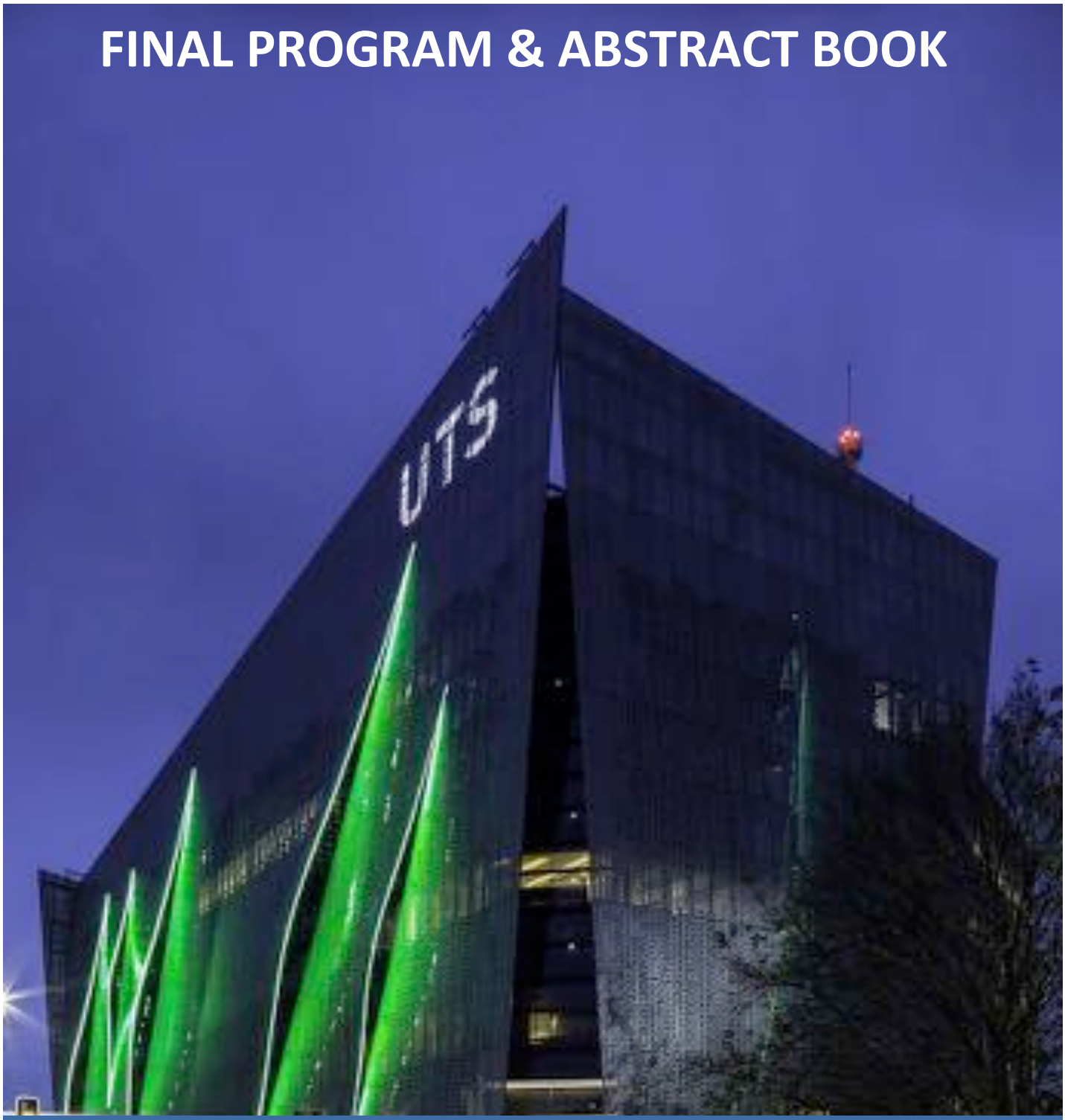
NEW HORIZONS
COMBINED HEALTH SCIENCE MEETING

University of Technology Sydney
14th – 15th November 2019

UTS
UNIVERSITY OF TECHNOLOGY, SYDNEY

FINAL PROGRAM & ABSTRACT BOOK



36th Combined Health Science Conference

New Horizons 2019

Innovative science with impact:
Strengthening alliances between research

ACKNOWLEDGEMENTS

The New Horizons 2019 Program Committee would like to thank the following who, at the time of printing, had given their support to this conference:

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WELCOME

DR KRISTINE McGRATH

Lecturer
School of Life Sciences
Faculty of Science
University of Technology Sydney

On behalf of the Organising Committee and all co-hosting organisations I would like to extend a very warm welcome to delegates, plenary speakers, presenters and invited guests of New Horizons 2019. This is the 36th Combined Health Science Conference co-hosted by the Kolling Institute, the University of Sydney, Northern Sydney Local Health District, the University of Technology Sydney and the Centenary Institute. Through this meeting, we look forward to forming new collaborations and strengthening the continuous relationship between our Institutions.

These annual conferences promote advancements in healthcare through research and education, and by building bridges between basic science, the clinic and delivery of care. There is a rich history of collaboration between the institutes involved which, over the past 35 years, has resulted in significant progress in all of these areas.

This year our conference will focus on research with impact - research that increases our understanding of disease and leads to the development of new therapies and better outcomes for patients. It will include presentations on the latest scientific research, new developments in technology, clinical excellence and the translation of research from bench to bedside.

New Horizons 2019 will be held at the University of Technology Sydney. We are very grateful to our plenary and invited speakers for agreeing to share their latest research with us. We also look forward to presentations and posters from health care providers, research assistants, Honours students, PhD students, Masters students, post-doctoral researchers as well as research leaders.

We acknowledge and sincerely thank all of those who have committed time and effort into the organising of this conference, our academic and health sponsors, as well as our commercial sponsors, who have made the meeting possible. A special thanks to our Gold sponsors, Spruson and Ferguson, for continuously supporting this Meeting.

We hope that you find this meeting productive and informative, and take the opportunity to form new cross-institutional and inter-disciplinary collaborative and personal relationships. We have tried to create a relaxed and friendly atmosphere that allows students and younger researchers to feel comfortable presenting their research and interacting with more experienced researchers.

Please join us for drinks and canapés after the meeting - take the opportunity to interact with the speakers and other delegates and enjoy being part of a vibrant research community.

Dr Kristine McGrath, *Organising Committee Co-Chairman, 2019*

PROGRAM AT A GLANCE

THURSDAY 15TH NOVEMBER 2019

0800 - 1700	**Registration desk open**
0915 - 0930	**Welcome and Introduction to Conference** **Professor Dianne Jolley** (Dean, Faculty of Science, UTS)
0930 - 1020	**Opening Plenary: Prof Mariapia Degli-Esposti** (Monash University, VIC) *'Cytomegalovirus and transplantation: new therapeutic approaches informed by discovery research'*
1020 - 1040	**Morning tea, Exhibitions**
1040 -1120	**Plenary Session 1: Neurosciences** **A/Prof Greg Neely** (University of Sydney, NSW) *'Functional genomics applied to pain biology'*
1120 - 1210	**Abstract Session 1: Honours Students and Research Assistants** 10 talks (4 mins each + 1 min questions)
1210 - 1230	**Guided Poster Session 1**
1230 - 1330	**Lunch, Exhibitions**
1330 - 1410	**Panel discussion and Q & A session:** **Career guidance for Students and E/MCRs** **Panel members**: **Dr Darren Saunders** (University of NSW) **A/Prof Caroline Ford** (University of NSW) **Dr David White** (Roche, NSW) **Chair: *Prof Michael Wallach*** *(UTS, Sydney, NSW)*
1410 - 1450	**Plenary Session 2: Microbiomes** **A/Prof Andrew Holmes** (University of Sydney, NSW) *'The different dimensions driving microbiome structure and its impact on health'*
1450 - 1510	**Afternoon Tea, Posters, Exhibitions**
1510 - 1610	**Abstract Session 2: Postdoctoral Researchers**, 5 talks (10 mins each + 2 mins questions)
1610 - 1650	**Plenary Session 3: Biomedical Engineering/Biotechnology** **Prof Alison Heather** (University of Otago, NZ) *'Sports doping: The endless chase'*
1650 -1800	**Networking with drinks**

FRIDAY 15th NOVEMBER 2019

0800 - 1700	**Registration desk open**
0915 - 0950	**Plenary Session 4: 3D Bioprinting** **A/Prof Payal Mukherjee** (University of Sydney, NSW) *'Bioprinting cartilage for ears'*
0950 - 1040	**Abstract Session 3: PhD Students Session 1 – Young Investigators,** 5 talks (8 mins + 2 mins questions)
1040 - 1105	**Morning Tea, Exhibitions**
1105 - 1145	**Plenary Session 5: Clinical Sciences** **Prof Wally Thomas (**University of Queensland) *'A bitter taste in your heart'*
1145 - 1235	**Abstract Session 4: PhD Students Session 2,** 5 talks (8 mins + 2 mins questions)
1235 - 1300	**Guided Poster Session 2**
1300 - 1350	**Lunch, Exhibitions**
1350 - 1430	**Plenary Session 6: Tumour Immunology** **Dr Tatyana Chtanova** (Garvan Institute of Medical Research, NSW) *'Neutrophils in cancer: From foe to friend'*
1430 - 1445	**Gold sponsor**
1445 - 1535	**Abstract Session 5: PhD Students Session 3,** 5 talks (8 mins + 2 mins questions)
1535 - 1600	**Afternoon Tea, Posters, Exhibitions**
1600 - 1640	**Plenary Session 7: Biochemistry and Cell Biology** **Prof Glen King (University of Queensland)** *'Gain from pain: using venomous animals to help understand and treat chronic pain'*
1640 - 1700	**Closing Remarks and Awarding of Prizes** **Prof Stella Valenzuela** (Associate Head of School for Research, UTS) **Prof Carolyn Sue** (Kolling Institute Executive Director) **Prof Mathew Vadas** (Centenary Institute Executive Director)
1700 - 1800	**Canapés Reception**

ORGANISING COMMITTEE

The Organising Committee of the New Horizons 2019 Conference includes (in alphabetical order):

- Dr **Lara Bereza-Malcolm**, *Henry Langley Postdoctoral Fellow, Kolling Institute, University of Sydney*
- Dr **Alessandro Castorina**, *Senior Lecturer, University of Technology Sydney*
- Dr **Yik (Jeremy) Chan,** *NHMRC Early Career Fellow, School of Life Sciences, University of Technology Sydney*
- Dr **Jaesung (Peter) Choi**, *Research Officer, Cardiovascular Signalling Group, Centenary Institute*
- Miss **Charlotte Fleming**, *PhD Candidate, School of Life Sciences, University of Technology Sydney*
- Dr **Alvaro Garcia**, *Chancellor's Postdoctoral Research Fellow, School of Life Sciences, UTS*
- Dr **Cindy Gunawan**, *Senior Lecturer, The ithree Institute, Core Member, ithree - Institute of Infection, Immunity and Innovation, UTS*
- Dr **Chunling (Helen) Huang**, *NHMRC Early Career Fellow, Kolling Institute, University of Sydney*
- Mr **Gerard Li**, *PhD Candidate, School of Life Sciences, University of Technology Sydney*
- Dr **Jiao Jiao Li**, *NHMRC Early Career Fellow, Kolling Institute, University of Sydney*
- Dr **Yiguang Lin**, *Lecturer, School of Life Sciences, UTS*
- Dr **Kristine McGrath**, *Lecturer, School of Life Sciences, UTS*
- Dr **Diana Quan**, *Research Officer, Tuberculosis Research Program, Centenary Institute*
- Miss **Claire Rennie**, *PhD Candidate, School of life Sciences, The University of Technology Sydney*
- A/Prof **Sonia Saad**, *Senior Research Fellow, Kolling Institute and Adjunct Professor, School of Life Sciences, UTS*
- Dr **Jessamy Tiffen**, *Research Officer, Melanoma Immunology and Oncology Program, Centenary Institute*
- Mr **Daniel Turkewitz**, *PhD Candidate, School of Life Sciences, UTS*

INVITED SPEAKERS

Invited Speakers of the New Horizons 2019 Conference:

Prof Mariapia Degli-Esposti

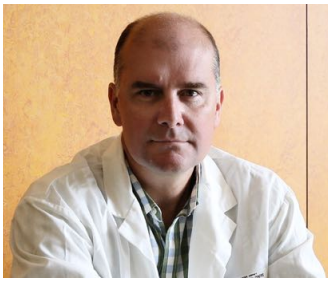
Professor Degli-Esposti studied immunology and immunogenetics at the University of Western Australia (UWA) and received a PhD in 1992. After her PhD and post-doctoral training in Perth, she moved to Seattle, USA, to undertake further post-doctoral studies at Immunex. She returned to Australia in 1998 and was appointed Group Leader in the Department of Microbiology at UWA. In 2000 she became an NHMRC Research Fellow. In 2001 she was awarded a Wellcome Trust Senior Research Fellowship in Biomedical Sciences, the only one ever awarded in Western Australia. She moved to the Lions Eye Institute in 2003 as Head of Immunology and Director of Research. Mariapia is a NHMRC Principal Research Fellow. In 2019 she moved to Monash University where she heads the Experimental and Viral Immunology Group within the Infection and Immunity Program at the Biomedicine Discovery Institute and the Department of Microbiology. She continues to hold an appointment at the Lions Eye Institute as an Honorary Fellow.

Her research focuses on understanding the regulation of complex immune responses, especially those involved in autoimmunity, infection and tumour control. Her laboratory has elucidated novel interactions between components of the innate and adaptive immune system and how they affect the outcome of immune responses in the setting of infection and autoimmunity. These findings have been key to both basic and translational research aimed at developing improved therapies to treat viral infections and their complications by harnessing the immune system.

A/Prof Greg Neely

Associate Professor Greg Neely completed his PhD in human immunology at the University of Calgary, Canada and went on to train in functional genomics with Josef Penninger in Vienna, Austria. Since 2011 he has been running a lab in Sydney Australia using functional genomics approaches to find novel human disease genes and pathways. His main interest is in age-related diseases involving the nervous system, including pain, neurodegeneration, and strategies to extend lifespan while preserving overall health. His lab has extensive experience using whole genome CRISPR screening in human cells, and they commonly use transgenic knock out mice or tissue-specific gene targeting in fruit flies.

Dr Darren Saunders (UNSW)



Darren is a research scientist and Associate Professor in Medicine at UNSW. He undertook post-doctoral training at the Garvan Institute and University of British Columbia and has held fellowships from the US Dept. of Defense and Cancer Institute NSW. Darren is secretary of Science and Technology Australia and Senior Research Advisor to Elizabeth Broderick and Co. He is a regular commentator on television and radio, resident scientist on ABC TV's The Drum and Channel 7's Daily Edition, and 2019 Eureka Prize winner. His written work covers everything from cancer, to science policy, masculinity and gender equity. When not in the lab, Darren loves being in the ocean or flying down a mountain. neurodegeneration, and strategies to extend lifespan while preserving overall health. His lab has extensive experience using whole genome CRISPR screening in human cells, and they commonly use transgenic knock out mice or tissue-specific gene targeting in fruit flies.

A/Prof Caroline Ford

Associate Professor Caroline Ford leads the Gynaecological Cancer Research Group at the University of New South Wales. She established her lab at the Lowy Cancer Research Group in 2010 after international postdoctoral fellowships at the University of Toronto, Canada and Lund University, Sweden. Her research aims to understand why gynaecological cancers develop, how and why they spread throughout the body, and how best to treat them. She leads major projects on the early detection of ovarian cancer and molecular targets in ovarian and endometrial cancer. A/Prof Ford is an experienced university lecturer, convening courses on medical research, cancer pathology and personalised medicine and is passionate about science communication and enhancing the health literacy of the wider community. A long-time advocate for women in science, Caroline has been named a "Superstar of STEM" by Science & Technology Australia, a program aimed at smashing the stereotype of what a scientist looks like. In 2018 she founded the STEMMinist Book Club a global and virtual community focused on feminism and women in STEMM, which has rapidly grown to include over 4500 members from 30 countries worldwide.

Dr David White

David White completed his PhD at the Baker IDI Heart and Diabetes Institute and the Alfred Hospital studying cardiovascular inflammation in both scientific models and clinical trials. He had the opportunity to complete a postdoctoral fellowship at the Brigham and Women's Hospital and Harvard Medical School studying genetics and first in man clinical trials for genetic cardiovascular disorders.

Upon returning to Australia, David transitioned to a pharmaceutical career as a medical science liaison at Roche working in immuno-oncology and targeted therapies in Lung Cancers. Currently, he is a Medical Manager at Roche delivering a jointly funded collaborative program examining comprehensive genomic profiling in Lung Cancer.

A/Prof Andrew Holmes

Associate Professor Andrew Holmes studied science at the University of Queensland where he completed a PhD in Microbiology in 1993. He held research positions at the University of Warwick, UK, and Macquarie University before taking his current academic position at the University of Sydney. Andrew is now Associate Professor in the School of Life and Environmental Sciences and Microbiome Project node leader in the Charles Perkins Centre.

Andrew was the recipient of the Fenner Prize from the Australian Society for Microbiology in 2006. He is a senior editor for The ISME Journal and a member of the editorial boards of Applied and Environmental Microbiology and Environmental Microbiology. He is currently working on the relationship between nutrition, gut microbiome and health.

Prof Alison Heather

After graduating with a PhD in Physiology from the University of Sydney, Australia, Alison received a University of Sydney Fellowship to undertake studies in Endocrinology at the Royal Prince Alfred Hospital in Sydney. She then spent 5 years at the Heart Research Institute studying the interaction between sex hormones and heart disease before moving back into mainstream academia with an Associate Professor position at the University of Technology, Sydney. Alison moved to the University of Otago, New Zealand as Professor of Cardiovascular Physiology in 2014. Alison's research interests focus on sex hormones and she leads an innovative and technology-focused team developing tests to detect the use of sports doping agents. Alison is a member of the WHISPA Project, High Performance Sport New Zealand. In her free time, Alison walks the talk, competing in Ironman triathlons. Alison was recently selected as a member of the Australian age-group team for the International Triathlon Union's long course triathlon world championship event.

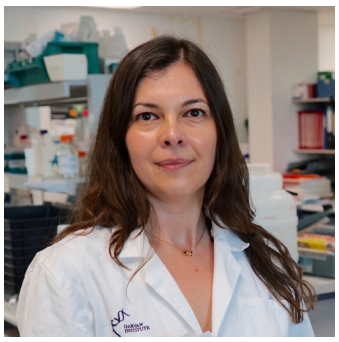
A/Prof Payal Mukherjee

A/Prof Payal Mukherjee is an Adult and Paediatric ENT Surgeon subspecialising in Ear Surgery, Cochlear Implantation and Skull Base Surgery. She is the deputy chair of Royal Australasian College of Surgeons NSW state committee, a committee member of the Section of Academic Surgery and the ENT Research Lead of the RPA Institute of Academic Surgery.

She is currently doing a PhD in disruptive technologies in ENT specialising in medical applications of Augmented Reality, Virtual Reality, 3D printing and Bioprinting with a focus on global translation of Australian innovation in biotechnology. She is also proud to have strong advocacy in promoting surgical innovation, on gender equity in surgery, domestic violence as well as developing STEMM skills in young girls. She was a finalist of the NSW Premier Women of the year 2019.

Prof Wally Thomas

Walter (Wally) Thomas is a PhD graduate (1992) from the University of Queensland. His postdoctoral training/research in the USA and Melbourne (Baker Institute) was supported by a NHMRC CJ Martin Fellowship and subsequent NHMRC Research Fellowships. In 2008, he was recruited to the University of Queensland as the Chair of General Physiology. In September 2009, he was appointed to the position of Head of the School of Biomedical Sciences. In October 2015, he was seconded to the Directorship of the University of Queensland Diamantina Institute. In 2017, he returned to his substantive position in the School of Biomedical Sciences, where he is Head of the Receptor Biology Laboratory with a specific focus on the molecular and cellular physiology of G protein-coupled receptors (GPCRs) – his group has a strong international reputation for studying the processes that activate and deactivate these receptors in health and disease. Since joining UQ, he has been awarded ~$6.5M in competitive grant funding.



Dr Tatyana Chtanova

Dr Tatyana Chtanova is the head of the Innate and Tumour Immunology lab at the Garvan Institute in Sydney. After undergraduate studies at the University of New South Wales, Dr Chtanova was awarded her PhD in 2005 for her thesis work on specific gene expression signatures for novel T cell subsets, performed at the Garvan Institute.

Following her PhD, Tatyana was awarded the Human Frontier Science Program Fellowship to train at the University of California, Berkeley. During her fellowship she gained expertise in in vivo two-photon microscopy and used it to characterise, for the first time, neutrophil dynamics in vivo, and to identify a novel mechanism of immune evasion by pathogens.

