initiatives - where to from here?”</i>
4.50 – 5.00	Discussion/Closing Remarks - Prof. Michael Good
5.00 – 6.00	Drinks and Canapés (all welcome)

Plenary Presentation (2)
From genome-wide association studies to genetic risk prediction.

Naomi R Wray

Common, complex, genetic diseases are caused by multiple genetic and environmental factors. In genome-wide association studies (GWAS), subjects are genotyped for ~500,000 genetic polymorphisms which capture the majority of the known common variation in the human genome and enable us to search for genetic variants associated with disease. Since the first GWAS in 2007, ~250 studies have now been published. Results have been greeted with a mixture of euphoria- “Compelling signals have been found, often highlighting previously unsuspected biology.” - and realism - “..but, for most of the traits studied, known variants explain only a fraction of observed familial aggregation.” Across the whole spectrum of diseases and traits studied, results demonstrate that there are few variants of large effect which implies that individually these variants are not useful for prediction of disease risk. However, we show that by combining information from many (perhaps thousands of) risk variants, accurate prediction of genetic risk of disease should be possible when GWAS sample sizes are of the order of 10,000s. These methods have been applied to real data giving insight into the genetic architecture of complex diseases, into genetic co-morbidity between diseases and provide optimism for prediction of genetic risk.

Breast Cancer Stem Cells as Targets for Immunotherapy

Brian J. Morrison^{1,2}, Chris Schmidt², Derek Kennedy¹, Sunil Lakhani^{2,3},
Brent A. Reynolds⁴ and **J. Alejandro López**^{1,2}

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The cancer stem cell model predicts that only a rare subpopulation of cells is capable of initiating a tumour or metastasising. This population is hypothesised to exhibit many of the cardinal properties of a somatic stem cell such as being an undifferentiated cell capable of proliferation, self-maintenance, and production of a large number of differentiated progeny. To assess the functional and phenotypic properties of breast cancer stem cells (BCSC) we have made use of the neurosphere assay for culturing mammospheres based upon work culturing neural stem cells. We cultured and analysed mammospheres from three established luminal and basal-like breast cancer cell lines. This work validates the use of the neurosphere assay for isolating stem-like cells in both luminal and basal-like breast cancer cell lines and for investigating functional and phenotypic characteristics of these cells. We showed that mammospheres cultured in neurosphere medium demonstrate sustained proliferation and a self-renewal capacity that is enriched on serial passage. Our findings challenge the view that the phenotypic characteristic of BCSC is necessarily CD44⁺CD24⁻. We show that the CD44⁺CD24⁻ phenotype is associated with basal-like cancer lines and that this phenotype is not further enriched in mammosphere cultures. Phenotypically, mammospheres of luminal origin were characterised as CD44⁻CD24⁺ and demonstrated increased expression of the cell surface markers ESA, CD49f, and HER2 compared to adherent culture. These molecules appear as attractive targets for immunotherapy. HER2 expression was decreased by culture with the HER2-specific antibody trastuzumab. Furthermore, systemic treatment with trastuzumab significantly reduced tumour growth following intra-brain injection of MCF-7-derived mammospheres in immunodeficient mice, demonstrating that HER2 is a potential target for cancer therapy of breast cancer stem cells. Overall, our data suggest that BCSC are attractive targets for immunotherapy.

Novel Insights into Iron Metabolism: The Role of ATM (Ataxia-Telangiectasia-Mutated)

Nathan Subramaniam¹, Dianne Watters², and Daniel Wallace³

¹Head, Membrane Transport Laboratory, QIMR and GMRC

²Eskitis Institute for Cell and Molecular Therapies, and School of Biomolecular and Physical Sciences, Griffith University, ³Membrane Transport Laboratory, QIMR and GMRC

Dysregulation of iron metabolism is associated with a wide range of clinical disorders. Iron levels are controlled by the hormone hepcidin which is produced in the liver. The production of hepcidin is regulated through four major pathways- HFE (hemochromatosis), TfR2 (transferrin receptor 2), hemojuvelin (HJV) and inflammatory cytokines. Recent data implicate ATM (Ataxia-telangiectasia-mutated) as having a role in iron metabolism and liver regeneration. Our studies will investigate the involvement of ATM in the regulation of iron homeostasis by examining signalling pathways leading to hepcidin production, iron absorption and trafficking in normal and Atm deficient mouse liver. The elucidation of the role of ATM in these processes is of fundamental importance in unravelling the mechanisms of disease processes and identifying therapeutic targets.