Dr Chtanova returned to the Garvan Institute to establish her research laboratory in 2009. Tatyana's main research interest is immune cell migration and function in inflammation and cancer. Dr Chtanova's group utilises a range of innovative approaches such as in vivo imaging and photoconversion to study immune cell dynamics in health and disease.

Prof Glen King

Glenn did his PhD at the University of Sydney before postdoctoral studies at the University of Oxford. After academic stints at the University of Sydney and the University of Connecticut Health Center, he joined the Institute for Molecular Bioscience at The University of Queensland in 2007. Professor King is a pioneer in the field of venoms-based drug discovery, in particular the development of drugs and environmentally-friendly insecticides derived from spider venoms. Professor King's early work on venoms lead to him to found an agricultural biotechnology company (Vestaron Corporation) that is developing bee-safe, eco-friendly insecticides.

Professor King's current research is focused on the development of venom-derived drugs to treat chronic pain, epilepsy, and stroke. His laboratory at the University of Queensland maintains the largest collection of venoms in the world, comprising more than 700 venoms from ants, assassin bugs, caterpillars, centipedes, cone snails, scorpions, spiders, and wasps. Professor King has published 3 books, 19 book chapters, and more than 250 peer-reviewed journal articles. Glenn is a former President of the Australian Society for Biophysics (ASB) and former Chair of the Australian & New Zealand Society for Magnetic Resonance (ANZMAG). He has served on the editorial board of numerous journals and is currently Editor-in-Chief of the journal Toxicon. Recent awards include the 2013 Beckman Coulter Discovery Science Award from the Australian Society for Biochemistry & Molecular Biology, 2013 ASB Sir Rutherford Robertson Award, 2015 ANZMAG Medal, and the 2016 IMB Impact Award for Discovery & Innovation.

DETAILED PROGRAM DAY 1 (Thursday 14th Nov)	
0800 - 1700	**Registration desk open**
0915 - 0930	**Welcome and Introduction to Conference** **Professor Dianne Jolley** (Dean, Faculty of Science, UTS)
0930 - 1020	**Opening Plenary Talk** **Prof Mariapia Degli-Esposti** (Monash University, VIC) *'Cytomegalovirus and transplantation: new therapeutic approaches informed by discovery research'* *Chair: Prof Robert Baxter (University of Sydney, Sydney, NSW)*
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1120 - 1210	**Abstract Session 1: Honours Students and Research Assistants** 10 talks (4 mins each + 1 min questions) *Chairs: Dr Jiao Jiao Li (Kolling Institute) and Dr Jess Tiffen (Centenary Institute)*
11:20	**Abstract 1-1: Adrian Schweinsber** (UTS) *Inhibition of DNA damage repair to improve sensitivity to chemotherapy in triple negative breast cancer*
11:25	**Abstract 1-2: Sargon Lazar** (UTS) *The role of an immunophilin protein, fkbpl, in cardiac endothelial dysfunction associated with type 2 diabetes*
11:30	**Abstract 1-3: Monique de Rooy** (HRI) *Intermittent pacap in the ventromedial hypothalamus evokes lasting elevations in blood glucose*
11:35	**Abstract 1-4: Johana Luhur** (UTS) *A ring-forming protein links spore shape to spore envelope assembly*
11:40	**Abstract 1-5: Krystal Louangaphay** (UTS) *Buspirone as an anti-neuroinflammatory drug: implications for Parkinson's disease*
11:45	**Abstract 1-6: Jisang Ryu** (Kolling Institute) *The effects of chronic polypharmacy, monotherapy and deprescribing on the kidneys of aged mice*
11:50	**Abstract 1-7: Lissy Hartnamm** (UTS) *Membrane ion channel properties of the pH-switchable peptide gala*
11:55	**Abstract 1-8: Andrew Sheheta** (UTS) *Cellular response of 3D printed implants*
12:00	**Abstract 1-9: Stuart Cook** (Centenary Institute) *Differential chemokine receptor expression and usage by immediate dendritic cell precursors*
12:05	**Abstract 1-10: Alan Wainwright** (Kolling Institute) *Does sole-of-foot electrical stimulation produce an RIII nociceptive flexor reflex recorded from tibialis anterior that responds to a conditioned pain modulation protocol?*
1210 - 1230	**Guided Poster Session 1**
1230 - 1330	**Lunch, Exhibitions**

DETAILED PROGRAM DAY 1 (Thursday 14th Nov)	
1330 - 1410	**Panel discussion and Q & A session:** **Career guidance for Students and E/MCRs** **Panel members**: **Dr Darren Saunders** (University of NSW) **A/Prof Caroline Ford** (University of NSW) **Dr David White** (Roche, NSW) *Chair: Prof Michael Wallach (UTS, Sydney, NSW)*
1410 - 1450	**Plenary Session 2: Microbiomes** **A/Prof Andrew Holmes** (University of Sydney, NSW) *'The different dimensions driving microbiome structure and its impact on health'* *Chair: Dr Alen Faiz (UTS, Sydney, NSW)*
1450 - 1510	**Afternoon Tea, Posters, Exhibitions**
1510 - 1610	**Abstract Session 2: Postdoctoral Researchers** 5 talks (10 mins each + 2 mins questions) *Chair: Dr Belinda Di Bartolo (University of Sydney) and Dr Melissa Farnham (HRI)*
15:10	**Abstract 2-1: Dr Joshua Neale** (Centenary Institute) *Getting a leg up on diabetic peripheral artery disease*
15:22	**Abstract 2-2: Dr Polina Nedoboy** (HRI) *The effects of short-term ketogenic diet on counter-regulatory response to hypoglycaemia in rats*
15:34	**Abstract 2-3: Dr Belinda Di Bartolo** (Kolling Institute) *Inflammation-induced angiogenesis was attenuated by Apolipoprotein C-III deficiency*
15:46	**Abstract 2-4: Dr Jiao Jiao Li** (Kolling Institute) *To treat or not to treat osteoarthritis with stem cell therapy*
15:58	**Abstract 2-5: Dr Alen Faiz** (UTS) *Understanding corticosteroid biology using transcriptional profiling of bronchial biopsies and CRISPR-Cas9 KO models*
1610 - 1650	**Plenary Session 3: Biomedical Engineering/Biotechnology** **Prof Alison Heather** (University of Otago, NZ) *'Sports doping: The endless chase'* *Chair: Prof Joanne Tipper (UTS, Sydney, NSW)*
1650 -1800	**Networking with drinks**

DETAILED PROGRAM DAY 2 (Friday 15th Nov)

0800 - 1700	**Registration desk open**
0915 - 0950	**Plenary Session 4: 3D Bioprinting** **A/Prof Payal Mukherjee** (University of Sydney, NSW) *'Bioprinting cartilage for ears'* *Chair: Dr Qian (Peter) Su (UTS, Sydney, NSW)*
0950 - 1040	**Abstract Session 3: PhD Students Session 1 – Young Investigators** 5 talks (8 mins + 2 mins questions) *Chairs: Dr Jaesung (Peter) Choi and Dr Diana Quan (Centenary Institute)*
9:50	**Abstract 3-1: Manisha Patil** (HRI) *Cell-specific functions of TRAIL critical for angiogenesis and vessel stabilisation*
10:00	**Abstract 3-2: Benjamin Larkin** (Kolling Institute) *Repurposing hydralazine for the treatment of obesity-related kidney disease*
10:10	**Abstract 3-3: Dr Sarah Glastras** (Kolling Institute) *The impact of preconception weight intervention on metabolic inflammation in mice*
10:20	**Abstract 3-4: Inah Camaya** (UTS) *A novel helminth-derived molecule, fhhdm-1, preserves β-cell function to prevent type 1 diabetes*
10:30	**Abstract 3-5: Karosham Reddy** (UTS) *Epigenetic-like changes to signalling proteins in chronic obstructive pulmonary disease*
1040 - 1105	**Morning Tea, Exhibitions**
1105 - 1145	**Plenary Session 5: Clinical Sciences** **Prof Wally Thomas (**University of Queensland) *'A bitter taste in your heart'* *Chair: Prof Jim Elliot (University of Sydney)*
1145 - 1235	**Abstract Session 4: PhD Students Session 2** 5 talks (8 mins + 2 mins questions) *Chairs: Dr Chunling (Helen) Huang (Kolling Institute) and Dr Polina Nedoboy (HRI, Sydney, NSW)*
11:45	**Abstract 4-1: Qinghua Cao** (Kolling Institute) *A novel single domain, i-body AD-114, attenuated kidney fibrosis through targeting CXCR4*
11:55	**Abstract 4-2: Mojtaba Moosavi** (UTS) *Investigation of FXYD1 as a novel signalling protein in cholesterol metabolism*
12:05	**Abstract 4-3: Gihani Manodara** (UTS) *Potential therapy for treating type 2 diabetes and hepatic steatosis*
12:15	**Abstract 4-4: Joshua Xu** (Kolling Institute) *The effect of various stem placement on global joint offset during total hip arthroplasty: a virtual study*
12:25	**Abstract 4-5: Senani Rathnayake** (UTS) *Longitudinal effects of 12 months smoking cessation on gene expression and DNA methylation in bronchial biopsies*
1235 - 1300	**Guided Poster Session 2**
1300 - 1350	**Lunch, Exhibitions**
1350 - 1430	**Plenary Session 6: Tumour Immunology** **Dr Tatyana Chtanova** (Garvan Institute of Medical Research, NSW) *'Neutrophils in cancer: From foe to friend'* *Chair: Prof Deborah Marsh (UTS, Sydney, NSW)*
1430 - 1445	**Gold sponsor** **Spruson & Ferguson** *'Protecting your Intellectual Property: Key Considerations for Researchers'*

DETAILED PROGRAM DAY 2 (Friday 15th Nov)	
1445 - 1535	**Abstract Session 5: PhD Students Session 3** 5 talks (8 mins + 2 mins questions) *Chairs: Dr Joshua Neale (Centenary Institute) and Dr Lara Bereza-Malcolm (University of Sydney)*
14:45	**Abstract 5-1: Behjat Sheikholesla** (UTS) *Therapeutic effects of synthetic phospholipids in inflammation*
14:55	**Abstract 5-2: Riti Mann** (UTS) *Unique Adaptation Strategy of* Pseudomonas aeruginosa *to silver nanoparticles*
15:05	**Abstract 5-3: Huan Wu** (UTS) *A low cost and novel lateral flow immunoassay for celiac disease test*
15:15	**Abstract 5-4: Danielle Stone** (Kolling Institute) *Oropharyngeal volume and self-reported dysphagia following whiplash injury*
15:25	**Abstract 5-5: Kieran English** (Centenary Institute) *CD4 T cell help promotes the expansion of CD8 T cells during persistent liver antigen but does not rescue T cell exhaustion*
1535 - 1600	**Afternoon Tea, Posters, Exhibitions**
1600 - 1640	**Plenary Session 7: Biochemistry and Cell Biology** **Prof Glen King (University of Queensland)** *'Gain from pain: using venomous animals to help understand and treat chronic pain'* *Chair: Prof Phil Hansbro (Centenary Institute, Sydney, NSW)*
1640 - 1700	**Closing Remarks and Awarding of Prizes** **Prof Stella Valenzuela** (Associate Head of School for Research, UTS) **Prof Carolyn Sue** (Kolling Institute Executive Director) **Prof Mathew Vadas** (Centenary Institute Executive Director)
1700 - 1800	**Canapés Reception**

Poster Number 4 14th Nov

A systematic review of clinical practice guidelines for the management of lumbar spinal stenosis

Anderson DB[1], de Luca K[2], Jensen RK[3], Eyles JP[1], Van Gelder JM[4], Friedly, JL[5], Maher CG[6], Ferreira ML[1]

[1]Institute for Bone and Joint Research, The Kolling Institute, Northern Clinical School, Faculty of Medicine and Health, The University of Sydney, Sydney, New South Wales, Australia
[2]Department of Chiropractic, Faculty of Science and Engineering, Macquarie University, Sydney, New South Wales, Australia
[3]Department of Sports Science and Clinical Biomechanics, University of Southern Denmark, Odense, Denmark
[4]Sydney Spine Institute, Sydney, New South Wales, Australia
[5]Department of Rehabilitation Medicine, The University of Washington, Seattle, Washington, The United States of America
[6]Institute for Musculoskeletal Health, Sydney School of Public Health, The University of Sydney, Sydney, New South Wales, Australia

Background: Lumbar spinal stenosis is a leading cause of pain and disability in older adults, but treatment recommendations can vary.
Aim & Objectives: To review and appraise both the methodological quality of the clinical practice guidelines and their recommendations for the assessment and management of lumbar spinal stenosis.
Methods: PubMed, MEDLINE, CINAHL, EMBASE, and Cochrane Central Register of Controlled Trials were searched up until Sep 2018 for clinical practice guidelines on the management of lumbar spinal stenosis. Guidelines needed to utilise a systematic process to generate their recommendations and needed to be publicly available.
Results: Nine guidelines were included, with four found to have satisfactory methodological quality when analysed with the AGREEE II instrument. Recommendations from the four satisfactory guidelines included: fair evidence endorsing decompression surgery for patients who did not respond to non-surgical care; conflicting recommendations endorsing epidural injections; poor evidence supporting a range of pharmacological approaches (e.g. Opioids, Non-Steroidal Anti-Inflammatories (NSAIDs), Paracetamol, Gabapentin); and poor evidence recommending whether physical therapy and exercise be used for treating lumbar spinal stenosis.
Conclusion: Guidelines made conflicting recommendations for the use of surgery and epidural injection in the management of lumbar spinal stenosis. High-quality clinical practice guidelines for lumbar spinal stenosis are needed, although their recommendations will remain limited until higher-quality evidence is available.

This review demonstrates that clinical practice guidelines are limited in their recommendations for lumbar spinal stenosis, given the poor evidence available for many common treatments.

Postdoctoral Researchers Session 14th Nov

Inflammation-induced angiogenesis was attenuated by Apolipoprotein C-III deficiency.

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Background: Inflammatory-driven pathological angiogenesis is associated with an acceleration of atherosclerosis and cancer. There is a strong positive association between apolipoprotein C-III (ApoC-III) and the risk of cardiovascular disease. ApoC-III is shown to promote mechanisms associated with inflammation-induced angiogenesis including induction of inflammatory gene expression and monocyte recruitment. The direct role of ApoC-III in angiogenesis is, however, yet to be established.

Methods and Results: Wildtype (C57Bl6/J) and apoC-III knockout (ApoC-III$^{-/-}$) mice aged 8-12 weeks underwent hindlimb ischemia (n=12) and periarterial cuff (n=12) surgery to induce pro-angiogenic and inflammatory responses. Deletion of ApoC-III suppressed the pro-angiogenic response induced by the cuff; attenuating both adventitial neovessel formation by 61% ($p<0.01$), assessed by CD31+ staining, as well as arteriole formation by 43% ($p<0.05$), assessed by α-actin+ staining. Cuff placement caused a marked increase in the mRNA expression of key angiogenic genes HIF-1α and VEGFA which were significantly attenuated in the ApoC-III$^{-/-}$ mice (33% and 79%, $p<0.05$ respectively). Similarly, there was an up-regulation in the mRNA expression of key inflammatory genes; NF-κB-subunit p65 and CD68, which were in the ApoC-III$^{-/-}$ mice (41% and 52%, $p<0.05$ respectively). Blood flow recovery and neovascularisation was assessed by laser Doppler perfusion imaging after hindlimb ischaemia and remained unchanged between ApoC-III$^{-/-}$ and wildtype mice.

Conclusion: ApoC-III gene deletion suppresses inflammatory-driven angiogenesis whilst, in contrast, had no effect on ischaemia-driven angiogenesis. Thus, ApoC-III inhibition may pose as an alternative therapy that specifically targets pathological angiogenesis without the adverse effects of inhibiting essential ischaemia-driven functions of physiological angiogenesis.

Poster Number 13 14th Nov

THE EFFECTS OF FATIGUE ON BLOOD GLUCOSE LEVELS – IMPLICATIONS FOR DIABETES

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Background: Individuals living with diabetes mellitus are commonly diagnosed with or experience some level of fatigue; however, the relationship is still to be fully explored. The effect of fatigue on blood glucose levels, both with and without a diabetes diagnosis, also requires further research.
Aim & Objectives: The aim of the study was to assess the following in individuals with and without diabetes: (i) the differences in fatigue levels and blood glucose, and (ii) the correlations between fatigue and blood glucose levels.
Methods: Participants who met the inclusion criteria signed a consent form before commencing the study. Three blood pressure measurements were taken before and after the study. Questionnaires targeting demographic and psychometric measures, as well as fatigue and sleepiness, were administered, followed by measurements of blood glucose levels and haemoglobin A1c.
Results: Blood glucose levels and Haemoglobin A1c were significantly higher in the test sample (n=16) in comparison to the control group (n=41) ($p<0.0001$). No statistically significant difference was established between the two samples for the fatigue measures. The Pittsburgh Sleep Quality Index reported a significantly higher score for those with diabetes when compared to the general population ($p=0.04$). However, the Fatigue Severity Scale was within the threshold for fatigue for the individuals with diabetes (36.3 ± 12.1). There were no significant associations between fatigue and blood glucose or haemoglobin A1c levels in the diabetes group, however, the Pittsburgh Sleep Quality Index displayed a trend towards a positive correlation with blood glucose levels in the control group ($p=0.089$, $r=0.269$).
Conclusion: The present study established that individuals with diabetes are more susceptible to poor sleep quality than the non-diabetes group. Future research is required in order to understand the relationship between fatigue and blood glucose levels, and its implications for diabetes.

Poster Number 15 14th Nov

NEWLY IDENTIFIED MIR-6770-3P DRAMATICALLY INDUCES ANGIOGENESIS IN HUMAN ENDOTHELIAL CELLS WHILE DECREASING PROLIFERATION

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Micro-RNAs (miRs) are small non-coding RNAs that alter the expression of multiple mRNA targets. Although they participate in physiological processes, dysregulation of their expression is implicated in various diseases. We investigated whether miRs could be involved in the regulation of FXYD1 expression, a sub-unit of the Na+/K+-ATPase pump, that we previously described as both cardio- and vasculoprotective under conditions of oxidative stress.

Using in silico analysis, we identified 3 potential miRs that could target FXYD1 mRNA: miR-3178, miR-3960 and miR-6770-3p. Using an FXYD1-3'UTR-luciferase reporter assay, we found that overexpressing miR-6770-3p in HEK293T cells resulted in the largest reduction in luciferase activity, showing a strong targeting of FXYD1 mRNA. A mutation of the binding site in the 3'UTR of FXYD1 restored luciferase activity, confirming the binding site of miR-6770-3p. Overexpression of miR-6770-3p in a human endothelial cell (EC) line, EA.hy.926, dramatically increased endothelial tube formation in a Matrigel angiogenesis assay (>4 fold change vs. control transfection, $p<0.05$) and was also associated with a 2 to 3-fold increase of VEGFR2 and Endoglin mRNA levels respectively. Interestingly, the overexpression of miR-6770-3p was associated with a decrease in cell proliferation, suggesting that the pro-angiogenic effect of miR-6770-3p was not due to increased proliferation. This effect was also specific to human ECs, and not replicated in mouse ECs.

We have identified a novel, pro-angiogenic miR which has the potential to increase vessel formation in vitro, and induce critical regulators of angiogenesis; however, further work is required to better understand how this miR performs these functions.

Poster Number 21 15th Nov

TARGETING THE 'GUARDIAN OF THE GENOME' AS A POTENTIAL THERAPEUTIC FOR OVARIAN CANCER

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Background: Ovarian Cancer is ranked 7th for incidence and 8th for mortality in global analyses of cancers affecting women. There is a high incidence of mutation of the tumour suppressor *TP53* in the most common type of ovarian cancer.
Aim & Objectives: We aimed to engineer a p53 isogenic ovarian cancer cell line panel (*TP53* wild-type (WT), null and pathogenic mutant) using CRISPR-cas9 genetic editing. This will allow for the screening of new therapeutics targeting p53, and fundamental research into the role of mutant p53 in malignancy.
Methods: Initial methods have focussed on engineering a p53 null line. A plasmid based (px458) CRISPR-cas9 system, integrated with specifically designed guide RNAs was used to transfect the A2780 WT p53 ovarian cancer cell line. Single cell sorting (based on transient GFP activation) was performed using flow cytometry, with cells expanded as p53 KO clonal populations. To screen the resulting clones for p53 levels, In-Cell Western (ICW) was employed along with Sanger sequencing.
Results: ICW analyses showed 10 of the 13 clones expanded from single cells, had absent p53 levels after treatment with the chemotherapeutic drug cisplatin to activate p53 in response to DNA damage. Of interest, one clone had increased p53 levels, indicating introduction of a variant that stabilises p53 levels. In a subset of potential p53 KO clones, Sanger sequencing has confirmed that frameshift mutations knocked out p53, identified by ICW, while a heterozygous in frame mutation (-9 and -6) was found for the clone with increased p53 levels.
Conclusion: Our preliminary data is proof-of-principle that we can use CRISPR-cas9 to knockout p53. Next, we will engineer pathogenic *TP53* mutants, and conduct experiments in a mutant p53 ovarian cancer cell line. Isogenic cell line panels are valuable as disease models that can be exploited to develop new cancer therapeutics.

PhD Session 1 – Young Investigator 15th Nov

A NOVEL HELMINTH-DERIVED MOLECULE, FhHDM-1, PRESERVES β-CELL FUNCTION TO PREVENT TYPE 1 DIABETES

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Background: Type 1 diabetes (T1D) is an autoimmune disorder characterised by the destruction of the insulin-producing pancreatic β-cells. Our team has discovered a novel anti-inflammatory molecule, termed *Fasciola hepatica* helminth defence molecule 1 (FhHDM-1) that prevents T1D development in non-obese diabetic (NOD) mice. Proteomic analysis of the pancreas of these mice suggests that FhHDM-1 promotes the activation of signalling pathways associated with cell survival and proliferation.

Aim & Objectives: The aim of this study was to investigate the putative effect of FhHDM-1 on pancreatic β-cells, specifically via readouts of proliferation, survival, apoptosis *in vitro,* and mass *in vivo*.

Methods: To evaluate the preservation of β-cell mass in vivo, pancreata from 10 week old NOD mice treated with of FhHDM-1 or vehicle control were harvested, sectioned and immunofluorescently stained for quantification of insulin to provide an indication of functional β-cell mass. To investigate the direct effect of FhHDM-1 on β cells, the survival and proliferation of NIT-1 cells (a NOD mouse-derived β-cell line) after exposure to inflammatory cytokines in the presence or absence of FhHDM-1 was examined using a variety of in vitro assays.

Results: Treatment with FhHDM-1 preserved β-cell viability ($p=0.0004$) as determined by XTT assays, and prevented pro-inflammatory cytokine-induced apoptosis ($p=0.0013$) in conditions akin to T1D pathogenesis, as determined by TUNEL staining and decreased levels of caspase 3 activity ($p=0.0056$). FhHDM-1 had no effect on β-cell proliferation, as evaluated by BrdU incorporation or DNA labelling with CyQuant dye. These outcomes corroborate preliminary *in vivo* studies that suggest treatment with FhHDM-1 preserves β-cell mass.

Conclusion: The positive effects on β-cells induced by FhHDM-1 treatment have significant therapeutic applications for the prevention of T1D and beyond. For instance, FhHDM-1 can also be used to preserve residual β-cell mass in recent onset T1D patients, prevent β-cell exhaustion and loss in type 2 diabetes and support β-cell viability during pancreatic islet transplantation.

A NOVEL SINGLE DOMAIN, I-BODY AD-114, ATTENUATED KIDNEY FIBROSIS THROUGH TARGETING CXCR4

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Background: Kidney fibrosis is the final common pathway of various forms of chronic kidney disease (CKD). However, the efficiency of current therapies is limited. The G-protein coupled C-X-C chemokine receptor 4(CXCR4) is a potential therapeutic target for tissue fibrosis. To date, the only approved CXCR4 antagonist (AMD3100) was terminated due to its off-target cardiotoxicity. Recently we have developed a fully human single-domain antibody-like scaffold termed i-body AD-114 with specific high binding affinity to CXCR4. AD-114 selectively blocks CXCR4 signaling and has shown anti-fibrotic effects in pulmonary fibrosis.
Aim & Objectives: The present study aims to evaluate the renoprotection of AD-114 in kidney fibrosis.
Methods: CXCR4 expression in the kidney biopsies from patients with diabetic kidney disease (DKD) and kidneys from three mouse models of CKD was detected using immunohistochemistry (IHC). To determine the preventive role of AD-114 in the development of CKD, a mouse model of folic acid (FA)-induced nephropathy was used. C57/BL6 mice were challenged with 250 mg/kg of FA followed by daily administration of AD-114 (10 mg/kg) intraperitoneally for 21 day. Nonspecific i-body that doesn't bind CXCR4 and AMD3100 served as negative and positive controls. To assess the therapeutic role, i-body was administrated on day 7-21. Renal function, histology and ECM deposition were assessed by urine creatinine/albumin kits, IHC and Masson's trichrome staining.
Results: CXCR4 expression was significantly upregulated in patients with DKD and fibrotic kidneys of three mouse models of CKD compared to control groups. In both prophylactic and therapeutic models, AD-114 markedly ameliorated albuminuria, fibrotic kidney remodeling and ECM in kidneys compared to negative control i-body.
Conclusions: AD-114 effectively ameliorated fibrotic kidney remodeling through targeting CXCR4 signaling in a murine model of kidney fibrosis. These data suggest that AD-114 has potential utility for therapeutic use in reversing kidney fibrosis.

Poster Number 8 14th Nov

Impact of traffic related air pollutant exposure on lung inflammation and mitochondrial wellbeing in mouse lungs

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Background: It is well accepted that traffic related air pollution (TRAP) is detrimental for respiratory health, causing inflammation. One of the core components of TRAP is particulate matter (PM). However, there is no consensus in animal models, and most models used high dose of PM acutely which might not be physiologically relevant.
Aims: In this study, we aimed to develop a mouse model of subchronic low dose PM exposure representing similar environmental exposure as the humans.
Method: Balb/c mice (7 weeks old, male) were exposed to saline or roadside PM10 (<10 micron; particle removed from Teflon filter) 1μg or 5μg daily for three weeks (n=10). Inflammatory response was assessed in bronchoalveolar lavage (BAL), and mitophagy markers (to measure recycling mechanism of mitochondria) was measured by Western blotting (n=8).
Results: Exposure to 1μg of PM10 did not affect inflammatory and mitochondrial markers in the lung, while 5μg of PM10 exposure increased lymphocytes and macrophages in BAL. Inflammatory cytokine IL-1β was increased and mediated through upstream NLRP3 in mice exposed to 5μg PM10 exposure ($P<0.05$). IL-6 protein level was not changed. PM10 reduced mitochondrial antioxidant manganese superoxide and mitochondrial fusion marker OPA-1 and increased mitochondrial fission marker Drp-1($P<0.05$). Autophagy marker LC3-II and AMPK were reduced with increased apoptosis marker caspase-3 ($P<0.05$). Fibrotic markers fibronectin, TGF-β1 and Collagen-III were not changed by PM10 exposure at either 1μg or 5μg.
Conclusion: Low level of PM10 exposure can elicit inflammation and alter mitochondrial fission, fusion and autophagy in the subchronic setting. This model can be used to study other TRAP exposure related conditions, such as asthma.

Poster Number 33 15th Nov

DIAGNOSTIC AND PROGNOSTIC POTENTIAL OF CURRENT BIOMARKERS IN HEART FAILURE WITH PRESERVED EJECTION FRACTION: A SYSTEMATIC REVIEW AND META-ANALYSIS

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Background: The diagnosis and treatment of heart failure with preserved ejection fraction (HFpEF) are poorly managed and remain an area of unmet clinical need due to the limited understanding of the pathogenesis of this condition.
Aim & Objectives: In this systematic review and meta-analysis, we aimed to evaluate the current biomarkers used for both the diagnosis and prognosis of HFpEF.
Methods: SCOPUS, Ovid MEDLINE, Web of Science, Cochrane Library and PubMed databases were searched until October 2019 by two independent authors. RevMan 5.3 was used to extract and pool the data from the included studies in relation to the biomarkers' sensitivity and specificity for HFpEF diagnosis and to assess the pooled hazard ratios for HFpEF-related hospitalisation.
Results: To date, a meta-analysis including a total of 617 patients with HFpEF from four studies was conducted, resulting in the evaluation of 12 biomarkers used for HFpEF diagnosis. Most of the biomarkers demonstrated good sensitivity (mean=0.82±0.13) with modest specificity (mean=0.61±0.22) for diagnosing HFpEF. Interestingly, NT-proBNP (N-terminal pro-B-type natriuretic peptide), the most commonly used biomarker to diagnose HFpEF, showed a modest sensitivity of 0.67 [95% CI, 0.61-0.73] and high specificity of 0.91 [95% CI, 0.85-0.95] for HFpEF diagnosis. In terms of the prognosis of HFpEF, high hazard ratios were demonstrated with the following biomarkers: cBIN1 (cardiac bridging integrator 1) of 3.8 [95% CI, 1.3-11.2; p-value=0.02] and NT-proBNP of 1.83 [95% CI, 1.44-2.33; p-value<0.0001].
Conclusion: The results of this meta-analysis suggest that the current biomarkers used for HFpEF diagnosis display either modest sensitivity or specificity and therefore there is an urgent need for better understanding of the pathogenesis of HFpEF and discovery of novel biomarkers for HFpEF diagnosis. In terms of the prognosis, cBIN1 and NT-proBNP as biomarkers show some promise in risk stratification of patients with HFpEF in terms of mortality.

Honours/RA 14th Nov

Differential chemokine receptor expression and usage by immediate dendritic cell precursors

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Background: Type 1 conventional dendritic cells (cDC1) derive from distinct precursor cells called pre-cDC1 in the bone marrow, which traffic through the blood to the periphery. Coordinated trafficking of these cells is necessary for anti-tumour immunity due to their unique ability to prime a T helper type 1 (Th1) immune response. Hence, understanding the way these cells traffic to tumours could reveal new targets for cancer therapy.
Aim & Objectives: To determine mechanisms of pre-cDC1 trafficking to melanoma tumours in both mouse and man.
Methods: This study combined single cell gene expression analysis with flow cytometry to identify potential mechanisms of pre-cDC1 migration. We also used genetic knock-out mice to create mixed bone marrow chimeric models to elucidate cell intrinsic uses of these pathways whilst trafficking to melanoma tumours. Furthermore, we screened human melanoma samples using a novel imaging mass cytometry (IMC) approach to identify these mechanistic components in human tumours.
Results: We show that pre-cDC1 distinctly express and use the Th1-associated chemokine receptor CXCR3 to traffic to melanoma tumours ($P < 0.01$) and consequently to tumour draining lymph nodes ($P < 0.001$) in mice. We also show you can enhance pre-cDC1 trafficking to melanoma tumours by inhibiting dipeptidylpeptidase-4 (DPP4) ($P < 0.05$), a known negative regulator of CXCR3-specific ligands CXCL9/10. Finally, we confirmed that human pre-cDC1 also express CXCR3 in normal blood and show that its expression is maintained on mature cDC1 in both healthy human blood and in melanoma tumours.
Conclusion: Our results identifies CXCR3 as a distinct regulator of pre-cDC1 kinetics during the anti-tumour response across species and provides evidence this pathway can be manipulated to enhance cDC1 presence in tumours, relevant for creating novel cancer immunotherapies.

Honours/RA 14th Nov

INTERMITTENT PACAP IN THE VENTROMEDIAL HYPOTHALAMUS EVOKES LASTING ELEVATIONS IN BLOOD GLUCOSE

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Background: Intermittent hypoxia is a key pathophysiological hallmark of obstructive sleep aponea (OSA), a condition that affects up to 30% of the population and 70% of diabetics. The central mechanisms behind OSA-induced effects are poorly understood. Of interest is the excitatory neuropeptide, pituitary adenylate cyclase activating polypeptide (PACAP) that is present in neurons of the ventromedial hypothalamus (VMH), when stimulated these neurons produce hyperglycaemia.
Aim & Objectives: To determine whether intermittent stimulation with excitatory neuropeptides, glutamate and PACAP in the VMH causes persistent increases in blood glucose.
Methods: In anaesthetised, mechanically ventilated Sprague-Dawley rats blood glucose was recorded prior and post treatment with intermittent microinjections. The carotid artery was cannulated for recording of mean arterial pressure. Heart rate, end-tidal CO_2, temperature and splanchnic nerve activity were monitored and recorded through the experiment. Post-treatment blood glucose changes from baseline and recorded parameters were compared to vehicle and volume control, PBS, using a two-way ANOVA.
Results: Intermittent unilateral microinjections of glutamate (n= 5, 10 x 0.5 μmol) was not sufficient to cause an increase in blood glucose compared to vehicle control. A bolus microinjection of 60 pmol of PACAP increased blood glucose from baseline (n=4, $\Delta 0.5 \pm 0.32$ mmol/L, P= 0.0212). Intermittent microinjections of a subthreshold dose (n=8, 10 x 5pmol PACAP) evoked lasting increases in blood glucose for up to one hour compared to vehicle control (60 min: $\Delta 0.09$ mmol/L $\pm$ 0.3 mmol/L vs. n=6, PBS: -0.5 ± 0.35 mmol/L, P=0.0043). PACAP-induced elevations in blood glucose occurred without significant changes from baseline in mean arterial pressure, heart rate, end-tidal CO_2 and temperature compared to vehicle control.
Conclusion: Intermittent stimulation with PACAP induces early plasticity changes in the VMH to mediate maintained elevations in blood glucose. Alterations in neuronal signalling in the VMH may have implications for the dysregulation of glucose control in patients with OSA.

Poster Number 31 15th Nov

MULTIPLEX RT-QPCR TO DETECT HPV16 ONCOGENES IN HEAD AND NECK CANCER PATIENTS

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Background: Over the last ten years, there has been a significant increase in human papillomavirus (HPV) infections associated with head and neck cancers. Today, this sexually transmitted virus is the driver of cancer progression in cases of tongue and throat cancers, referred to as oropharyngeal cancers (OPC). More than 85% of these patients are infected with the high-risk HPV strain, HPV16.
Aim & Objective: We are developing a robust diagnostic assay to accurately detect HPV16 RNA oncogenes using blood and saliva from OPC patients.
Method: High-risk strains of HPV encode for several viral oncogenes such as E6/ E7. We have developed and optimise a RT-qPCR multiplexing assay to detect these two oncogenes.
Results: For proof-of-concept, our multiplex approach was able to detect E6 and E7 in HPV positive cell lines with no significant difference to a traditional singleplex reaction. We then carried out serial dilutions of starting RNA input to determine the LOD. Finally, we assessed our method in OPC patient tissue which accurately differentiated between HPV positive and negative specimens. Using this multiplex RT-qPCR approach, we are aiming to develop a non-invasive approach for the detection of HPV using the serum and saliva of OPC patients.
Conclusion: Development of a rapid and accurate test to accurately measure HPV is crucial for clinical decision making and treatment planning for OPC patients. We have shown that HPV16 E6 and E7 mRNA can be detected using hydrolysis probe RT-qPCR in both cell lines and patient tissue specimens. The combination of multiplexing would reduce sample input and reagent costs. Our assay is different from other commercial or diagnostic kits as we measure the RNA, which is confirmation of active oncogene transcription and viral replication.

CD4 T CELL HELP PROMOTES THE EXPANSION OF CD8 T CELLS DURING PERSISTENT LIVER ANTIGEN BUT DOES NOT RESCUE T CELL EXHAUSTION

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Background: Studies show that both CD8 and CD4 T cells play critical roles in protecting humans and chimpanzees against hepatotropic pathogens, Hepatitis C virus and Hepatitis B virus, that persist as a chronic infection in many individuals. While a robust anti-viral $CD8^+$ CTL response is a predictor of resolution of hepatotropic viral infections, $CD8^+$ T cell exhaustion leads to the inability for the host to clear the pathogen. $CD4^+$ helper T cells likely play an essential role in pathogen control by supporting CD8 T cell expansion and differentiation, a process known as "CD4 help". Although studies have reported the determinant role of CD4 T cells in hepatotropic viral responses, the role of CD4 help on $CD8^+$ T cell exhaustion in the liver has not been investigated.

Aim & Objectives: We aim to investigate the role of CD4 T cell help in influencing the CD8 T cell response and exhaustion during persistent hepatocyte expressed antigen.

Methods: We have generated recombinant adeno-associated viral (rAAV) vectors that mediate hepatocyte specific expression of a model antigen containing both CD8 and CD4 epitopes recognised specifically by T cell receptor (TCR) transgenic CD8 T cells and CD4 T cells, allowing us to investigate how CD4 T cells influence the CD8 T cell response in the mouse liver.

Results: In absence of CD4 help, CD8 T cells responding to persistent hepatocyte expressed antigen quickly become exhausted. The presence of CD4 help increases the number of CD8 T cells however cannot rescue them from exhaustion. Interestingly, CD4 help also facilitates the accumulation of a large number of activated endogenous $CD8^+$ T cells with an unknown specificity and function in the liver.

Conclusion: These results suggest a model in which the CD4 T cell response boosts the number of effector virus-specific CD8 T cells but cannot rescue them from exhaustion during persistent antigen expression in chronic hepatotropic viral infections.

UNDERSTANDING CORTICOSTEROID BIOLOGY USING TRANSCRIPTIONAL PROFILING OF BRONCHIAL BIOPSIES AND CRISPR-CAS9 KO MODELS

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Background: Corticosteroids are known for their anti-inflammatory effects in asthma and COPD. Severe asthma and COPD share common pathophysiologic traits such as airflow obstruction and corticosteroid insensitivity.
Aim & Objectives: We aimed to investigate genes upregulated by corticosteroid treatment and to determine their functional role in corticosteroid resistance.
Methods: A meta-analysis of 4 studies (Healthy (GSE83233 n = 11), Asthma (MAST n = 12, SAGE n = 20), COPD (GLUCOLD n = 26)) was conducted on bronchial biopsies matched for pre- and post-corticosteroid treatment. From this analysis, the top candidate gene was chosen to be knocked out in the lung epithelial cell line A549 using CRISPR-Cas9. To identify the functional role, glucocorticoid receptor (GR) and NFkB reporter assay and ELISA for the pro-inflammatory cytokine CXCL8 were performed on knockout cells treated with Fluticasone Propionate (FP) 10-8 M (n = 6).
Results: The meta-analysis identified 93 genes increased and 170 genes decreased by corticosteroids (meta Bonferroni adjusted $P < 0.05$). FKBP5, identified as the most significantly increased gene, was knocked out in A549 cells using CRISPR-Cas9. In the absence of FKBP5, the GR reporter activity increased ~6x further upon FP treatment ($P < 0.05$) compared to wildtype, while the NFkB reporter assay was decreased at baseline. Additionally, the effectiveness of FP to supress CXCL8 release upon TNFalpha stimulation was enhanced in the FKBP5 knockout compared to control A549 cells ($P < 0.05$).
Conclusion: Based on our findings we propose that the expression of FKBP5 not only acts to supress corticosteroid function but also aids in the activation of the NF-kB signalling leading to enhanced inflammation. This duel function of FKBP5 indicates that it plays an important role in regulating the function of inflammatory during corticosteroid treatment. Therefore, FKBP5 provides a novel therapeutic target to improve corticosteroid sensitivity.

Poster Number 2 14th Nov

INVESTIGATING THE METABOLIC EFFECTS OF DEPRESSION AND BURNOUT IN NURSES

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Background: Due to their inherently stressful occupation, nurses are highly susceptible to psychological disorders such as depression and burnout, both of which may be risk factors for diabetes mellitus. These three conditions affect not only the health outcomes of nurses, but also patient care.
Aim & Objectives: The study aims to investigate, in nurses compared to non-nurses: (i) the differences in psychometric and metabolic variables; (ii) the relationship between psychometric and metabolic variables.
Methods: If the inclusion criteria were met, subjects signed the consent form. Three blood pressure measurements were obtained before and after the study. Questionnaires were administered to collect demographic and psychometric data, followed by blood glucose levels and haemoglobin A1c assessment.
Results: Both sample groups scored within the normal range for depression, with the nurses scoring slightly higher. As for burnout, the nurses scored significantly higher for Emotional Exhaustion than the non-nurse group ($p=0.04$), with an average score of 26.25 indicating moderate severity of burnout. The nurse group scored an average of 7.94 for Depersonalisation, also in the moderate range and slightly higher than the non-nurse group. As for Personal Accomplishment, the nurses presented significantly higher levels than the non-nurses ($p<0.01$), scoring an average of 40.81, which indicates low severity of burnout for this measure. Both the nurses and non-nurses had normal fasting blood glucose levels and haemoglobin A1c values, however, the nurses had slightly higher haemoglobin A1c levels than the non-nurses. No significant correlations were established between the psychometric variables and either blood glucose or haemoglobin A1c levels.
Conclusion: While it was established in the present study that nurses were significantly more susceptible to developing burnout than non-nurses, further research is required in order to determine the associations between psychometric and metabolic measures.