A tale of two tumour suppressors

Dianne J Watters¹ and Sergei Kozlov²

1. *Eskitis Institute for Cell and Molecular Therapies and School of Biomolecular and Physical Sciences Griffith University, Nathan Campus*
2. *Queensland Institute of Medical Research, P.O Royal Brisbane Hospital*

Nuclear ATM has a well established role in DNA repair. ATM has also been localized outside the nucleus, suggesting that ATM has other, as yet undetermined, functions. ATM has been demonstrated to participate in the insulin signaling pathway by phosphorylating eIF-4E binding protein (4EBP1). 4EBP1 is also phosphorylated by components of the Mammalian target of Rapamycin (mTOR) pathway in response to insulin. The Tuberous Sclerosis Complex (TSC) proteins, hamartin (TSC1) and tuberlin (TSC2), are regulators of the mTOR pathway. Mutations in either TSC1 or TSC2 lead to Tuberous Sclerosis, an autosomal dominant multisystem disorder of benign tumour growth and neurological abnormalities. Studies in our laboratory have revealed a link between these pathways. Evidence of an interaction between ATM, TSC1 and TSC2 was shown by mammalian two-hybrid analysis. This has been confirmed by immunoprecipitation experiments. In addition, *in vitro* kinase assays have shown that hamartin is phosphorylated by ATM after insulin activation. ATM and TSC represent two different cellular approaches to tumour suppression. ATM functions through the cell cycle checkpoint controls, while the TSC exerts its effects through its response to nutrient and growth signals to control protein synthesis. These processes need to be coordinated in order to provide a basis for the effective control of tumour growth.

The aspartyl aminopeptidase of *Plasmodium falciparum*

**Don Gardiner¹, John Dalton². Tina Skinner-Adams¹, Chris Brown³,
Katharine Trenholme¹.**

1. Malaria Biology Laboratory, QIMR; University of Technology Sydney; School of Biomolecular and Physical Sciences. Griffith University

Aspartyl aminopeptidases are exopeptidases of the M18 family that specifically remove acidic amino acids (Glu and Asp) from the unblocked N-termini of peptides and proteins. Little is known about the general function of this family of proteases although a role in protein catabolism or processing has been suggested. Investigation of their function is hampered by the lack of potent inhibitors. We have shown that a *P. falciparum* aspartyl aminopeptidase gene is transcribed and translated in intra- erythrocytic stage parasites and its activity can be detected in soluble extracts of malaria parasites. Immunolocalisation and immunoblotting experiments show that the *P. falciparum* aspartyl aminopeptidase is expressed in the cytosol and also exported to the parasitophorous vacuole of the parasite and is, therefore, likely to play a role other than in protein catabolism. Using antisense RNA technology to knockdown gene function we have shown that the aspartyl aminopeptidase activity identified in parasite extracts is the product of the PFI1570c gene (Plasmodb.org). Significant morphological differences were also seen in antisense-mediated knockdown parasites, consistent with a lethal phenotype. These results suggest that the PfM18 aspartyl aminopeptidase is suitable target for chemotherapeutic intervention. In a joint collaboration between the three Institutes we are undertaking high throughput screening of the M18 aminopeptidase to identify novel compounds that may lead to the development of new antimalarial agents

Nasal Associated Lymphoid Tissue (NALT) and Olfactory Epithelium as Portals of Entry for Burkholderia pseudomallei in Murine Melioidosis

Ifor Beacham

Burkholderia pseudomallei is the causative agent of melioidosis, a potentially fatal disease endemic in northern Australia. *B. pseudomallei* is a Gram-negative bacterium found in soil and water in endemic regions. Infection is generally considered to be acquired *via* inhalation of dust or water droplets from the environment, with infections strongly associated with the wet season. In this study we have used intranasal inoculation of mice to simulate inhalation.