Poster Number 14 14th Nov

INVESTIGATING THE EFFECTS OF AIR POLLUTANT NANOPARTICLES IN ALZHEIMER'S DISEASE

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Background: Air pollution nanoparticles are considered a major risk factor in the development of Sporadic Alzheimer's disease (AD). Despite this, the underlying mechanisms between air pollutant nanoparticles and the development of AD is yet to be established.
Aim & Objectives: This study aimed to determine whether inhalation of air pollutant nanoparticles will exacerbate neuropathology changes associated with AD.
Method: Air pollutant nanoparticles were derived from (i) diesel emission particles (DE), (ii) micro abraded iron (IRON) and (iii) magnetite nanoparticles (MNPs). Four study groups, each including 3month-old C57BL/6 (n=36) and APP/PS1 (n=35) mice, received either of the aforementioned nanoparticles or saline (vehicle control), every third day, via intranasal administration [66µg] over 17-weeks. An elevated plus maze (EPM) test and *in-vivo* imaging of the brain using probes (CRANAD 58 and 2) was used, to assess changes. Human neuroblastoma cells (SH-SY5Y) and mouse microglia cells (BV2) were exposed to air pollutant nanoparticles before MTT assay, RT-qPCR, Griess and DCF assays were performed.
Results: The EPM test showed an increase in stress anxiety levels in (i) C57BL/6 exposed to IRON and DE compared to C57BL/6 controls, and (ii) APP/PS1 exposed to IRON compared to APP/PS1 controls. *In-vivo* imaging showed an increase in Aβ load in (i) C57BL/6 exposed to DE and MNPs, and (ii) APP/PS1 exposed to IRON, DE and MNPs compared to controls. At the cellular level, both cell lines exposed to the air pollutant nanoparticles showed (i) an increase in nitric oxide and reactive oxygen species levels; (ii) decrease in cell viability and (iii) an increase in mRNA expression of neuroinflammatory markers (TNF, IL-6, IL-1β and IL-1α), compared to vehicle control.
Conclusion: Exposure to air pollutant nanoparticles can result in changes to pathways associated with inflammation and oxidative stress in key cells related with AD. These changes subsequently may lead to Aβ load and the onset of AD.

Honours/RA 14th Nov

MEMBRANE ION CHANNEL PROPERTIES OF THE PH-SWITCHABLE PEPTIDE GALA

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Background: GALA is a 30-residue, pH-switchable peptide that contains the amino acid repeat sequence glutamic acid – alanine – leucine – alanine. It was designed to facilitate endosomal drug release but its ability to form stable membrane pores makes it an ideal model system to study the structure and formation of membrane pores. Protonation of the glutamic acid side chains induces a conformational change from unstructured in solution at physiological pH to helical at low pH, enabling insertion into phospholipid bilayers where multiple peptides aggregate to form stable pores. There was little information on pore size and no data investigating the ion selectivity of the pore.

Aim & Objectives: To determine cation selectivity and estimate the GALA pore size in model phospholipid bilayers using a series of cations of varying size and charge.

Methods: Tethered bilayer lipid membranes (tBLMs) and electrical impedance spectroscopy (EIS) were used to measure conduction of different sized cations through GALA pores formed in tBLMs composed of POPC phospholipids in the presence and absence of 20% cholesterol.

Results: We show that GALA forms a stable, cation selective pore that allows passage of mono- and divalent cations, but not larger organic cations like choline. Monovalent sodium and potassium have a significantly larger conduction through the GALA pores relative to divalent magnesium, calcium and strontium ($p \leq 0.003$). We also report that cholesterol modulates the pore formed by GALA and subsequently changes the conduction of cations.

Conclusion: We can conclude that GALA forms small stable ion selective pores and thus shows the potential to be used to manipulate the ion concentration gradient across cell membranes. This could be clinically used to disrupt the function of mammalian or bacterial cells in acidotic cellular microenvironments, leading to targeted cytotoxicity. The newly defined cation selectivity makes GALA pores excellent model systems to study ion selectivity.

Poster Number 36 15th Nov

THE INFLUENCE OF ONCOGENIC MIR-21 ON THE EXPRESSION OF MIRNAS

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Background: On a global scale, Head and Neck Squamous Cell Carcinoma (HNSCC) currently affects more than 500,000 people per year. The survival rate for HNSCC has remained at 50% for over 30 years, with an increasing incidence rate. MicroRNAs (miRNAs) have been found to have a role in HNSCC development. MicroRNAs convey post-transcriptional control of messenger RNA (mRNA). However, recent studies have found that miRNAs infer regulation of other miRNAs through a miRNA:miRNA interaction.
Aim & Objectives: Our lab aims to investigate the miRNA:miRNA interactions of the oncogenic miRNA, miR-21, in HNSCC, and uncover its effects on gene regulation and tumorigenesis.
Methods: A miRNA OpenArray was used to detect changes in miRNA expression in response to miR-21 transfection in hypopharyngeal squamous cell carcinoma (UMSCC22B) cells. Cytoscape was utilised to identify network pathways between the identified miRNAs, and analysed with GO and KEGG. Select miRNAs were confirmed with qRT-PCR. HNSCC patient data was extracted from the Cancer Genome Atlas (TCGA), and analysed in R Studio to corroborate the findings of the array.
Results: miR-21 was found to upregulate 10 miRNAs by greater than 2-fold. Additionally, the 10 most downregulated miRNAs were chosen for further analysis. Networks of the upregulated and downregulated miRNAs and their targets had 2383 nodes and 5232 edges, and 4166 nodes and 14646 edges respectively. GO and KEGG analysis identified an oncogenic role for these miRNAs by identifying roles in the P53 and MAPK signalling pathways. Both analysis of HNSCC TCGA patient data and qRT-PCR reflected the miRNA changes observed in the array.
Conclusion: This study is the first to identify miRNA:miRNA interactions in HNSCC, map their targets, and predict their potential role in oncogenesis. These findings are significant to our understanding of cancer biology, and have implications on the design of novel therapeutics.

Poster Number 38 15th Nov

DUAL ROLE OF GOLD NANOPARTICLES IN LUNG SURFACTANT MONOLAYER: A MOLECULER DYNAMICS STUDY

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Background: The rapid development of nanotechnology increases the huge aspects of Nanoparticles (NPs) in biomedical applications particularly gold nanoparticles (AuNPs) and the potential health risk associated in instigation of lungs diseases. Being nanoscale size, the NPs easily enter our organism through lungs, where the NPs primarily interact with a thin barrier usually called lung surfactant (LS). The stability of lungs through normal breathing entirely controlled by the intrinsic LS functions, therefore it is crucial to understand the functions of the LS exposed to AuNPs at molecular level.
Aim & Objectives: The overall aim of the study is to explore the dual-role of AuNPs in lungs area and elucidate the nano-bio interactions molecularly. To achieve the aim successful, it is indispensable to study the model LS layer (first biological barrier inside lungs) at air-liquid interface exposed to AuNPs, so that the lung diseases caused by the NPs can be revealed with the role of NPs' concentrations, sizes, shapes and surface properties.
Methods: In this investigation, coarse-grained (CG) molecular dynamics simulations are performed to a series of LS monolayer models with AuNPs at the interface during breathing cycles.
Results: It is observed that the bare AuNPs and its' concentration structurally deform the monolayer, change the biophysical properties of LS and create pores in the monolayer, which all interfere with the normal lung functions including surface tensions at the interface. It is also found that AuNPs significantly disrupt the monolayer packing during monolayer in inhalation state than exhalation state. In case of coated AuNPs in model LS, the surfactant monolayer associated hydrophobic peptide aggregates in the monolayer during the course of the simulations.
Conclusion: Overall, these findings could help to design nanomedicines to improve drug delivery capacity in lungs as well as in identifying the possible consequences of airborne NPs inhalation at molecular level.

Poster Number 5 14th Nov

INTRACEREBROVENTRICULAR PAC1 RECEPTOR ANTAGONIST ABOLISHES THE GLUCOSE RESPONSE TO ACUTE INTERMITTENT HYPOXIA

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Background: Obstructive sleep apnoea (OSA) is a risk factor for developing type 2 diabetes. Repetitive activation of the sympathetic nervous system may cause long-term dysfunction in autonomic control of glucose metabolism. The excitatory neuropeptide, Pituitary Adenylate Cyclase–Activating Polypeptide (PACAP), is important for normal functioning of these autonomic pathways.
Aim & Objectives: To determine the contribution of central vs peripheral PACAP receptor signalling in the sympathetic blood glucose (BG) response to acute intermittent hypoxia (AIH).
Methods: Conscious, male Sprague-Dawley rats (n = 78; 300-500g) were given 2h of AIH (6%O2). 1min intervals of hypoxia were interspersed with 3min of room air (21%O2). BG was measured pre and post-AIH and compared with intermittent room air. 10nmol of PAC1 receptor antagonist, VPAC1/2 receptor antagonist, or vehicle (0.9% saline) was injected intracerebroventricularly (ICV), or intraperitoneally (IP), before the sequence. Plasma was collected and assayed for adrenaline and PACAP. Brain tissue was injected with dye post-mortem for intracerebroventricular cannula site confirmation
Results: Rats given ICV vehicle had elevated post-AIH BG compared to rats given intermittent room air. Neither antagonist had any effect on BG levels in the absence of AIH. AIH treated rats that were given the PAC1 antagonist had no elevation in BG whereas VPAC1/2 antagonist treated rats had an elevation similar to those given vehicle ($P < 0.05$). AIH-induced increases in BG were unaffected by IP injection of either antagonist ($P > 0.05$). No significant changes were detected in plasma [PACAP] and [Adrenaline].
Conclusion: The study reveals that central PACAP-PAC1 signalling is important for the blood glucose response to AIH and is not mediated by adrenaline on this time scale. This offers new insight into how repetitive activation of the sympathetic nervous system may lead to dysfunction of glucose control, a potential mechanism underlying the relationship between OSA and diabetes.

Poster Number 3 14th Nov

Chemical modification of *t*-BLM biosensor for real time monitoring

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Background: The demand for rapid real time monitoring of small analyte present in the biological and chemical samples has increased the interest in the development of biosensors. Tethered bilayer membrane biosensors are one of the promising tool which can be used for such application. The *t*BLM based biosensors are highly sensitive, robust and relatively inexpensive to make.

Aim & Objectives: The overall aim of this project is to chemically modify the *t*BLM biosensor which will allow for real time continuous monitoring of small analyte present in the biological and chemical samples.

The objective of this work is largely around the chemistry associated with the biosensor and creating the hybrid macromolecule species which can be incorporated to the biosensor for continuous monitoring.

Methods: The hybrid molecules were chemically synthesized. These hybrid molecules were incorporated to the antibody via site specific homogenous conjugation using click chemistry**.** The extent of the conjugation was measured using surface plasma resonance (SPR).

Results: For click conjugation azide group was attached to the monoclonal antibody. The chemically synthesized biotin-DBO (triple bond component) derivatives with different linker lengths were conjugated to the antibody. According to the SPR analysis the conjugation was occurred nearly 13%. These biotinylated antibody was attempted to attach to membrane spanning lipid (MSL) via streptavidin. These results prove that the antibody can be directly attached to the ion channel gramicidin of the biosensor. These results will be used to select the linker length and appropriate protocol to achieve necessary antibody flexibility when coupling MSL-DBO to whole antibody.

Conclusion: It has been shown that the antibody can be incorporated to the gramicidin ion channel present in the membrane. This chemical modification will allow the biosensor to be use in real time continuous monitoring of analyte present in the biological and chemical samples and to build the next generation diagnostic tool.

Poster Number 34 15th Nov

Future of phospholipids in the treatment of asthma

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Background: Steroids are the mainstay treatment targeting airway inflammation, however are associated with several side effects. Natural phosphatidylcholines are proven to be anti-inflammatory with lesser side effects. Synthetic phosphatidylcholine such as DOPC has not been explored for its anti-inflammatory potential.
Aim & Objectives: The aim of this study was to evaluate the potential of UTS-L containing DOPC as an anti-inflammatory treatment to improve lung function.
Methods: UTS-Liposomes were prepared by thin film hydration method. To induce acute allergic asthma, 4 W/O female C57BL/6 mice were sensitized on day 0 and day 14 with ovalbumin. On days 19, 21, 23, 25 and 27, OVA challenge was performed with 1% ovalbumin in PBS. Sham mice were sensitized and challenged with PBS. For the OVA-UTS-L mice, UTS-L (6 mg/mice) was injected every day from day 0. 24 hours after last aerosol challenge (day 28), mice were anaesthetized and lung function was performed.
Results: The size of UTS-L liposome was 190.86 ± 6.95 nm with a polydispersity index of 0.28 ± 0.01. The zeta potential of UTS-L was found to be -1.39 ± 0.06. Total elastance (Ers), a parameter of airway hyperreactivity following 50 mg/ml of methacholine was significantly higher ($P<0.01$) in the OVA-challenged group (76.54 ± 7.14 cmH2O.s/ml) when compared to PBS group (46.65 ± 1.86 cmH2O.s/ml). In OVA-UTS-L group, total elastance was measured to be (54.76 ± 1.38 cmH2O.s/ml), significantly lower ($P<0.05$) in comparison with OVA challenged group.
Conclusion: Airway hyperresponsiveness is the key feature of asthma. Our findings indicate daily injection of UTS-L in OVA challenged mice reduced AHR. Further studies are required to understand the mechanism of liposomes in lowering the asthma. UTS-L, will provide an innovative and effective approach to managing asthmatic symptoms in those affected.
Conclusion: Airway hyperresponsiveness is the key feature of asthma. Our findings indicate daily injection of UTS-L in OVA challenged mice reduced AHR. Further studies are required to understand the mechanism of liposomes in lowering the asthma. UTS-L, will provide an innovative and effective approach to managing asthmatic symptoms in those affected.

Conclusion: Airway hyperresponsiveness is the key feature of asthma. Our findings indicate daily injection of UTS-L in OVA challenged mice reduced AHR. Further studies are required to understand the mechanism of liposomes in lowering the asthma. UTS-L, will provide an innovative and effective approach to managing asthmatic symptoms in those affected.

PhD Session 1 – Young Investigator 15th Nov

REPURPOSING HYDRALAZINE FOR THE TREATMENT OF OBESITY-RELATED KIDNEY DISEASE

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Background: Obesity is a significant risk factor for the development and progression of chronic kidney disease (CKD). Renal fibrosis is the final pathophysiological pathway in the development of end stage kidney disease. Recent studies demonstrated the role of epigenetics in CKD progression. The antihypertensive agent hydralazine acts as a demethylating agent when used at low dose independent of its effect on hypertension, suggesting a potential therapeutic role in CKD.
Aim & Objectives: Use a mouse model to determine whether low dose hydralazine prevents CKD progression in obesity, and elucidate the underlying mechanisms.
Methods: From 8 weeks, male C57/BL6 mice were fed either high fat diet (HFD) or chow, and received either hydralazine dissolved in drinking water (25mg/L), or normal drinking water. Prior to harvesting at 32 weeks, mice underwent intraperitoneal glucose tolerance testing, and blood pressure measurement via a non-invasive tail vein cuff method. Urinary albumin:creatinine ratio was determined via bladder puncture. Renal pathology, markers of fibrosis, inflammation and oxidative stress were assessed histologically, by Western blotting or real-time PCR.
Results: Mice fed HFD demonstrated increased adiposity and glucose intolerance. Hydralazine did not significantly change body weight or glucose intolerance. Obesity increased albuminuria and this was reversed by hydralazine. Increased glomerulosclerosis, observed in obese animals, was ameliorated by hydralazine independent of its effect on blood pressure. Obese mice demonstrated increased kidney fibrosis, inflammation and oxidative stress markers. Such markers were not significantly improved by hydralazine administration.
Conclusion: In a mouse model of obesity, hydralazine is renoprotective with reduced albuminuria and glomerulosclerosis. This occurs independently of alterations in body weight, blood pressure, glucose intolerance, renal fibrosis, inflammation or oxidative stress. Although the renoprotective effect of hydralazine is unknown at this stage, the data provide a potential novel therapy for patients with CKD.

Poster Number 30 15th Nov

INTERPLAY BETWEEN BONE MARROW-RESIDENT CD69^{HI} AND CLONALLY EXPANDED TERMINAL EFFECTOR T CELLS IN MULTIPLE MYELOMA PATIENTS

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Background: Multiple myeloma (MM) is preceded by the clinically-stable condition Monoclonal Gammopathy of Undetermined Significance (MGUS). Most MM patients have clonally expanded V_β restricted $CD8^+CD57^+$Terminal Effector T cells (T_{TE}), detectable in the peripheral blood (PB), which potentially engage in immunological control of myeloma. Differentiation of clonally expanded T_{TE} cells particularly in chronically inflamed myeloma-infiltrated bone marrow (BM) can be altered, leading to failure in disease control.

Aim & Objectives: To identify changes in T_{TE} cells during the progression from MGUS to MM by defining 1) discrete subsets of T_{TE} cells which are differently distributed between MGUS and newly-diagnosed (ND)MM patients and 2) their relationship with clonally expanded V_β restricted T_{TE} cells.

Methods: Paired BM and PB of MGUS (n=4) and NDMM (n=10) patients were analysed using mass cytometry, flow cytometry and unsupervised Flow Self-organising Map (FlowSOM) clustering.

Results: Within entire T_{TE} cells, the FlowSOM clustering identified 4 discrete $CD69^{hi}$, subsets which were more prevalent in the BM of NDMM than MGUS patients. These $CD69^{hi}T_{TE}$ cells were not detectable in the PB and as such are BM-resident. They have a transitional phenotype between effector memory T cells ($CD45RO^+$, $CD28^+$, $CD27^+$) and T_{TE} ($CD57^+$, $KLRG1^+$) cells, express multiple inhibitory receptors: PD-1, TIGIT, Tim3 and CD160 suggesting their exhaustion status. They have high IFNγ and TNFα, but low granzyme B and perforin expression, regulated by $Eomes^{hi}$ expression. Higher accumulation of $CD69^{hi}T_{TE}$ cells was detected in NDMM patients with low expansion of clonally V_β restricted T_{TE} cells suggesting inverse relationships between these two types of T_{TE} cells.

Conclusion: We identified a novel type of BM-resident $CD69^{hi}T_{TE}$ cells which are prevalent in NDMM patients with low expansion of clonally V_β restricted T_{TE} cells suggesting that interplay between those two types of T_{TE} cells may be a key to disease control in MM patients.

Honours/RA 14th Nov

THE ROLE OF AN IMMUNOPHILIN PROTEIN, FKBPL, IN CARDIAC ENDOTHELIAL DYSFUNCTION ASSOCIATED WITH TYPE 2 DIABETES

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Background: Cardiovascular disease is the leading cause of death globally and up to three-fold more common in people with diabetes mellitus (DM). Although endothelial damage has been implicated, the mechanisms underlying the association between these two conditions, however, remain poorly defined.
Aim & Objectives: To elucidate the expression and role of the immunophilin protein, FKBPL, within the cardiac endothelium using *in vitro* and *in vivo* models of DM.
Methods: Primary human coronary artery endothelial cells (HCAECs) were exposed to the FKBPL peptide mimetic, AD-01 (1 nM) or vehicle control and cultured for a period of 24 h in media containing physiological (5 mM) or high (25 mM) glucose. Angiogenesis and inflammatory mRNA expression were analysed using RT-qPCR and Western blotting, concurrent with endothelial tubule formation assays. Additionally, endothelial FKBPL protein expression was assessed in a streptozotocin and high fat diet induced mouse model of type 2 DM (T2DM) at two different time points.
Results: When cultured in high glucose media, FKBPL mRNA expression in HCAECs was significantly reduced at 24 h ($n \geq 3$, $p < 0.05$), compared to the physiological glucose control, mirroring the results obtained in the T2DM *in vivo* model, where there was a significant decrease in endothelium-associated FKBPL expression within the aorta of mice ($n \geq 3$, $p < 0.01$, 9 weeks; $p < 0.05$, 16 weeks). In addition, exposure of HCAEC to AD-01 significantly increased the mRNA expression of the pro-fibrotic mediator collagen-1α ($n = 3$, $p < 0.05$) under normoxia, whilst decreasing endothelial tubule formation ($n = 3$, $p < 0.05$). An increase in ET-1 mRNA expression ($n = 3$, $p < 0.05$) was further indication of inducement of pro-inflammatory mechanisms.
Conclusion: Reduced levels of FKBPL in diabetes appear to be protective of the endothelium and restoring the levels of FKBPL in diabetes using a peptide mimetic leads to increased likelihood of fibrosis and restricted angiogenesis.

Poster Number 28 15th Nov

NUMERICAL SIMULATION TO THE RELATIONSHIP BETWEEN THE AORTIC VALVE CALCIFICATION AND HEMODYNAMIC PARAMETERS USING COMPUTATIONAL FLUID DYNAMICS

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Background: Aortic stenosis (AS), as a result of degenerative calcific change, is the commonest form of valvular heart disease worldwide, with an increasing prevalence owing to the aging population. The onset of symptoms, in the form of angina, dyspnoea or syncope and arrhythmia is associated with a significantly poor prognosis. However, predicting which patients will develop symptomatic severe aortic stenosis, or indeed anatomically where degenerative changes will occur is unknown.
Aim & Objectives: To overcome this problem, an engineering approach using numerical simulation may be a useful way of predicting which patients will develop AS and hence who may benefit from closer monitoring and intervention. The aim of the study was to predict the relationship between the distribution of aortic valve calcification and hemodynamic parameters.
Methods: Five patient-specific left ventricle models were reconstructed from multiple computed tomography (CT) images. Volumetric flow rate was applied as the input data and appropriate boundary conditions were considered for the simulation. A mesh independence test was performed to choose appropriate mesh size before main simulation.
Results: As a result of the simulation, hemodynamic parameters were calculated with respect to each case. Wall shear stress at the non-coronary cusp was lower than at the borderline between the right coronary cusp and left coronary cusp for all cases. Furthermore, it was found out that low turbulence kinetic energy would be related to the calcification of the aortic valve.
Conclusion: It was expected to figure out the mechanism of the onset of aortic valve calcification in terms of fluid dynamics. This finding will be helpful to make a decision for the cardiologist.

Poster Number 7 14th Nov

INTRAUTERINE E-VAPOUR EXPOSURE CAUSES METABOLIC AND HEPATIC CHANGES IN MICE

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Background: Approximately 15% of pregnant women vape e-cigarettes during pregnancy, exposing the developing foetus to a range of toxic compounds. Nicotine is a developmental toxin, hampering healthy brain and lung growth, promoting behavioural disorders and asthma. Furthermore, several studies have shown that the e-vapour possesses cytotoxic, inflammatory and oxidative properties, especially when heated to 300^{o}C during vaping. However, the safety of other e-vapour components have not been established and as a result, the health impacts to the child are unknown.
Aim & Objectives: Therefore, the aim of this study was to understand the impacts of intrauterine e-vapour exposure, with and without nicotine, on liver and metabolic health outcomes.
Methods: E-cigarette vapour was created using a 3rd generation e-cigarette device filled with tobacco flavoured e-liquid containing either 18mg/mL or 0mg/mL of nicotine. Female Balb/c mice were exposed to e-vapour with or without nicotine for 6 weeks before mating, through gestation and lactation. Liver and plasma from 13 weeks old male offspring were examined. Data were analysed by one-way ANOVA with Fisher's LSD *post hoc* analysis.
Results: Maternal e-vapour exposure caused glucose intolerance in the offspring, independent of nicotine. Intrauterine exposure to nicotine containing e-vapour increased hepatic lipid accumulation concomitant with reduced mitochondrial antioxidant levels. Furthermore, maternal exposure to nicotine free e-vapour during pregnancy resulted in increased hepatic inflammatory and oxidative stress markers in the offspring.
Conclusion: E-vapour exposure during pregnancy represents an adverse developmental environment, leading to metabolic disorders and hepatic changes in the offspring. **Therefore, e-cigarettes cessation should be encouraged among pregnant women to ensure healthy offspring are produced.**

TO TREAT OR NOT TO TREAT OSTEOARTHRITIS WITH STEM CELL THERAPY

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Background: Osteoarthritis is a leading cause of chronic pain and disability, for which there is no cure. Mesenchymal stem cells (MSCs) have recently brought new hope for treating osteoarthritis due to their ability to send anti-inflammatory and trophic signals to surrounding tissues. Interestingly, the few available clinical trials utilising MSCs to treat knee osteoarthritis have not demonstrated consistent benefits.
Aim & Objectives: This study aims to unravel the mechanisms behind the low efficacy of stem cell injections for osteoarthritis using an *in vitro* model of a human osteoarthritic joint.
Methods: MSCs were co-cultured with diseased cells isolated from human osteoarthritic joint tissues, for up to 21 days in growth, osteogenic and chondrogenic medium (simulating the relevant conditions in a joint environment). Cell interactions were assessed using RT-PCR (n=4) and histology (n=2).
Results: MSCs co-cultured with osteoarthritic cells showed increased inflammation (MMP2, ADAMTS5 upregulation) and impaired ability to form new bone (reduced BSP, SPP1 expression and calcium deposition) and cartilage (reduced COL2A1, ACAN expression and proteoglycan deposition) at 21 days, suggesting that the osteoarthritic joint is a highly inhibitory environment that negatively influences MSCs and reduces their therapeutic effects. Furthermore, short-term (3 days) exposure of the osteoarthritic cells to MSCs was insufficient for sustained modifications to their diseased phenotype. The osteoarthritic cells, whether previously exposed to MSCs or not, had similar expression profiles of inflammatory markers, and also had similar negative effects on MSCs (inflammatory marker upregulation e.g. IL-8, ADAMTS4; impaired chondrogenesis).
Conclusion: Diseased cells in an osteoarthritic joint create an inflammatory environment that impairs healing. Although MSCs have anti-inflammatory and trophic functions, they can adopt the same diseased phenotype of the osteoarthritic cells following injection and cease to have a therapeutic effect. Future regenerative therapies for osteoarthritis may have greater success by focusing on the biological derivatives of stem cells.

Poster Number 17 14th Nov

THE PARASITE-DERIVED PEPTIDE, FhHDM-1, ALTERS THE METABOLIC ACTIVITY OF MACROPHAGES TO PREVENT PRO-INFLAMMATORY RESPONSES

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Background: Macrophages acquire distinct functional states triggered by specific environmental factors. The cellular metabolism of macrophages profoundly affect this polarization to ensure the different energy demands of each functional phenotype are met. Thus, M1 macrophages activated by pro-inflammatory ligands (such as bacterial LPS) predominantly utilise glycolytic pathways to provide sufficient ATP to support anti-microbial and inflammatory activities. In contrast, the anti-inflammatory/regulatory M2 phenotype requires oxidative phosphorylation to support its functions of tissue repair and remodelling.
Aim & Objectives: To survive in its mammalian host, the parasite worm *Fasciola hepatica*, secretes immune-modulatory proteins to switch the phenotype of macrophages away from inflammatory M1 cells towards the regulatory M2 phenotype. The aim of this study was to investigate whether this switch was driven by the metabolic reprogramming of macrophages.
Methods: A single peptide, secreted by *F. hepatica* (FhHDM-1), was used to treat macrophages *in vitro*. The preference of macrophages for different fuels (fatty acids, glucose or glutamine) to drive metabolism and the metabolic status of cells was determined by a combination of mass spectrometry and extracellular flux assays. The phenotype and activity of cells was characterised by qPCR, gene array and ELISA.
Results: FhHDM-1 inhibited the activation of M1 pro-inflammatory macrophages by directing metabolic activity away from glycolysis, towards oxidative phosphorylation. This was mediated by increasing macrophage lysosomal pH, causing Ca^{2+} release, which in turn triggered the TCA cycle to drive an increase in oxidative phosphorylation. Surprisingly, despite this switch in metabolism and biological function, treatment with FhHDM-1 did not induce the expression genes characteristic of an M2 phenotype.
Conclusion: This study has revealed a novel mechanism by which a single parasite protein modulates the functional activity of innate immune cells. Importantly, it has also determined that an anti-inflammatory state in macrophages is independent of a switch to an M2 phenotype.

Honours/RA 14th Nov

BUSPIRONE AS AN ANTI-NEUROINFLAMMATORY DRUG: IMPLICATIONS FOR PARKINSON'S DISEASE

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Background: Parkinson's disease (PD) is an increasingly prevalent neurodegenerative disease with no direct treatment. Buspirone is a drug currently used to treat anxiety via its serotonin 5HT1a-mediated mechanism of action. However, pharmacological studies have found that buspirone also targets dopamine D3 receptors (D3Rs) to arrest brain inflammation, suggesting that the drug could be repurposed to slow down PD by blocking its inflammatory component.
Aim & Objectives: This study aims to test if buspirone reduces the inflammatory response in lipopolysaccharide (LPS)-stimulated microglial cells and investigate if D3R blockade partakes in its mechanism of action (MoA).
Methods: BV-2 microglial cells were activated by exposure to LPS and treated or not with either buspirone, a 5HT1a agonist (8-OH-DPAT), a D3R antagonist (SB277011a) or both for 24h. Cell morphology, viability (MTT assay) and expression of a panel of pro-inflammatory mediators were analysed by real-time qPCR and Western blot. Finally, Griess reagent assays were conducted to measure nitrites levels, a further indicator of inflammation.
Results: Buspirone significantly reduced the expression of several pro-inflammatory markers both at mRNA and protein level, including IL-1β, iNOS and MMP9 ($p<0.001$). Griess assays showed 15% reduction of nitrite levels when compared with LPS-treated cells ($p<0.05$). Western blots demonstrated that iNOS, CD11b and IL-17a were significantly reduced. 8-OH-DPAT slightly diminished IL-1β mRNA expression whereas SB277011a did not. However, combined treatment with 8-OH-DPAT and SB277011a further reduced IL-1β. Again, 8-OH-DPAT or SB277011a alone reduced iNOS mRNA expression but had no further effects when combined.
Conclusion: These data demonstrate that buspirone reduces inflammation in BV-2 microglial cells. Buspirone MoA seems to involve both the agonist activity at 5HT1a receptors and the antagonist activity at D3Rs, which in several instances act synergistically to attenuate LPS-driven inflammation. Collectively, these findings suggest that buspirone may be repurposed to treat inflammation in neuroinflammatory diseases, including PD.

Poster Number 11 14th Nov

DISTINCT EFFECTS OF THE NEUROPEPTIDES PACAP AND VIP ON CELL MIGRATION IN ACTIVATED MICROGLIAL CELLS

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Background: Microglia are resident immune cells that are involved in innate inflammatory responses in the central nervous system (CNS). Microglia have the capacity to restore injured tissue and are critical for maintaining a healthy CNS environment. However, this response requires the active migration of microglia to the damaged CNS site.
PACAP and VIP are two neuropeptides that modulate inflammation, and both are present in microglia. However, whether these peptides regulate cell migration in activated microglia remains unknown.
Aim & Objectives: Our goal is to investigate if PACAP or VIP affect cell migration in lipopolysaccharide (LPS)-activated microglial cells. In addition, we seek to unveil the underlying molecular mechanisms.
Methods: We utilised morphological and wound healing assays (WHAs) to evaluate the effects of PACAP or VIP on cell migration in LPS-treated BV2 microglia. Real-time qPCR and Western blots were used to measure the expression of extracellular matrix (ECM)-degrading enzymes critical for cell motility, tissue and urokinase plasminogen activators (tPA and uPA).
Results: We identified distinct effects of PACAP and VIP on both cell morphology and migratory capacity in LPS-stimulated BV2 cells. Specifically, PACAP significantly reduced the abundance of activated cells and increased the number of resting cells whereas VIP increased a subset of cells exhibiting an 'intermediate' phenotype at the expenses of resting cells (##$p<0.01$ Vs LPS). Conversely, WHAs revealed that PACAP was more effective than VIP in rescuing LPS-induced cell immobility. These differences were corroborated by the changes in the expression of uPA, but not tPA.
Conclusion: Our findings demonstrate that PACAP and VIP differently affect microglial morphology and motility during inflammation. These differences are crucial to determine how well cells can reach target sites, and should be taken into account when establishing the best therapeutic route to restore homeostasis in the inflamed CNS.

Honours/RA 14th Nov

A RING-FORMING PROTEIN LINKS SPORE SHAPE TO SPORE ENVELOPE ASSEMBLY

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Background: Spores are one on the toughest cell types on Earth. They are dormant cells that resist heat, oxidizing chemicals and antibiotics. Spores are a major problem in hospitals worldwide, because they lead to new and recurring infections in pathogens, such as *Clostridioides difficile*. Spores are tough because of their complex cellular envelope. But little is known about how the spore envelope is built.

Aim & Objectives: Cell envelope assembly is linked to shape in growing bacteria. Thus, in an effort to understand how the spore envelope is built, and identify its weaknesses, we characterized YdcC, a poorly-defined protein implicated in spore shape in *Bacillus subtilis*.

Methods: To reveal YdcC's subcellular localization, we used 2D and 3D fluorescence microscopy and image analysis. To identify genetic partners of *ydcC*, we used genetic screens based on Transposon-Sequencing. To understand the genetic relationship between YdcC and the genes identified in the screens, we carried out spore shape comparisons using fluorescence microscopy and image segmentation, on double mutant combinations with *ydcC*.

Results: Our results reveal that YdcC forms a ring-like structure at one end of the spore, which then disperses as foci. We found that YdcC ring-formation depends on SpoIVA, a protein required for spore envelope assembly and cells lacking *ydcC* or *spoIVA* produce spores of similar shape. Finally, we identified an inverse shape relationship between *ydcC* and the genes required for the assembly of the spore cell wall.

Conclusion: Collectively, our results support a model whereby YdcC, through SpoIVA, maintains spore shape by regulating the assembly of the spore envelope. Our results thus reveal new weak spots in spore envelope assembly that could be exploited to develop strategies aimed at spore eradication.

Poster Number 29 15th Nov

THE IDENTIFICATION OF NEW INTERACTION PARTNERS OF WILD-TYPE AND MUTANT P53 – EXPANDING THE FAMILY OF ENZYMES THAT ASSOCIATE WITH THE GENOME GUARDIAN

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Background: Ovarian cancer is the most lethal gynaecological malignancy with a 5-year survival rate of only 45.7% in Australian women, categorising it as a low survival cancer. Mutation of the tumour suppressor *TP53* is highly prevalent in the most common form of this malignancy. To date, there is no clinically approved therapy that targets mutant p53. Factors that associate with mutant p53 have potential as therapeutic targets.
Aim & Objectives: We aimed to determine the physical interaction between both wild-type (WT) and mutant p53 and the E3 ubiquitin ligase Ring Finger Proteins RNF20 and RNF40 known to act on histone H2B to remodel chromatin in the nucleus and on other non-histone substrates.
Methods: We employed two independent techniques, co-immunoprecipitation (co-ip) and the Proximity Ligation Assay (PLA) visualised by confocal microscopy, to assess protein-protein interactions between WT or mutant p53 with RNF20 and RNF40 that function as a complex. WT p53 interactions were assessed using the A2780 endometrioid ovarian cancer cell line, and mutant p53 using the high-grade serous ovarian cancer cell line OVCAR3 that harbours the p53 gain-of-function mutation p.R248Q.
Results: Co-ip of endogenous proteins in p53 wild-type and mutant ovarian cancer cell lines identified both RNF20 and RNF40 as p53 interaction partners. Interestingly, PLA analyses showed that while the interaction between wild-type p53 and both RNF20 and RNF40 was predominantly nuclear, consistent with these E3 ligases interacting with a histone substrate, interactions in the p53 mutant cell line were predominantly cytoplasmic, indicating an entirely different function of this interaction.
Conclusion: The interaction of mutant p53 with the E3 ubiquitin ligases RNF20 and RNF40 is an entirely novel discovery, warranting further exploration of these enzymes as potential therapeutic targets for mutant p53 driven malignancy. The functional significance of this interaction that occurs predominantly in the cytoplasm remains to be elucidated.

Unique Adaptation Strategy of *Pseudomonas aeruginosa* to silver nanoparticles

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Background: The widespread and indiscriminate use of silver nanoparticles (AgNPs) in medical devices and an increasing array of consumer products has triggered a concern for the development of silver-resistant bacteria.
Aim & Objectives: The project seeks to investigate the emergence of AgNP adaptations in the biofilm-forming priority pathogen *Pseudomonas aeruginosa* strain PAO1.
Methods: Assays were performed to observe and compare the antibacterial effects of AgNP, ionic silver (Ag^+) and the antibiotic gentamicin (GM) on the growth of PAO1. The bacterium was exposed to the sub-lethal concentrations of each antibacterial agent for a prolonged timeframe and subsequently tested to determine the nature of the adaptive response.
Results: Our work has found that PAO1 shows a unique adaptation strategy to AgNP, distinct from Ag^+ and GM. After prolonged exposure, there was an increase in the minimum inhibitory concentration for GM, while the biofilms formed by the GM-adapted strains could not be eradicated at any tested concentrations; demonstrating the ability of PAO1 to develop resistance to GM. Although no increase in MIC was observed for AgNP and Ag^+ adapted strains, the time kill assays revealed the development of persistence in AgNP-adapted strains, with the simultaneous development of small colony variants. By visualizing such variants under the microscope, we hypothesize the role of cell division inhibition in AgNP-mediated persistence development in PAO1.
Conclusion: This work provides insights into the antibacterial capabilities of AgNP and Ag^+ in comparison to the antibiotic GM on PAO1 planktonic growth and biofilm. While PAO1 develops resistance to GM, we show that bacteria can enter into a persister state in response to AgNP treatment. As this metabolically dormant state can lead to antibiotic tolerance, causing chronic recurrent infections; our work highlights an escalating concern that just like antibiotics, AgNP treatment can also increase the rate of recurrent infections.

POTENTIAL THERAPY FOR TREATING TYPE 2 DIABETES AND HEPATIC STEATOSIS.

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Background and Aim: Obesity is associated with an increased risk of non-alcoholic fatty liver disease (NAFLD) that characterised by the accumulation of lipids in the liver. Excessive intrahepatic lipid accumulation is associated with alteration of glucose, fatty acid metabolism and is known to drive inflammation and oxidative stress, ultimately leading to the development of hepatic and systemic insulin resistance.

Aim & Objectives: The aim of this study was to assess the effects of a nitroxide, Tempol, on the accumulation of lipid and inflammation induced by palmitic acid (PA) in human liver cells.

Methods: To assess the effects of Tempol, HepG2 cells were exposed to PA for 24 hours before exposure to Tempol (200μM, 500μM, 1mM, 2mM) for 5 hours. The effects of PA induced-cellular steatosis and inflammation were then assessed using an (i) oil red O staining and extraction method to assess lipid accumulation, (ii) MTT assay to detect cell viability, (iii) RT-qPCR to assess the mRNA gene expression level of inflammatory markers, (iv) dichlorofluorescein assay to assess reactive oxygen species (ROS) levels and a (v) glycogen assay to assess glycogen levels.

Results: The results show HepG2 exposed to TEMPOL reduced palmitic acid induced- (i) lipid accumulation, (ii) inflammation, (iii) insulin-mediated glycogenesis and (iv) reactive oxygen species levels with no effect on cell viability.

Conclusions: These findings suggest that Tempol plays a protective role in PA-induced hepatic steatosis that is associated with reduced hepatic inflammation, oxidative stress and insulin-mediated glycogenesis, thus indicating Tempol may be useful as a pharmaceutical therapy for improving hepatic steatosis and insulin sensitivity.

Poster Number 41 15th Nov

AN INTEGRATIVE APPROACH TO TISSUE-SPECIFIC EFFECTS OF MICRO-RNA REGULATORY NETWORKS

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Background: miRNAs are small noncoding RNAs with role in post-transcriptional regulation of gene expression. Even though the basic mechanisms for miRNA action have been described, we are still unable to efficiently predict their impact on cellular function. The ability of a given miRNA to act upon a target is influenced by the transcriptome environment it is in. Thus, when predicting targets for a miRNA, the context in which it is expressed needs to be accounted for.

Aim & Objectives: The aim of this work is to comprehensively understand the interaction dynamics between miRNAs and their target transcriptome across different tissues.

Methods: Paired miRNA and mRNA normalized count data corresponding to normal samples of seven tissues present in TCGA were downloaded. The samples were clustered to understand if any outliers were present and how well they represented the tissue. The profile of miRNA expression was accessed, and categories to include the miRNA or transcripts were created according to their level of expression and tissue specificity. The interactions of miRNAs and their targets were accessed through correlation analysis and compared across tissues.

Results: The clustering analysis revealed that, overall, the tissues cluster well together. The categories and levels of expression of miRNA do not reflect a higher number of negatively correlated transcripts (-0.5). For example, miR-21, a ubiquitous miRNA, has a higher expression in all tissues when compared to miR-34c but does not have a higher number of negatively correlations. miR-34c expression is higher in the lung and head and neck tissues. However, the prostate tissue, where miR-34c does not have a high expression is where this miRNA has more negative correlations with transcripts.

Conclusion: The preliminary results of this work provide a deeper understanding of the regulatory networks governing gene expression regulation and allow further explorations of miRNA action.

Poster Number 27 15th Nov

Nanosensor for Non-Invasive Diagnosis of Neurodegeneration

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Background:
The inability of direct and non-invasive access to the brain structure has made it impossible to visualize brain neurodegenerative disorders such as Alzheimer's disease (AD). Lanthanide-doped upconversion nanoparticles (UCNPs) are capable of converting near-infra-red excitation into visible and ultraviolet emission, making them a suitable candidate for biomedical application.