Infection was monitored by bioluminescence imaging and by immunohistological analysis of coronal sections of the heads of infected animals. Bacterial load in organs and tissues were also monitored.

Bioluminescence imaging shows colonisation and replication in the nasal cavity, including the nasal associated lymphoid tissue (NALT). Coronal sections and immunofluorescence microscopy further demonstrates that there is infection in respiratory epithelium, olfactory epithelium, including associated nerve bundles, and olfactory bulbs, as well as NALT. Significantly, olfactory epithelium and brain were rapidly infected before bacteria were detected in blood, and a capsule-deficient mutant infected brain without significantly infecting blood.

These data suggest that the olfactory nerve is the route of entry into the brain, which may be paralleled in cases of human neurological melioidosis. This study focuses attention on the *upper* respiratory tract as a portal of entry: NALT as a route to systemic infection *via* the blood stream and the olfactory epithelium as a direct route to the brain.

Bacterial colonisation of intravascular devices

**David J McMillan¹, L Zhang², J Gowardman³, B Patel⁴, KS Sriprakash¹
and C. Rickard²**

¹*Bacterial Pathogenesis Laboratory, Queensland Institute of Medical Research;* ²*Research Centre for Clinical and Community Practice Innovation, Griffith University;* ³*Dept Intensive Care Medicine, Royal Brisbane & Women's Hospital;* ⁴*School of Biomolecular & Physical Sciences, Griffith University*

Intravascular devices (IVDs) are the single most important cause of hospital acquired blood stream infection. The standard international diagnostic test for colonisation of IVDs is Maki culture-dependent roll plate technique. This technique requires a minimum of one day before a result is returned, delaying antibiotic treatment of life threatening infections. Additionally, the Maki method can only identify bacteria on the external surface of an IVD. In the current project, we have used culture independent molecular techniques to identify bacterial species present on the interior and exterior surfaces of IVDs. Uncolonised (n=10) and colonised (n=10) IVDs, as determined by the Maki technique, were collected from the Royal Brisbane hospital. For culture independent bacterial identification, genomic DNA was extracted from each IVD and used as template for the amplification of DNA encoding the 16S rRNA gene. These products were then cloned and used to create a 16S rRNA clone library. Four hundred clones from the library were randomly selected and sequenced to identify the bacterial species present on the IVDs. The culture-dependent results showed that *S. epidermidis*, coagulase-negative staphylococci and *P. aeruginosa* were found on the IVDs. In contrast our culture independent molecular methods identified many more bacterial species. Some of the bacterial species found by culture-dependent studies were confirmed by the molecular methods. However, large numbers of other bacterial species were present. Some of these bacteria are known pathogens; some have not been described in relation to human health and have only previously been described in environmental samples. Colonization of arterial catheters by multiple bacterial species appears to be more common than suspected from culture-dependent studies.

Quantitative profiling of EBV microRNA expression in EBV-driven B-cell differentiation

Jamie Nourse

The Epstein Barr Virus (EBV) is associated with several lymphomas. Current consensus supports the notion that EBV infects and activates naïve B-cells driving a differentiation process that parallels germinal centre (GC) activation. In some individuals, this process may be interrupted by a transforming event resulting in a clonal proliferation of B-cells blocked at this differentiation state.

MicroRNAs (miRNAs) are small non-coding RNAs which act as negative regulators of gene expression. EBV expresses at least 39 miRNAs from two clusters in the viral genome. These miRNAs have been demonstrated to be differentially expressed in tumour cell-lines, suggesting distinct roles during EBV-driven B-cell differentiation and lymphogenesis. The relationships between EBV miRNAs, B-cell differentiation during infection and EBV associated lymphoma have not been characterised.

In an initial investigation of the influence of EBV miRNAs in B-cell differentiation and transformation we have established an *in vitro* model in which isolated naïve B-cells are infected with EBV. Using quantitative real time RT-PCR the expression of EBV miRNAs, as well as markers of B-cell differentiation were profiled.