Aim & Objectives:
We developed upconversion nanosensor for specifically targeting ZnT3 proteins in the brain tissue.

Methods
$NaYF_4$:Yb,Er nanoparticles (UCNPs) were synthesized using the co-precipitation method. Anti-ZnT3 antibody was conjugated to the surface of UCNPs. Localization and concentration of zinc, UCNPs, and ZnT3 were characterized using laser ablation inductive coupling plasma mass spectrometry (LA-ICP-MS) and fluorescence microscopy in normal aged mice (WT, 25 months) and AD mice model (APP/PS1, 25 months).

Results
LA-ICP-MS and fluorescence microscopy results demonstrated that the decrease in the ZnT3 concentration causes an increase in the zinc ion concentration in the brain tissue of AD mice models comparing with the healthy aged mice. We discovered the same trend in the retina of eye as well. Therefore, it would be possible to design a fluorescence nanosensor based on UCNPs to detect changes in ZnT3 through the eye.

Conclusion:
In summary, nanosensors based UCNPs offer a promising platform for the non-invasive identification and visualization of neurodegeneration processes in people with AD.

Investigation of FXYD1 as a novel signalling protein in cholesterol metabolism

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Background: Bioavailability of nitric oxide (NO) is often compromised in early atherosclerosis, driving disease onset. This is usually due to dysfunctional endothelial nitric oxide synthase (eNOS). We have found that the transmembrane protein, FXYD1, is highly concentrated in the caveolae sub-cellular region and closely associated with eNOS. Our preliminary evidence suggests that FXYD1 protects eNOS from redox-dependent inactivation. Therefore, we hypothesise that FXYD1 may protect against atherosclerosis.

Aim & Objectives: We aimed to test the protection role of FXYD-1 protein in a rodent model of atherosclerosis.

Methods: We produced a novel mutant mouse line by cross breeding FXYD1 heterozygote ($FXYD1^{+/-}$) and apolipoprotein E knock out ($ApoE^{-/-}$) mice. $FXYD1^{-/-}/ApoE^{-/-}$ and $FXYD1^{+/+}/ApoE^{-/-}$ littermates were fed a high fat/high cholesterol diet from 6-8 weeks of age for 16 weeks. At sacrifice blood was taken and plasma was separated and stored for analysis of total cholesterol using ELISA. The thoracic aorta was isolated and formalin-fixed to assess atherosclerotic plaque development using oil red O stain. Immunoblotting for eNOS expression was performed in heart lysates.

Results: Plasma cholesterol in $FXYD1^{-/-}/ApoE^{-/-}$ mice (n = 21) was significantly increased compared to $FXYD1^{+/+}/ApoE^{-/-}$ mice (n = 12; $p<0.05$). Interestingly, this only occurred in female mice, suggesting a sexually dimorphic response. Despite the higher total cholesterol, there was no effect on plaque size in either sex, as determined by oil red O stain of fixed aortae. In addition, eNOS expression was significantly decreased in tissue from $FXYD1^{-/-}/ApoE^{-/-}$ vs. $FXYD1^{+/+}/ApoE^{-/-}$ female mice. Ongoing studies include comprehensive lipidomic measurements and further analysis of plaque composition and stability.

Conclusion: $FXYD1^{-/-}$ atherosclerotic female mice have higher circulating cholesterol, but this does not result in plaque development in the short term. FXYD1 may be a novel signalling protein in cholesterol metabolism or handling.

Poster Number 26 15th Nov

IN-VITRO MODEL FOR INTERACTION BETWEEN RESPIRATORY MICROBIOME AND HUMAN EPITHELIUM

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Background: Chronic rhinosinusitis (CRS) is a chronic inflammatory disease of the nose and sinuses impacting quality of life with its prevalence ranging from 4% to 25% around the globe. Observational studies show increasing evidence for role of respiratory microbiota in CRS emphasizing the importance of *in vitro* model systems to test the role of imbalanced microbiota towards disease symptom exacerbations.
Aim & Objectives: Development of an *in-vitro* model system to assess the effects of multispecies microbial communities on the human respiratory epithelium. This would include optimizing the multi-species bacteria communities which will then be co-cultured with host respiratory epithelial cells.

Methods: Microbial communities for "Healthy" and "Diseased" state are represented by commensal bacteria *Staphylococcus epidermidis* & *Corynebacterium amycolatum* and potential pathogens *Staphylococcus aureus* & *Haemophilus inflenzea* respectively. Bacteria are characterized and grown as biofilm (single and multispecies) with varying initial bacterial load (10^3-10^7) for 24-72 hours. Each bacteria is labelled with different colour fluorescent dye for imaging and quantifying relative abundance. These microbial communities will be co-cultured with human respiratory epithelial cells (cell line and primary from healthy and CRS donors). This model would assess host response to "healthy" and "disease" associated microbiota to understand differences between healthy and CRS patients. Furthermore, the effect of manipulation of microbial communities on host response will be assessed.

Results: Experiments so far have involved optimising conditions for multispecies biofilm cultures. The total biofilm biomass remains similar between single species and multispecies biofilm with same initial bacterial load, however more biomass was observed with higher bacterial load and longer culture time. Live cell imaging using fluorescent dyes indicates changes in growth rate of bacteria in multispecies culture in comparison to single culture.

Conclusion: Current results point to interactions between members of bacteria in multispecies environment, however biomass alone does not explain much and use of dyes for imaging was not ideal. It is important to better visualize each bacteria member in single and multi-species cultures to estimate relative abundance. Future work will involve labelling of species with fluorescent proteins in plasmid followed by incorporation of host cells to multi-species bacterial communities.

Postdoctoral Researchers Session 14th Nov

Getting a leg up on diabetic peripheral artery disease

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Background: Diabetic peripheral artery disease (PAD) is a significant cardiovascular disease, and one of the most common in diabetic patients. No effective medical therapies are currently available to induce angiogenesis (the growth of new blood vessels) and promote blood flow recovery in severe diabetic PAD patients. We have recently reported the hormone ghrelin to be a novel factor that can induce angiogenesis in a mouse model of non-diabetic PAD. However, the therapeutic potential of ghrelin in diabetic PAD and its potential role in human diabetic PAD remain unknown.

Aim & Objectives: We aimed to 1) investigate the therapeutic potential of ghrelin in a diabetic mouse model of PAD; 2) elucidate the role of ghrelin in human diabetic PAD.

Methods: Femoral artery ligation and electrocoagulation (FAL) were used as an *in vivo* preclinical PAD model. Experiments including laser Doppler perfusion imaging, microcomputed tomography, microangiography, functional measures, immunoblot analysis, ELISAs, immunostainings, and quantitative polymerase chain reaction analysis were performed to determine the role of ghrelin in diabetic PAD.

Results: The administration of ghrelin significantly improved post FAL blood flow recovery, and increased reparative angiogenesis in response to ischaemia. The latter was demonstrated by a 50% increase in capillary density and a 44% increase in the density of small arterioles in the ischaemic muscle. Ghrelin treatment also significantly improved vascular function, and significantly reduced cell death and toe necrosis. Mechanistically, we implicated microRNAs –126 and –132 in orchestrating many of these events. Clinically, patients with diabetic and non-diabetic PAD, have reduced plasma levels of ghrelin, which appears to be significantly associated with PAD.

Conclusion: Our findings suggest that ghrelin is a novel factor capable of inducing therapeutic angiogenesis during diabetic PAD, and provides the foundation for phase 1 clinical trials with ghrelin for the effective treatment of diabetic PAD.

THE EFFECTS OF SHORT-TERM KETOGENIC DIET ON COUNTER-REGULATORY RESPONSE TO HYPOGLYCAEMIA IN RATS

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Background: Hypoglycaemia counter-regulation is an essential survival mechanism activated to correct low glucose, because severe hypoglycaemia can lead to seizures, coma and death. Ketones can provide the brain and other organs with an alternative fuel. Ketogenic diets (KD) are becoming a popular tool for diabetes management, however KD effects on hypoglycaemia counter-regulation are largely unknown.
Aim & Objectives: We investigated KD as a potential strategy in preventing the detrimental consequences of hypoglycaemia by testing the effects of KD on the sympathoadrenal counter-regulatory response: adrenal sympathetic nerve activity (ASNA), adrenal gland activity and plasma adrenaline.
Methods: Sprague-Dawley rats fed KD or chow diet (CD) for 3wk then anaesthetised and ASNA recorded. Insulin (5 U/kg; iv) induced hypoglycaemia and the counter-regulatory response. Blood glucose (BG) and β-hydroxybutyrate (β-HB, ketone) were measured every 15min post-insulin for 2h. Plasma adrenaline was determined *via* ELISA. Adrenal gland activity was assessed by immunohistochemistry for Fos.
Results: Rats on KD weighed less (361±29g vs. 420±36g) and had elevated β-HB (3.2±0.4mmol/L vs. 1.57±0.43mmol/L) compared to the CD group, but with similar BG. None of the KD rats developed seizures post-insulin, while 4/7 CD rats did. β-HB levels in KD rats declined in the first 30min post-insulin, then stabilised. CD rats had either a strong ASNA (%Δ222±38) response without seizure, or a failed ASNA (%Δ-2±6.2) response with seizure. All KD rats responded to hypoglycaemia with a robust increase in ASNA (%Δ279±97), which occurred at lower BG levels compared to non-seizure CD rats. Both adrenal gland activity and adrenaline levels reflected ASNA response.
Conclusion: Short-term KD preserved a strong sympathoadrenal counter-regulatory response to hypoglycaemia at lower BG levels and protected rats from seizures. **If the same effects are observed in humans, adherence to KD may mitigate the symptoms and severe consequences of hypoglycaemia in people with insulin-dependent diabetes mellitus.**

Poster Number 1 14th Nov

A longitudinal mouse model to study the development and progression of type 2 diabetic nephropathy

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Background: Type 2 diabetes (T2D), which is affecting 8% of the population, is the leading cause of chronic kidney disease (CKD). Apart from hyperglycaemia, there are other factors involved in the development and progression of diabetic nephropathy.
Aim & Objectives: The aim of this study is to develop a longitudinal animal model of T2D-CKD to investigate the step-by-step progression and identify novel biomarkers and/or therapeutic targets of this disease.
Methods: C57BL/6 male mice were fed a control or high-fat diet (HFD) for 6 weeks, 24 weeks and 32 weeks and examined for established markers of CKD such as urinary albumin/creatinine ratio and kidney injury marker (KIM-1). as well as a range of potential markers regarding oxidative stress, inflammation and epigenetic regulation processes.
Results: At 6 weeks of HFD feeding, mice developed characteristics of T2D including glucose intolerance and insulin resistance, with a modest increase of urinary albumin excretion but no change in KIM-1, suggesting the initial stage of CKD. At 24 weeks, microalbuminuria was established, and KIM-1 elevation was evident; however, there was no correlation between the two markers. At 32 weeks, 1/3 of the animals showed advanced CKD with both albuminuria and elevated KIM-1, which closely resembles clinical statistics. Examining the mRNA expression in the kidney, we identified several candidates of early CKD markers such as the oxidative stress marker NOX2 and DNA methylation markers DNMT1 and DNMT3a. Meanwhile, the expression of DNMT3b and Ten-eleven translocation (TET)1 and 3 are associated with advanced CKD progression.
Conclusion: Our study suggests that HFD consumption can be used as a model of T2D-induced CKD. Oxidative stress and epigenetic markers are associated with the progression levels.

Poster Number 18 14th Nov

EPIGENETIC AND TRANSCRIPTOMIC CHANGES DURING CORTICOSTEROID TREATMENT IN COPD PATIENTS

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Background: Chronic obstructive pulmonary disease (COPD) is a complex progressive inflammatory disease resulting in accelerated lung function decline. COPD affects approximately 20% of people globally. The major cause of COPD is smoking, but also genetics and epigenetics. Inhaled corticosteroids (ICS) have been shown to reduce the decline of FEV1 in a subset of COPD patients. However, there is heterogeneity of response, therefore it is important to perform studies on therapy response in COPD.
Aim & Objectives: The aim of this project is to investigate the effects of ICS on methylation DNA methylation and gene expression in COPD patients.
Methods: Bronchial biopsies of COPD patients were previously obtained at baseline and 6 months post treatment with ICS (n = 42). Samples were analysed for changes in methylation and mRNA expression. We used a linear model to identify alterations after treatment with ICS. We correlated the identified methylation sites to gene expression and performed pathway analysis. Finally, we used GR Chip-seq analysis of A549 in response to Dexamethasone 100nM to identify methylation sites close to Glucocorticoid Receptor (GR) binding sites.
Results: When comparing methylation after 6 months of exposure to ICS to baseline we found 990 significant alterations. We found 1925 correlations between the identified methylation sites altered by ICS and gene expression. Genes correlated to the identified methylation sites were associated to inflammation. Chip-seq analysis of the GR receptor in A549 cells identified 78 methylation in close proximately to GR binding sites including Hydroxysteroid 11-Beta Dehydrogenase 2 (HSD11B2).
Conclusion: ICS treatment alters DNA methylation, which influences gene expression in part by being positioned in GR binding site regions.

Poster Number 35 15th Nov

USE OF A SMARTPHONE ELECTROCARDIOGRAM, ELECTRONIC PROMPTS AND ELECTRONIC DECISION SUPPORT FOR ATRIAL FIBRILLATION SCREENING IN METROPOLITAN GENERAL PRACTICE (AF-SMART)

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Background: Atrial fibrillation (AF) screening in people aged≥65 years is recommended by national guidelines. Guideline-indicated treatment (oral anticoagulants (OAC)) can reduce stroke risk by 67%. Gaps in screening and treatment exist in practice. The estimated rate of AF screening in Australian general practice is 11%. Our previous study screened 16%, leading to refinement of the electronic tools.
Aim & Objectives: To investigate the impact of an AF screening program in rural general practices using custom-designed eHealth tools designed to increase the proportion screened and treated for AF in accordance with guidelines.
Methods: practices (n=8) in rural NSW participated between September 2018–June 2019. General practitioners (GPs) and nurses conducted opportunistic screening of eligible patients (aged≥65 years without existing AF diagnosis) using a smartphone electrocardiogram during practice visits. Practices were provided electronic prompts, electronic decision support based on Australian treatment guidelines, and regular screening data reports. A clinical audit tool extracted deidentified data from practices.
Results: 3,103 eligible patients who attended during the study were screened (median screening period 4.6 months, mean age 75.1±6.8 years, 47% male). 35% of eligible patients were screened (range 9-51%/practice), with 4/8 practices screening >40% of eligible patients. 36(1.2%) new cases of AF were confirmed (mean age 77.0 years, 64% male, mean CHA_2DS_2-VA=2.9). OAC treatment rates of patients with AF aged≥65 with CHA_2DS_2-VA≥2 were 82% (screen-detected) compared with 75% (pre-existing AF)(p=NS).
Conclusion: an AF screening program supported by eHealth tools resulted in 35% of eligible people screened, which is substantially higher than 16% achieved in our previous study. Numerous practices screened 40-50% of eligible patients, suggesting this may represent a 'ceiling' of patients captured by opportunistic screening programs. OAC treatment rates were high at baseline and were trending upwards during the study. eHealth tools, particularly customised data reports, may be a valuable addition to future programs.

CELL-SPECIFIC FUNCTIONS OF TRAIL CRITICAL FOR ANGIOGENESIS AND VESSEL STABILISATION

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Background: Angiogenesis requires endothelial cells (ECs) and pericytes to generate microvascular capillary networks, critical for tissue development and wound repair. We previously identified TNF-related apoptosis-inducing ligand (TRAIL) as an exciting new molecule that stimulates angiogenesis *in vitro*, and *in vivo* in mice with peripheral artery disease, restoring blood flow, and preserving tissue survival and function.

Aim & Objectives: Our aim was to elucidate how cell-specific TRAIL facilitates angiogenesis by assessing the contribution of EC- and pericyte-specific TRAIL expression to angiogenesis *in vivo* and identifying the effect of TRAIL on pericyte processes *in vitro*.

Methods: *In vivo*, EC- and pericyte-specific *Trail*$^{-/-}$ mice (*Trail*$^{EC-/-}$ and *Trail*$^{Pc-/-}$) were injected with Matrigel into the flank to form a plug. After 28 days, plugs were removed for histology and qPCR and assessed by Mann-Whitney *U*-test. *In vitro*, pericytes isolated from *Trail*$^{+/+}$ and *Trail*$^{-/-}$ brain were cultured in 0.5-2% serum to assess proliferation and migration using one-way ANOVA. Furthermore, *Trail*$^{+/+}$ and *Trail*$^{-/-}$ pericytes were co-cultured with ECs on Matrigel for 24 hours to compare tubule formation by student's *t*-test.

Results: EC and mural cell content in plugs from *Trail*$^{EC-/-}$ was ~50-60% less than in plugs from *Trail*$^{EC+/+}$ mice, whereas capillary density in plugs of *Trail*$^{PC-/-}$ mice was unchanged. Pericyte and angiogenesis markers, namely RGS5, PDGFRβ, NG2 and VEGF were also reduced ~50% in *Trail*$^{EC-/-}$ plugs, suggesting that EC-, but not pericyte-expressing TRAIL is critical for angiogenesis. *In vitro*, TRAIL showed no effect on pericyte proliferation and migration. In contrast, ECs cultured with *Trail*$^{-/-}$ pericytes displayed significantly less EC tubule formation than those cultured with TRAIL-expressing pericytes, suggesting that TRAIL assists pericyte stabilisation.

Conclusion: We have identified novel cell-specific functions of TRAIL critical for angiogenesis and vessel stabilisation. Understanding how TRAIL signals regulate angiogenesis may identify new targets for therapeutic intervention in patients with cardiovascular disease.

Poster Number 23 15th Nov

Molecular basis of the 'sticky platelet' phenotype in diabetes

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Background: Diabetes affects 1.2 million Australians and is the largest risk factor for thrombosis. Oxidative stress is a hallmark feature of diabetes. Additionally, the disease is associated with hyperactive or 'sticky' platelets. Although the molecular basis for this phenotype has been elusive, overactivation of the platelet integrin, αIIbβ3, has been implicated.

Aim & Objectives: αIIbβ3 integrin exists in a bent conformation on resting platelets and undergoes conformational change to engage fibrin(ogen). We aimed to identify whether redox sensitive disulphide bonds are involved in αIIbβ3 conformational change and activation, as well as whether conditions of oxidative stress such as diabetes would affect these mechanisms.

Methods: Differential cysteine alkylation and mass spectrometry allows the quantification of αIIbβ3 disulphide bond redox states on the surface of human platelets.

Results: We identified a disulphide bond in the αIIb subunit, Cys490-Cys545, that is involved in integrin conformational change. The bond is reduced in 39±10% of the integrin in platelets from healthy human donors and Cys545 of the disulphide is S-nitrosated, a modification that is most often a transient intermediate in the formation of disulphide bonds. C490A/C545A disulphide mutant integrin expressed on BHK cells binds fibrinogen poorly and, compared to wild type integrin, exists in a higher proportion of the bent conformation. These results indicate that the redox state of the Cys490-Cys545 disulphide bond controls integrin extension and activation, and we hypothesized that this control may be impaired in diabetes. Indeed, only 4±2% of the bond is reduced in the platelet integrins of patients with diabetes.

Conclusion: The redox state of the Cys490-Cys545 disulphide bond in the αIIb domain of αIIbβ3 is involved in extension and ligand binding. This bond is differentially S-nitrosated in diabetic platelets, which is predicted to enhance integrin activation and may underlie the molecular basis of the sticky platelet phenotype in diabetes.

Poster Number 20 14th Nov

NAVIGATING THE AUSTRALIAN INSTITUTE OF HEALTH AND WELFARE (AIHW) ETHICAL APPLICATION PROCESS TO REQUEST DATA-LINKAGE WITH THE NATIONAL DEATH INDEX (NDI) – THE KOLLING INSTITUTE TUMOUR BANK (KITB) EXPERIENCE

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Background: The Kolling Institute Tumour Bank (KITB) was established in 1992. It currently houses approximately 30,000 blood and tissue samples from more than 10,200 patients. Cancer types include adrenal, brain, breast, cervical, colorectal, endometrial, gastric, liver, nerve, oesophagus, ovarian, pancreas, parathyroid, pituitary, spinal, thyroid and vulval. A universal consent form was introduced in 2017 to facilitate participant consent for data-linkage with State and National data registries. Importantly, data-linkage has the potential to enable annotation of biobanked specimens with health data that is often missing from local hospital medical records.
Aim & Objectives: To document the process of applying to access the Australian National Death Index (NDI) to ascertain date and cause of death through the Australian Institute of Health and Welfare (AIHW).
Methods: As of 2019, the AIHW has a rigorous 2-step application process for data-linkage. A technical assessment form must first be completed and approved before an ethics application can be submitted *via* the online ethics submission portal EthOS.
Results: The technical assessment form requests detailed information about security policies, confidentiality agreements, governance arrangements, data storage, the research proposal, consent arrangements, data flow and re-identification risks. The ethics application then addresses privacy arrangements, local ethics approval, project details, external reviews and the requirements of Section 4 of the National Statement of Ethical Conduct in Human Research. The Technical Assessment Form submitted by the KITB will provide guidance for Australian biobanks planning to apply for data-linkage with the NDI. Applicants to the KITB conducting research outside of Australia and wishing to access NDI data will need to apply individually to the AIHW HREC for approval.
Conclusion: Streamlined access to biobank samples that have been linked to NDI data will enable researchers to examine questions such as the association of specific clinical and molecular features with survival of cancer patients.