Examination of 28 EBV miRNAs revealed the majority to exhibit distinct expression profiles within 72 hours of infection. Interestingly one group was rapidly expressed within 8 hours of infection and then down regulated after 24 to 48 hours. Alterations in the expression of genes associated with the differentiation of naïve B-cell was indicative of differentiation taking place within four days of infection, in a process exhibiting many similarities to the GC reaction. These findings suggest the possibility EBV miRNAs may be involved in this differentiation process. Current work in our lab involves the elucidation of EBV miRNA cellular targets that may play a role in EBV driven B-cell differentiation.

Genome Credentialing and Vaccine Development

Denise L. Doolan

Queensland Institute of Medical Research

The *Plasmodium* parasite, the causative agent of malaria, has a large genome and a complex life cycle with multiple stages and stage-specific expression of ~ 5300 putative proteins. A vaccine has proved elusive and the increasing drug resistance of the parasite and insecticide resistance of the vector highlight the urgent need for an effective malaria vaccine. Many believe that such a vaccine will need to target several antigens and multiple stages simultaneously and will require the generation of both antibody and cellular immune responses. Vaccine efforts to date have been stage-specific and based on proteins representing < 0.3% of the genome. The genomic sequences of *P. falciparum*, *P. vivax* and selected nonhuman primate and rodent malarias are now available, providing a foundation for the identification of promising new vaccine targets. In addition, the combination of micro-liquid chromatography and tandem mass spectrometry has led to the identification of over a thousand new proteins from key stages of the parasite life cycle that represent potential targets for protective immunity. Data from transcriptional profiling of timepoints from sporozoites, asexual stages, and gametocytes and can also be used to characterize and assign function to hypothetical proteins. We are mining this genomic, proteomic, transcriptomic and comparative genomic information to generate a prioritized list of antigens for proteome-wide screening of antibody and T cell reactivity using specimens from individuals exposed to malaria and technology platforms such as protein arrays, high throughput protein production, and epitope prediction algorithms. Information from these studies will help “credential” the *Plasmodium* genome to identify and prioritize promising new target antigens for vaccine development. Combined with molecular vaccine technologies such as plasmid DNA or recombinant viral vaccine delivery systems, these prioritized vaccine candidate antigens can be incorporated into a rational vaccine development process that targets specific stages of the malaria parasite life cycle with immune responses that are thought to be required for parasite elimination and control.

Dendritic cells as source of T cell antigens: the *Chlamydia muridarum* experience

Jose Rey-Ladino, Allen Ross & Allan Cripps

Griffith University Health Group

Chlamydia infections cause a wide spectrum of diseases worldwide and an effective prevention program will ultimately depend on finding a suitable vaccine. *Chlamydia* immunity is T cell-mediated but one of the major drawbacks for developing a vaccine is the lack of relevant T cell antigens. Another problem is the lack of appropriate adjuvants that target the vaccine to T cells in vivo. In this study, we used a combination of affinity chromatography and tandem mass spectrometry to identify 13 novel *Chlamydia* peptides among 331 self-peptides presented by MHC class II molecules derived from bone marrow murine dendritic cells (BM-DCs) infected with *Chlamydia muridarum*. The MHC class II-bound peptides were recognized by *Chlamydia*-specific CD4 T cells harvested from immune mice. Adoptive transfer of dendritic cells pulsed ex vivo with the peptides reduced up to 10 fold the bacterial load in lungs or genital tract of mice challenged intranasally or intravaginally, respectively. The results provide clear evidence for the utilisation of dendritic cells in T cell antigen (s) discovery and its applicability for other disease models.

From volcanoes to bedside, *hssb1* a potential diagnostic/prognostic tool and cancer therapy target

Derek Richard

Cells have developed a vast array of surveillance, repair and signalling proteins in order to prevent the loss of valuable genetic information as a result of DNA damage. It has been estimated that each cell can suffer up to 30000 DNA damaging insults in a 24 hour period, each damage event if not repaired correctly could consequently result in a loss of cellular programming leading to cancer development. Our initial studies examined the ability of an extremophile, to protect its genetic code from the volcanic environment in which it survived. We identified SSB as a key protein required for its volcanic existence. We have subsequently identified an un-annotated human homologue of SSB (hSSB1), which is the centre of this study. Our initial data suggests that hSSB1 is central to a number of DNA repair processes including homologous recombination. hSSB1 over expression is also linked to cancer, with expression levels being linked to tumor grade and patient survival.