Poster Number 37 15th Nov

The Role of the Lysine Demethylase KDM6A in Melanoma.

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Background: Melanoma is an aggressive form of skin cancer and the most common type of cancer in young adults. Australia has one of the highest incidences of melanoma in the world. Current treatments for metastatic melanoma are plagued by the resistance melanomas develops against current targeted therapies or immunotherapies. Lysine demethylases (KDMs) are epigenetic enzymes that remove methyl groups from the amino acid lysine on histone proteins, which effects gene expression. One of these KDMs is KDM6A (an X linked gene, also known as UTX), that removes methyl groups from histone 3, lysine number 27 (H3K27me3) inducing activation of gene expression. KDM6A has been reported to play roles in the progression of multiple cancers however the role of KDM6A in melanoma is yet to be investigated.
Aim & Objectives: 1. To investigate the effect of KDM6A expression on overall survival and gene expression in a cohort of melanoma patients. 2. Determine the effects of the KDM6A inhibitor, GSK-J4, on cell viability, apoptosis, cell cycle and colony formation in melanoma cells *in vitro*.

Methods: mRNA profiles from 458 patients with cutaneous melanoma was obtained from The Cancer Genome Atlas (TCGA) and tumour KDM6A expression levels were correlated with overall survival. Gene Set Enrichment Analysis (GSEA) was performed on 'high' vs 'low' KDM6A expressing melanomas. The effects of GSK-J4 on melanoma cell lines were determined using cell titre glow assays, Annexin V/PI and cell cycle flow cytometry assays and colony formation.

Results: High KDM6A expression was associated with better overall survival, significantly in females but not in male melanoma patients. High KDM6A expression was associated with upregulation of interferon pathways and downregulation of pro-survival pathways that may impede melanoma growth. Unexpectedly, KDM6A inhibitor treatment with GSK-J4 reduced cell viability and colony formation in melanoma cells as well as increased apoptosis, but had no significant effect on cell cycle.

Conclusion: KDM6A appears to have a protective effect in female melanoma patients indicative of a tumour suppressive role. However, growth inhibition was observed in melanoma cell lines treated with a KDM6A inhibitor, regardless of basal KDM6A expression. Future studies using knockdown or overexpression of KDM6A will help clarify this role.

Poster Number 6 14th Nov

CHARACTERISING AGE-RELATED RETINAL FUNCTIONAL AND STRUCTURAL CHANGES IN THE APP/PS1 MOUSE MODEL OF ALZHEIMER'S DISEASE

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Background: Alzheimer's disease (AD), is a neurodegenerative disorder affecting nearly 44 million people worldwide. Many studies suggest that there are retinal structural and functional changes that occur in AD, however, the time-line for these changes are still unknown. In this study, we characterised retinal functional and structural changes in the double transgenic APP/PS1 mouse model of AD and wild type (WT) control mice over 12 months.
Aim & Objectives: To investigate the time-line of retinal functional and structural changes in relation to neuropathological changes in the brain of APP/PS1 mouse across age.
Methods: Electroretinogram (ERG) and optical coherence tomography (OCT) were performed to assess retinal functional and structural changes. Amyloid beta (Aβ) plaque distribution in the retina and hippocampus were also visualised using Thioflavin S staining. Inner and outer retinal thickness and several components of the ERG including the a- and b- wave, amplitude of oscillatory potentials, and the positive scotopic threshold response (pSTR) were quantified, every 3 months, from 3 to 12 months of age.
Results: We observed a significant difference in the inner retinal thickness from 9 months of age between the two groups. A significant decline in the b-wave from 3 months, coinciding with hippocampus Aβ deposition was also observed. We found a significant difference in pSTR amplitudes between the two groups starting from 6 months ($p < 0.001$).
Conclusion: The results suggest an overall age-dependent decline in both retinal structural and functional parameters in both groups. However, the inner retinal decline is accelerated in the APP/PS1 mice. Further investigations are required to confirm the occurrence of such findings in a human population.

LONGITUDINAL EFFECTS OF 12 MONTHS SMOKING CESSATION ON GENE EXPRESSION AND DNA METHYLATION IN BRONCHIAL BIOPSIES

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Background: COPD is characterized by the chronic inflammation in lungs in response to noxious particles mainly in cigarette smoke leading to an accelerated decline in lung function. However once COPD developed even though patients quit smoking the inflammation associated with smoke exposure remains present suggesting, persistent epigenetic changes.
Aim & Objectives: This study aims to investigate the longitudinal effects of smoking cessation on gene expression and DNA methylation and to examine whether the persistent inflammation following smoking cessation in COPD is driven by persistent epigenetic changes resulting from the initial smoke exposure.
Methods: Bronchial biopsies were collected from 19 individuals (healthy= 7, COPD= 12) before and after 12 months smoking cessation followed by DNA, RNA extraction.
DNA methylation was measured using Infinium-HumanMethylation850k Bead Chip and RNA-sequencing was done using Illumina-NovaSeq6000 sequencing to measure gene expression. A Benjamini–Hochberg corrected P-value < 0.05 and the fold change > |1.5| considered significant. Expression quantitative trait methylation (eQTM) analysis was done to correlate the gene expression with DNA methylation.
Results: The differential gene expression analysis between before and after 12 months smoking cessation resulted 613 differentially expressed genes including *ALDH3A1*, which was found among top five genes and was decreased after smoking cessation. The differential DNA methylation analysis between before and after smoking cessation resulted in 261 hypomethylated, 289 hypermethylated significant CpG-sites, where the *cg19171383* was hypermethylated after smoking cessation. CpG site cg19171383 was found to be differentially methylated and was negatively correlated with *ALDH3A1* in eQTM analysis.
Conclusion: Smoking cessation influences DNA methylation and gene expression in bronchial biopsies. The *ALDH3A1* is involved in the oxidation of toxic aldehydes and is a well-known as a protector of airway epithelial cells from cigarette smoke induced oxidative stress. Together these findings indicate that methylation increased by smoking cessation, decreases the expression of oxidative stress related genes.

EPIGENETIC-LIKE CHANGES TO SIGNALLING PROTEINS IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE

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Background: Chronic obstructive pulmonary disease (COPD) is characterised by lung airway inflammation, drastically reducing lung capacity and function. Epigenetic modifications are closely linked to COPD disease processes with epigenetic inhibitors altering expression of inflammatory mediators in non-COPD airway smooth muscle (ASM), yet have no significant effect on COPD ASM cells, however, the nature of this alteration is unclear.
Aim & Objectives: The investigation aimed to evaluate whether prominent COPD pro-inflammatory marker C-X-C ligand 8 (CXCL8) expression is impacted by alterations to transcription proteins in ASM cells due to epigenetic inhibitors; Trichostatin-A (TSA) and 5-Azacytidine (5-Aza).
Methods: Primary human ASM cells from smoking and age matched COPD and non-COPD susceptible patients were used. The difference in response by COPD vs non-COPD cells to TSA (100nM) and 5-Aza (10μM) when stimulated by TGF-β (10ng/ml) was investigated. Cells were treated with TSA or 5-Aza prior to TGF-β stimulation. CXCL8 levels in cell-free supernatant were analysed via ELISA, whilst western blot analysis of total and phosphorylated protein levels was conducted. Data was analysed using two-way ANOVA with post-hoc Fisher's LSD multiple comparisons test.
Results: ELISA detection of CXCL8 reported a significant increase in CXCL8 production by non-COPD cells when stimulated by TGF-β in conjunction with the inhibitors, which was not observed with either treatment in isolation. Non-COPD cells showed peak increased phosphorylation of NF-kB, p38 MAPK and JNK after 20min stimulation by 5-Aza with TGF-β. Peak increased phosphorylation was recorded in COPD cells for p38 MAPK after 10min TGF-β stimulation with TSA and 5-Aza.
Conclusion: We show for the first time, non-COPD ASM cells have an epigenetic-like modifications on transcription proteins ensuring correct regulation of CXCL8, which are apparently lost in COPD cells. These modifications are altered by TSA and 5-Aza, impacting the activity of the signalling proteins; NF-kB, p38 MAPK and JNK.

THE IMPACT OF PRECONCEPTION WEIGHT INTERVENTION ON METABOLIC INFLAMMATION IN MICE

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Background: Maternal obesity affects 20% of pregnant women and negatively impacts on metabolic health in the mother. Maternal complications include miscarriage, gestational diabetes, preeclampsia, fatty liver disease and increased rates of cardiovascular disease. While the mechanisms underlying these complications are not fully elucidated, metabolic inflammation, of which the liver is a key regulator, is emerging as a crucial factor. To date, no studies have addressed whether pre-conception maternal weight loss improves inflammatory markers in obese mothers.
Aim & Objectives: We aimed to determine if weight loss prior to pregnancy, with liraglutide treatment, improves maternal metabolic outcomes, in particular liver metabolic markers.
Methods: Maternal obesity was modelled in C57BL/6 mouse; with dams fed a high fat diet (HFD) for 8 weeks versus chow diet as control. In obese dams, liraglutide (0.3mg/kg, s.c., for 4 weeks) was utilised to induce pre-conception weight loss. Pregnancy rates were observed after mating. Maternal anthropometric measures, glucose tolerance and metabolic markers were measured before and 1 week after intervention, and at late gestation. Pregnant dams were sacrificed at gestational Day 18-20 and blood and liver were collected. Western blotting and real-time PCR were used to measure tissue-specific lipid profiles, oxidative stress, inflammation, and fibrosis-related changes.
Results: Dams fed a HFD had greater body weights and reduced glucose tolerance compared to chow-fed dams. Following intervention with liraglutide, insulin resistance and body weight were reduced. Weight intervention with liraglutide improved conception rates and normalised foetal number in HFD-fed dams. Liver inflammatory markers and metabolic markers were improved in the intervention groups compared to the non-treated HFD-fed group.
Conclusion: Preconception weight loss can improve maternal weight leading into pregnancy. It further improves maternal insulin resistance, liver inflammation and metabolic markers. This research has great translational capacity into clinical practice with improved maternal and foetal outcomes.

THE EFFECTS OF CHRONIC POLYPHARMACY, MONOTHERAPY AND DEPRESCRIBING ON THE KIDNEYS OF AGED MICE

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Background: Polypharmacy (use of ≥5 medications) with increasing DBI (Drug Burden Index: a measure of total exposure to anticholinergic and sedative medications) in older adults is associated with functional impairments, which may be reversed with deprescribing (withdrawal). The effect of polypharmacy and deprescribing on the kidneys - the major organs involved in drug clearance - remains unclear.
Aim & Objectives: We aim to investigate the effects of chronic polypharmacy, monotherapy and deprescribing on the kidney function and histology of aged mice.
Methods: At 12 months, healthy male C57BL/6 mice received control or treatment diet with therapeutic doses of medications (~±10-30%). The regimens included zero DBI (simvastatin, metoprolol, omeprazole, paracetamol, irbesartan), low DBI (simvastatin, metoprolol, omeprazole, paracetamol, citalopram), high DBI (simvastatin, metoprolol, oxybutynin, oxycodone, citalopram), or single medication from high DBI diet (n=40/group). At 21 months, treated mice continued treatment or underwent deprescribing (n=20/group). At 26 months, kidneys, serum and urine samples were collected for histology and biochemistry assessments (n=4-15/group).
Results: Compared to control, all treatments had no differences in serum cystatin C and creatinine levels, and urinary creatinine/albumin ratio and albumin levels, and tubular atrophy scores. Deprescribing had no effect on the above markers. Compared to control, zero DBI, low DBI, high DBI and metoprolol groups had elevated blood urea nitrogen levels, which were reversed with deprescribing ($p<0.05$). simvastatin group had elevated urinary creatinine levels, compared to high DBI group ($p<0.05$). Preliminary results (n=4-5/group) showed no change in the extent of glomerulosclerosis and interstitial fibrosis in high DBI group compared to control.
Conclusion: Chronic polypharmacy and monotherapy of selected medications and deprescribing did not affect renal function or structure in old age. Further histological analysis will confirm these outcomes, which contribute to development of evidence-based policies for clinicians to provide optimal prescribing and deprescribing practices of medications for elderly.

Poster Number 22 15th Nov

mRNA EXPRESSION PROFILING IN LUNG TISSUE OF CIGARETTE SMOKE INDUCED COPD IN MICE

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Background: Chronic obstructive pulmonary disease (COPD) is a multifactorial complex inflammatory disease of the lungs whose pathophysiology is poorly understood. Genome-wide expression profiling in experimental COPD mouse model that mimics the human COPD features can provide novel insights into the molecular mechanisms underlying the pathogenesis of disease.
Aims & Objectives: Thus, we aimed to investigate the genome-wide dynamic regulation of mRNA expression in a time-series experiment (4, 6, 8 and 12 weeks) in a COPD mouse model.
Methods: A short-term mouse model of cigarette smoke (CS)-induced COPD that mimics the characteristic features of the disease was used in our study. In which, tightly controlled amounts of CS were delivered directly into the airways of the mice. The exposed mice exhibit the major characteristics features of COPD observed in human after only 8 weeks of smoke exposure. Expression profiling was performed at each time-points. We examine the smoke effect as well as disease effect in a longitudinal study to underpin the key molecules involved in COPD progression.
Results: The results indicate 287 smoke signature mRNAs in our short-term COPD mouse model. In mouse lung tissue we found about 104 mRNAs to be associated with disease status. We observed that the smoke protective genes or xenobiotic response elements that expressed high in response to CS exposure, dramatically reduced their expression without affecting the expression level of their regulatory molecules including *AHR* and *ARNT* upon disease development. However, the expression level of *ARNT2* and *AHRR* is significantly altered during disease induction and developmental phase in the presence of constant CS exposure.
Conclusions: We conclude that the *ARNT2* and *AHRR* might explain the rationale finding of cell exhaustion affecting the expression level of smoke protective genes that would help in understanding the disease pathogenesis.

Honours/RA 14th Nov

INHIBITION OF DNA DAMAGE REPAIR TO IMPROVE SENSITIVITY TO CHEMOTHERAPY IN TRIPLE NEGATIVE BREAST CANCER

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Background: Triple negative breast cancer (TNBC), an aggressive subtype of breast cancer found in 12-18% of breast cancer patients, is defined by a lack of expression of the estrogen receptor, progesterone receptor, and human EGF receptor 2 (HER2), making it unresponsive to current breast cancer targeted therapies. Chemotherapy is the current frontline treatment, but resistance often develops, in part caused by the ability of the cancer cells to repair potentially lethal DNA double-strand breaks induced by therapy.
Aim & Objectives: The overall aim of this project is to improve chemosensitivity in TNBC patients. Specifically, this study examines the effects of the PARP1 inhibitor veliparib, the EGFR inhibitor gefitinib, and knockdown of the long noncoding (lnc) RNA, LINP1, in their ability to sensitise the TNBC cell lines MDA-MB-468 and HCC1806 to the chemotherapy drug etoposide.
Methods: MTT assays were used to detect cell viability after inhibitor-chemotherapy treatment; phosphorylated histone H2AX immunofluorescence was used to monitor DNA damage repair complexes and resulting rate of double-strand break repair over 4 h; and clonogenic survival assays studied the long-term effects of inhibitor-chemotherapy combination therapy on the overall survival of TNBC cells.
Results: Veliparib-etoposide therapy reduced the clonogenic survival of MDA-MB-468 cells by 65% ($p=0.0133$), providing evidence for a combined effect on cell survival but not for chemosensitisation. Gefitinib did not sensitise cells to etoposide chemotherapy but caused a mild independent reduction of survival. Significantly, LINP1 knockdown in combination with etoposide in HCC1806 cells delayed repair of DSBs after treatment, and strongly reduced clonogenic survival by 73% ($p<0.0001$), whereas control cells treated with 20 nM etoposide saw no reduction in survival, demonstrating a chemosensitisation effect.
Conclusion: This study suggests that silencing the lncRNA LINP1 increases the sensitivity of TNBC cells to chemotherapy, providing evidence for a potential new therapeutic target.

Honours/RA 14th Nov

CELLULAR RESPONSE OF 3D PRINTED IMPLANTS

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Background: With an ageing population, there is a demand for the optimisation of patient-specific 3-D printed titanium implants in terms of its alloy composition and surface topography, in order to improve osseointegration and subsequent implant success.
Aim & Objectives: To determine the cellular morphology and gene expression profile of titanium alloy compositions, specifically Ti-12Nb-12Zr-12Sn (T12), Ti-6Al-4V (T64) and Commercially Pure Titanium (CPT), and to examine the effects of porosity on cell morphology and gene expression.
Methods: Osteoblast (MC3T3-E1) and osteocyte (OCY454) cells were proliferated, seeded and fixed onto 3-D printed, collagen-coated T12, T64 and CPT, as well as onto SLA, 29% and 40% porous T64 titanium alloy samples. Each sample was stained prior to microscopic imaging. Cell morphology was evaluated using surface area, circularity, and aspect ratio. RT-PCR was utilised to measure gene expression of the target genes (RUNX2 and COL1α1 for osteoblasts, RANKL and SOST for osteocytes) relative to the GAPDH gene. ANOVA and multiple comparisons were performed using GraphPad Prism Version 7.0.
Results: T12 surface composition was found to significantly increase both osteoblast and osteocyte cells' surface area compared to those seeded onto T64. Additionally, osteoblast and osteocyte cells seeded onto 29% or 40% T64 exhibited significantly greater surface area than those seeded onto SLA-coated implants. Osteoblast cells exhibited significantly greater fold change of gene expression in porous samples than in SLA. No significant differences were found in the gene expression of osteocytes between the porous samples and SLA.
Conclusion: The present findings show that the composition of T12 and the porosity of 40% T64 are integral in achieving greater cell adhesion and spread. Developing 3D printed, patient-specific implants that reflect the composition of T12 and the porosity of 40% T64 may lead to greater osseointegration and diminish the need for unnecessary surgical intervention due to failed implants.

PhD Session 3 15th Nov

THERAPEUTIC EFFECTS OF SYNTHETIC PHOSPHOLIPIDS IN INFLAMMATION

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Background: Inflammation as an important biological defence mechanism reflects the body reaction against the injury and infection to remove the initial source of cell injury and to repair the damages. However, chronic inflammation can be destructive as it may cause tissue damage. Phospholipid-based therapies are deemed to be safe and have shown anti-inflammatory properties, and therefore have been investigated for their potential therapeutic efficacy in inflammatory conditions.

Aim & Objectives: Our aim was to investigate the anti-inflammatory application of a pharmaceutical formulation (referred to as UTS-L; Au patent AU2019900939) containing 1,2-dioleoyl-sn-glycero-3-phosphocholine (DOPC), in the brain following a systemic inflammation.

Methods: UTS-Liposomes were prepared via thin-film hydration method and characterized for the size and zeta potential. Systemic inflammation was induced via repeated intraperitoneal administration of lipopolysaccharide (250 ug/Kg, 7 days) to male C57BL/6 mice. Control animals were injected with phosphate buffer saline. For UTS-L mice, UTS-L was intraperitoneally injected simultaneously with LPS for either 7 or 14 consecutive days. On days 14, mice were culled and the brain and other organs were harvested. The mRNA expression level of IL-6, IL-1β, and TNF-α, TLR-4, NOX4 and iNOS in Cortex, Hippocampus and Striatum were studied using rt-PCR.

Results: The liposomes were 190.86 ± 6.95 nm with a polydispersity index of 0.28 ± 0.01 and zeta potential of -1.39 ± 0.06. LPS administration caused an increase in mRNA expression level of all the mentioned markers in cortex and hippocampus, while treatment with UTS-L decreased their expression level ($P<0.05$ for TNF-α in cortex and IL-1β in hippocampus).

Conclusion: Inflammation in each and every organ, especially when chronic, can be injurious. Our preliminary findings suggest that daily UTS-L administration in LPS induced mice can alleviate the brain inflammation by reducing inflammatory cytokines. Future studies will investigate the therapeutic efficacy of UTS-L in different models of inflammation.