Bone marrow mediated tumour progression: The Enemy Within

Mellick AS

Bone marrow (BM) derived hematopoietic and endothelial lineages have in recent times been shown to play a critical role in cancer progression through: the promotion of tumour cell proliferation; breakdown of the extracellular matrix; the angiogenic switch and establishment of the metastases. While it has been known for a long time that the BM responds to cancer growth in a very specific way, this paradigm of cancer progression suggests that host BM and cancerous tissues engage in an active-interdependent conspiracy to promote disease development. Novel tools have allowed us to track and genetically modify cells of BM lineages to block tumour growth, and prevent metastatic spread. This work has led to a greater understanding of the role of small noncoding RNAs as key regulators of lineage differentiation in the BM as well as to the development of novel methods for modifying the BM *in vivo*, with the potential of modulating the aberrant effects associated with the host response to cancer.

***P. falciparum* histone deacetylases as new antimalarial drug targets**

Thanh Tran, Tina Skinner-Adams, Andrew Lucke, Don Gardiner, Boyle, G., David Fairlie, Kathy Andrews

Parasite resistance to current antimalarial drugs is driving the search for new agents that act on novel malaria parasite targets. Histone deacetylases (PfHDACs) have been proposed as possible new targets in *P. falciparum*, the parasite responsible for most of the 1-2 million malaria related deaths that occur annually. In this study, a panel of new synthetic hydroxamate-based HDAC inhibitor analogues derived from l-cysteine or 2-aminosuberic acid (2-ASA) were examined for their antimalarial potential. These compounds demonstrated potent activities against *in vitro* cultured *P. falciparum* parasites at low nanomolar concentrations. In comparison to the activity of these compounds against mammalian cells, the 2-ASA compounds display better selectivity for malaria parasites (>100 fold) than the l-cysteine compounds (<10 fold). Two representative 2-ASA compounds were found to preferentially kill trophozoite-stage parasites over ring stages and to inhibit deacetylase activity in *P. falciparum* nuclear extracts. Northern blot analysis shows that as in other eukaryotes, HDAC inhibitors alter the transcription profile of some parasite genes. With a view to better understanding the potential of this class of compounds as possible new antimalarial drugs, combination studies were carried out. Compound 2-ASA-9 was found to antagonize chloroquine but displayed an additive trend when combined with quinine. Oral treatment of *P. berghei* infected mice with this same compound resulted in a significant reduction in parasitemia. Together these data extend our understanding of how hydroxamate-based HDAC inhibitors act on malaria parasites and this may contribute to further development of this class of compounds as new drugs for use against malaria.

Maternal ethanol consumption alters the epigenotype and phenotype of offspring in a mouse model

**Nina Kaminen¹, Arttu Ahola¹, Kylie-Ann Mallitt¹, Emma Whitelaw¹,
Timothy Cox² and Suyinn Chong¹**

¹*Division of Genetics and Population Health, Queensland Institute of Medical Research;*
²*Center on Human Development and Disability, University of Washington*

Exposure to environmental triggers such as poor nutrition or high levels of alcohol *in utero* can lead to compromised foetal development and adult disease in humans. The underlying mechanisms remain unknown. We have developed a model of moderate ethanol exposure in the mouse based on maternal ingestion of 10% ethanol from fertilisation to mid-gestation. This strategy produces offspring with craniofacial and growth restriction phenotypes that are reminiscent of foetal alcohol syndrome in humans. We also observe increased DNA methylation and transcriptional silencing at an epigenetically sensitive allele, *Agouti viable yellow*, which is linked to changes in mouse coat colour. Our results show that ethanol can affect adult phenotype by altering the epigenotype of the early embryo. Interestingly, maternal ethanol consumption prior to conception had a similar effect on *Agouti viable yellow*, suggesting that ethanol-induced epigenetic changes can also occur in maturing oocytes. Future work is directed towards genome-wide DNA methylation and gene expression analyses as well as further characterisation of foetal alcohol syndrome-like phenotypes in our mouse model.

The QCL - a major technology platform to support biomedical research

David Camp

The Queensland Compound Library was established in March 2008 at the Eskitis Institute of Cell and Molecular Therapies as national resource to synergise interactions between Australasian chemists, biomedical researchers, and their international colleagues.[1] By promoting collaborations, value can be added to the already excellent basic biomedical research, synthetic organic chemistry and natural product expertise in the region.

Importantly, a unique IP model that lies somewhere between the propriety culture of industry and the NIH policy of placing data in the public domain was developed for the Australasian situation. The Queensland Compound Library model allows synergies to develop and mature into projects that are prosecuted in a way best suited to the collaboration.

The *modus operandi* to engage the chemical and biological communities is a three step process:

1. Chemists deposit their small molecules (compounds with a molecular weight < 500 Daltons) and natural product extracts into Australia's only small molecule repository;
2. Biologists select screening sets from the available suite of molecules;
3. A collaboration is pursued by the biology group and chemistry group that supplied the active molecule

This presentation will outline the Queensland Compound Library's technological platform and capabilities, recent activities and progress / process to make compounds available to biomedical research groups.

1. Camp, D., et al., *Progress towards establishing an open access molecular screening capability in the Australasian region*. ACS Chem. Biol., 2007. 2: p. 764-767.

Posters

- 1. Cellular characterisation of mammalian mon1a: a putative trafficking protein and modifier of the haemochromatosis phenotype.**
Daniel Wallace
- 2. Targeting Bone Marrow Mediated Tumour Angiogenesis.**
Prue Plummer
- 3. MMP-2 and MMP-9 in Oral Cancer Progression using in vivo and in vitro models**
Jin Gao
- 4. A holistic view of the long term impact of malaria intervention strategies**
Michelle Gatton
- 5. Mechanism of Interferon resistance in melanoma**
James Amalraj
- 6. Antimalarial efficacy of the HIV protease inhibitor tipranavir**
Tina Skinner-Adams
- 7. Title; SerpinB2 is a regulator of Th1 responses**
Andreas Suhrbier
- 8. Heparan sulfate proteoglycans and the stem cell niche**
Larisa Haupt
- 9. Potential haemolysins of hookworms**
Charlene Willis
- 10. Lipid-core peptide group a streptococcal vaccine: immunological evaluation in a murine model**
Colleen Olive

List of Participants

Name	Position	e-mail address	Expertise
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David Camp	Director, Queensland Compound Library	david.camp@griffith.edu.au	compound management natural product extract screening
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Don Gardiner	Laboratory Head	Don.Gardiner@qimr.edu.au	Malaria Biology
Emma Whitelaw	Head, Epigenetics Lab	emma.whitelaw@qimr.edu.au	epigenetic modifications in mammalian cells
Fernanda Caldas Cardoso	Research Officer	fernanda.caldascardoso@qimr.edu.au	Vaccinology: Molecular biology and Immunology
George Mellick	Associate Professor	G.Mellick@griffith.edu.au	Clinical Neuroscience with particular interest in neurodegenerative disease and neurogenetics.
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James Amalraj	PhD Student	j.amalraj@griffith.edu.au	Molecular biology - Interferon resistance mechanism in malignant melanoma.
Jamie Nourse	Research Officer	jamie.nourse@qimr.edu.au	EBV microRNA and lymphoma
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Jenny Gamble	DHOS, School of Nursing & Midwifery	j.gamble@griffith.edu.au	RCTs relating to perinatal mental health. Survey methods and decision making.
Jin Gao	Snr Lecturer and Team Leader	j.gao@griffith.edu.au	cellular and molecular biology, immunohisto-chemistry, role of MMP-2 and -9 in cancer progression, Head&Neck cancer in vivo model and cell culture model
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