PhD Session 3 15th Nov

OROPHARYNGEAL VOLUME AND SELF-REPORTED DYSPHAGIA FOLLOWING WHIPLASH INJURY

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Background: Whiplash injury gives rise to the maximal extension and flexion of the cervical spine. Swallow deficits have been reported following whiplash injury, however the underlying mechanisms are unknown.
Aim & Objectives: This study examined 1) changes in self-reported dysphagia to 12-months post whiplash injury and 2) the relationship between changes in oropharyngeal volume as measured on Magnetic Resonance Imaging (MRI) and self-reported dysphagia.
Methods: Secondary analysis was carried out on 37 adults from a longitudinal cohort study. All had whiplash injury following motor vehicle collision. Serial MRI of the cervical spine were collected at acute (< 1- and 2-weeks) and chronic (3- and 12-months) stages post-injury. OsiriX image processing software was used to manually contour the oropharynx for each structural T1-weighted axial slice between C2 and C5. Axial slices were stacked and summed to calculate total volume. The Dysphagia Handicap Index (DHI) was completed at each time point and mean DHI for acute and chronic stages were calculated. DHI and % volume change scores were calculated for acute vs. chronic stages and dichotomised to represent positive or negative change. A paired-samples t-test was conducted to test differences in DHI from acute to chronic. A chi-square test of independence was used to evaluate the relationship between volume and DHI change.
Results: Overall, dysphagia was self-reported by 32% of the cohort at least once in the 12 months post-injury. At the acute stage 12.5% self-reported dysphagia, increasing to 48.8% in the chronic stage. Mean acute DHI score was 0.5 (SD: 1.14; Range 0-5) with a significant ($p<0.001$) increase in symptom score by the chronic stage review (M=2.5, SD: 3.81; range 0-19). There was a greater than expected proportion of patients with both increased oropharyngeal volume and higher (worse) DHI scores ($p=0.019$) between acute and chronic stages.
Conclusion: Almost one in 5 self-reported dysphagia in the first 12-months following whiplash, with significant worsening of symptoms over 12 months. Findings reflect the need to consider swallowing deficits in the management of this complex population.

Poster Number 24 15th Nov

USING GENOMICS AND PROTEOMICS TO UNDERSTAND THE ANTIBIOTIC RESISTANCE CAPABILITIES OF A BACTERIAL PATHOGEN

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Background: Next-generation genomic sequencing has shown potential as a predictor of phenotype and for understanding genes thought to confer antimicrobial resistance (AMR) in bacterial communities. Despite the availability of genome sequencing and improvements to proteomic workflows enabling robust, sensitive and comprehensive discovery and quantitation of biomolecules, there are still little to no experimental studies evaluating how the bacterial proteome responds to antimicrobial challenge in the case of AMR.
Aim & Objectives: Our research aims to understand the AMR capabilities of an isolate on a molecular level through examination of its genome and proteome, with and without antibiotic challenge. This research seeks to evaluate how effectively genome sequences predict the phenotype by connecting AMR genes to gene end-products on the proteoform-level, which has yet to be experimentally shown using a systems biology approach.
Methods: Long- and short-read genomic sequencing and assembly was conducted in-house on multi-drug resistant E. coli isolates to confirm the presence of AMR-related genes. A shotgun LC/MS/MS proteomics pipeline measured proteome changes with and without antibiotic challenge. PEAKS Studio X, UniProt, and STRING databases was used to analyse data.
Results: Several proteins related to AMR were found to be upregulated, despite no antibiotic challenge, including multi-drug resistance proteins. Additionally, several proteins previously annotated as hypothetical were observed.
Conclusion: Our research findings are one of the first to experimentally link an AMR-related gene to the AMR-related protein using a systems biology approach, providing evidence that the genotype and the phenotype do differ. Results highlight that more proteoform-level evidence is required to validate the insights made by genomic sequencing projects, especially in cases which define the “resistance” status of an isolate based on the presence or absence of particular gene elements. Finally, this study supports genomic sequencing as having a strong potential to replace current clinical tests and provide more specificity in antibiotic selection in the clinic.

Poster Number 16 14th Nov

THE OXIDOREDUCTASE ACTIVITY OF HIS-TAGGED AND NON-HIS TAGGED CLIC PROTEINS REVEALS CHANGES IN ENZYME EFFICIENCY

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Background: The human chloride intracellular ion channel protein (CLIC) family are a unique set of ion channels that also demonstrate oxidoreductase enzymatic activity when in their soluble form. Use of purified recombinant proteins with a six amino terminal Histidine tag have been an important means of characterising protein activity, with the His tags often quoted as having minimal to no effect on a protein's native activity.

Aim & Objectives: To characterize the enzymatic profile of members of the CLIC family and expand upon the knowledge gap of CLICs' functions.

Methods: Purified recombinant his- or non-his tagged proteins were prepared using pET28a(+) plasmids containing the genes for human CLIC1, CLIC3 and the CLIC1-Cys24A mutant transformed into *E. coli* BL21 (DE3). Cells were harvested and lysed, with soluble lysates run through an immobilised nickel metal affinity column and proteins eluted using an imidazole containing buffer. Purified proteins with or without removal of the His-tag were then subjected to size exclusion chromatography. The HEDS (2-Hydroxyethyl disulphide) Assay system was used to measure glutaredoxin activity.

Results: We demonstrate that the enzymatic activity of the recombinant proteins in the HEDS assay, display distinct profiles dependent upon their storage buffer and the presence or absence of the amino terminal 6xHistidine tag. We demonstrate that the presence of the His-tag decreases the oxidoreductase enzymatic activity using 2-hydroxyethyl disulfide as a substrate, as well as observing changes in Km and Vmax of the CLIC proteins through Michaelis-Menten Plots.

Conclusion: Based on our findings, we conclude that use of His-tagged CLIC proteins and / or the presence of imidazole in the storage buffers are not a suitable model for characterising native oxidoreductase enzymatic activity. This also puts into question other published studies that have used this His-tag system, for the characterisation of oxidoreductase protein enzymatic activity.

Poster Number 25 15th Nov

PREPARATION, CHARACTERISATION AND BIOLOGICAL APPLICATIONS OF RUTIN LOADED LIQUID CRYSTALLINE NANOPARTICLES IN TARGETTING AIRWAY DISEASES

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Background: Natural compounds such as bioflavonoids have been recognised as a unique class of therapeutic compounds. Rutin, a bioflavonoid has been known for its pharmacological activities due to significant antioxidant, non-toxic and non-oxidizable properties.
Aims & Objectives: The present study aims to formulate rutin loaded liquid crystalline nanoparticles (LCNs) and investigate their anti-inflammatory activity in human bronchio-epithelial cell line (BEAS-2B) induced with TNF-α. In addition, the anticancer activity of the LCNs was also investigated in adenocarcinomic human alveolar basal epithelial cell lines (A549).
Methods: The formulated LCNs were characterised in terms of particle size, zeta potential as well as the drug encapsulation efficiency. Furthermore, their morphology and *in vitro* release profile were also studied. In addition, the anti-inflammatory activity of rutin LCNs was evaluated by measuring the concentration of pro-inflammatory markers in BEAS-2B cell lines and the anti-cancer activity was studied by *in vitro* proliferation and migration assay.
Results: The physicochemical properties of the LCNs were found to be optimal with a size of 160±2nm and drug entrapment efficiency of 70%. Rutin LCNs also exhibited significant ($p<0.05$) reduction in the production of IL-8. Similarly, rutin LCNs attenuated proliferation and migration in A549 cells.
Conclusion: Rutin loaded LCNs could be a potential therapeutic intervention in treating airway diseases and subsequently benefiting the pulmonary clinics.

Honours/RA 14th Nov

A PILOT STUDY EXAMINING THE EFFECT OF CONDITIONED PAIN MODULATION ON A NOVEL NOCICEPTIVE FLEXOR REFLEX RECORDED FROM TIBIALIS ANTERIOR.

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Background: The nociceptive flexor reflex (NFR) is an established measure in pain neurophysiology[1, 2, 3] however generating this response via sural nerve stimulation can be aversive for subjects. An alternative method of generating an NFR using sole of foot stimulation and recording from tibialis anterior has been reported in the literature[4] however whether it allows a sensitive clinical measure of descending pain modulation remains unknown.
Aim & Objectives: To examine whether a novel method of generating a NFR is useful for measuring conditioned pain modulation (CPM).
Methods: An n=11(7f) convenience sample had baseline assessments of right hand pressure pain threshold (PPT) and mean area under the curve (AUC) output from the right leg tibialis anterior (TA) and biceps femoris (BF) after a painful sole of foot electrical stimulus. Subject's left hands were submerged for 2-minutes in cold-water bath (12°C) as the conditioning stimulus (CS). During the second minute of the CS the measures were repeated. A fixed post-stimulus window (55ms-180ms) was analysed and results were noise corrected. We compared baseline and parallel CS measures using paired t-tests.
Results: PPT demonstrated a statistically significant CPM effect. Neither TA nor BF AUC showed a measurable CPM effect (decrease in the CS AUC).

	Baseline				Conditioning Stimulus				p-value
	Min	Average	Max	SD	Min	Average	Max	SD	(2-tail)
PPT (kPa)	103	318	781	198.3	156	400	937	234.8	0.0083
TA AUC (μVms)	211	4449	23029	6605.4	149	4105	21272	6330.3	0.3332
BF AUC (μVms)	294	1444	4559	1219.1	183	1846	5619	1832.7	0.3606

Conclusion: Our pilot data does not indicate sole-of-foot stimulation produces a CPM effect when the AUC of the muscle response is measured from either the TA or BF muscles over a fixed, post-stimulus window.

References

1. Willer, J.C. (1977). Pain 3(1):69-80.
2. Andersen, O.K. (2007). Acta Physiol 189 Suppl 654:1-35.
3. Biurrun Manresa, J.A., et al. (2011). Eur J Appl Physiol 111(1):83-92.
4. Jensen, M.B., et al. (2015). J Neurosci Methods 253:110-115.

Poster Number 12 14th Nov

L-Carnitine mitigates impact of maternal smoking on lung health in mice offspring

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Background: Cigarette smoke exposure (SE) during pregnancy is the largest modifiable risk factor for the development of asthma. We have previously shown that maternal L-Carnitine treatment reduces renal and brain adverse impacts in SE offspring, but its effect on the lung is unknown.

Aim & Objectives: Here, in order to investigate the effect of maternal L-Carnitine supplementation on lung proinflammatory signalling pathways we measured inflammasome NLRP3 activation, signalling pathway activation (ERK1,2, JNK1,2, MAPK, and NF-KB), and markers of autophagy (LC3A/B-I, II) and mitophagy (Drp-1 and Opa-1).

Methods: Female Balb/c mice (8 weeks) were exposed to cigarette smoke before mating for 6 weeks, during gestation and lactation. Half SE mothers were given L-Carnitine supplementation through drinking water during gestation and lactation. Lung samples were collected at postnatal day 1 and 13 weeks from both male and female offspring.

Results: At P1, there was an increase in phospho-ERK1,2, total ERK1,2, total JNK1,2, phospho-P38 MAPK and P38 MAPK, phospho-NFKB, NFKB and NLPR3 protein levels in male offspring. The mitochondrial fission marker Drp-1 and autophagosome markers (LCA3A/B-I,II) were increased in SE offspring, L-Carnitine significantly reduced protein levels of phospho-ERK1 and Drp-1. At 13 weeks, there was an increase in autophagosome markers (LCA3A/B-I,II) and MAPK signaling pathway markers (phospho-ERK2, total ERK2, total P38 MAPK and phospho-NFKB), which were partially normalized by L-Carnitine treatment. Maternal SE did not affect the female offspring with no changes found after L-Carnitine treatment.

Conclusion: L-Carnitine supplementation during pregnancy may alleviate the adverse impact of maternal smoking in the male offspring's lung.

Poster Number 9 14th Nov

Maternal low dosage particulate matter exposure induced transgenerational hyperairwayresponsiveness in the mice

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Background: In humans, maternal particulate matter (PM) exposure during pregnancy is known to negatively affect offspring's lung. Most murine models used high doses regime to investigate mechanisms.

Aim & Objectives: The aim of this study was to investigate the effect of low dose in-utero PM exposure on offspring's lung health.

Methods: Female BALB/c mice were divided into SHAM, PM and PM cessation groups. PM group was exposed to PM_1 (5ug/day) before mating for 6 weeks, during gestation and lactation. PM cessation group only exposed during the pre-gestational period. Lung were collected from both dams and female offspring at age of postnatal day P1 , P20 and 13 weeks. Lung function were tested in the dams and bronchoalveolar lavage fluid was assessed for inflammation. Oxidative stress (MnSOD), mitophagy (Drp-1, Opa-1, Parkin1 and PINK1), autophagy (LC3A/B-I, II), pro-inflammatory mediator (NF-KB, MAPK signalling pathway (ERK1,2, JNK1,2 and P38)), and inflammasome NLRP3 were measured by western blotting.

Results: In the dams, PM exposure caused airway hyperresponsiveness and increased infiltration of macrophages and neutrophils into the lung. This was accompanied by low body weight. Lung pathology showed epithelial cell swelling and more immune cells around airway.

In the female offspring, maternal PM exposure caused airway hyperresponsiveness and increased infiltration of macrophages into the lung. Lung pathology showed more immune cells around airway.

Conclusion: Chronic low dosage PM_1 exposure caused adverse effects in the lungs of dams and offspring, which need to raise our concern of environmental air pollution.

LOW COST AND NOVEL LATERAL FLOW IMMUNOASSAY FOR CELIAC DISEASE TEST

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Background: Celiac disease is an auto-immune disease, triggered by ingested gluten which are from barley, wheat, and rye, resulting in damage to small intestine among human leukocyte antigen predisposing-genotypes (HLA-DQ2/8) gene carriers. Around 83% potential celiac patients remain undiagnosed or misdiagnosed due to the torturous gold standard detection and not cheap screening tests. Thereby, the rapid and low cost detection methods development for celiac disease is important.
Aim & Objectives: To develop a low cost lateral flow immune-device for celiac disease on-site screening test.
Methods: A cost-effective lateral flow immunoassay for the detection of celiac antibody based on celiac antigen was developed. Gold nanoparticles conjugate with a capture protein, which can absorb antibody from sample, as the signal reagent. Celiac antigen, which can react with the specific antibody from the sample was dispersed as the test line, and primary antibody from human was dispersed as the control line. Two red lines mean a positive result and only the control line becoming red means a negative result. Neither of the two lines become red, or only the test line turns red representing invalid results.
Results: Gold nanoparticles can conjugate with the capture protein easily and rapidly. And the conjugate is pretty uniform. What is more, the conjugate can move forward very well on the lateral flow immunoassay platform, especially after all the possible conditions optimized. A good linear detection range can be obtained when a series of concentrations of spiked antibodies were added to the platform. Besides, the designed method can test celiac disease with serum and saliva samples.
Conclusion: A simple, fast, and low cost lateral flow immunoassay method to detect celiac disease was successfully developed. It has great potential for converting it into commercial medical device. Once commercialized, the device will greatly reduce the cost of celiac disease detection.

Poster Number 19 14th Nov

SENSITIVITY OF OVARIAN CANCER CELLS TO PHARMACOLOGICAL INHIBITION OF THE DNA REPAIR ENZYME PARP

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Background: Ovarian cancer is a low survival cancer, with 5 year survival rates showing minimal improvement over several decades. A new therapy that targets the enzyme poly-adenosine diphosphate-ribose polymerase (PARP) has the potential to improve outcomes for some women with this malignancy. PARP inhibitors (PARPi) perform optimally in the presence of defective homologous recombination (HR) where synthetic lethality leads to cell death. Around 50% of ovarian cancers are HR defective, a large proportion of these due to mutations of *BRCA1* or *BRCA2*.

Aim & Objectives: The aim of this study is to investigate pre-clinical ovarian cancer cell line models with known *BRCA1/2* status for differential sensitivity to PARP inhibitors, both clinically approved for the treatment of ovarian cancer and those under investigation.

Methods: Two-dimensional (2D) cell culture, as well as 3D bio-printing to generate spheroids are being used. Functional assays include MTS for cell proliferation and clonogenic cell survival assays. PARP inhibitors undergoing testing are Olaparib, Niraparib, Talazoparib, Rucaparib and Niraparib, in ovarian cancer cell line pairs - UWB1.289 and UWB1.289+BRCA1, and PEO1 (*BRCA2* mutant c.5193C>G) and PEO4 (*BRCA2* wild-type).

Results: While all *BRCA* mutant cell lines were more susceptible to PARP inhibitors compared to their wild-type pair, an end point proliferation assay (MTS) at 5 days post treatment showed differential efficacy of these inhibitors, with Talazoparib being the most potent and Veliparib the least. Clonogenic cell survival assays are currently underway. Upon 3D bio-printing with the bio-ink “RASTRUM hydrogel”, PEO1 was unable to form spheroids while its chemoresistant pair PEO4 formed large spheroids after 14 days.

Conclusion: Different PARP inhibitors are differentially potent in ovarian cancer cell line pairs with known *BRCA* defects leading to HR deficiency when cultured in 2D. Similar experiments will be conducted in 3D bio-printed ovarian cancer cells to better mimic the tumour environment.

Poster Number 10 14th Nov

COMPARISON OF OUTPATIENT VERSUS INPATIENT TOTAL HIP AND KNEE ARTHROPLASTY: A SYSTEMATIC REVIEW AND META-ANALYSIS OF COMPLICATIONS

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Background: Patients undergoing TKA or THA have traditionally been managed post-operatively as inpatients. However, with current surgical techniques and pain management, there is evidence that outpatient joint arthroplasty can be safely performed in selected patient.
Aim & Objectives: To compare the post-operative complication rates of outpatient and inpatient TJA with subgroup analysis of TKA and THA.
Methods: Electronic searches were performed using five databases from their date of inception to October 2018. Relevant studies were identified, with data extracted and meta-analysed from the studies.
Results: From seven included studies, 176,179 patients were inpatient TJA and 1613 were outpatient TJA. The outpatient and inpatient TJA cohorts had similar mean age and BMI, with a greater proportion of females in the inpatient group. For TJA we found no significant difference in total complications (P=0.06), major complications (P=0.59), readmissions (P=0.60), DVT (P=0.94), UTI (P=0.50), pneumonia (P=0.42) and wound complications (P=0.50) between the outpatient and inpatient groups. However, there were fewer transfusions (P=0.05) but increased reoperations (P=0.02) in the outpatient TJA group. Subgroup analysis of TKA (P=0.25) and THA (P=0.39) also found no significant differences in total complications between the outpatient and inpatient groups.
Conclusion: Outpatient TJA had comparable total complication rates to inpatient TJA. Along with that outpatient TJA can significantly reduce costs to healthcare systems but careful pre-operative patient selection is required to optimize outcomes. More quality randomised controlled trials with longer follow-up periods are needed to add to this body of evidence.

THE EFFECT OF VARUS STEM PLACEMENT ON GLOBAL JOINT OFFSET DURING TOTAL HIP ARTHROPLASTY: A VIRTUAL STUDY

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Background: With total hip replacement (THR), varus alignment of an uncemented stem will increase offset which can have significant effects on muscular balance, leg length and overall satisfaction. However, no studies that have quantified the relationship between the degree of varus stem placement and increase in global offset.
Aim & Objectives: To use 3D planning software to determine the change in global joint offset with increasing varus stem placement.
Methods: Eight patients undergoing THR had routine CT scans to allow for 3D hip planning. Each set of CTs was templated with the straight, quadrangular MetaFix stem and an uncemented press-fit acetabular Trinity cup. Initial templating was performed to reproduce native leg length and global offset. The templated stem was then rotated into varus at 1° intervals, up to 6° varus while maintaining the desired leg length. The global offset changes for all varus positions were noted. This was repeated for three neck angles of 125°, 135° and 135° lateral with stem sizes 1, 3, 5 and 7.
Results: Twelve simulations were conducted for 3 neck angles at 4 different stem sizes. Overall, there was a mean 1.5 mm increase in global offset for every 1° of varus. The stems with a 125° neck angle had the greatest increase in mean global offset at 1.6 mm for every 1° of varus. The stem neck angles of 135° lateral offset and 135° standard offset, had a mean increase in global offset of 1.5 mm and 1.4 mm for every 1° of varus respectively. A greater mean increase in global offset for every 1° of varus was observed with increasing stem size. For size 1, size 3, size 5 and size 7 stems, there was respectively a 1.3 mm, 1.4 mm, 1.6 mm and 1.8 mm increase in global offset for every 1° of varus.
Conclusion: We have quantified the relationship between alignment and offset with every 1° of varus placement increasing global hip offset by 1.5 mm. This can be used as a guide for surgeons during THR so that they have a better quantitative understanding of how varus placement of the stem affects the global hip offset.

Poster Number 40 15th Nov

NANOSILVER IN THE ENVIRONMENT: AN EMERGING THREAT TO HUMAN AND ENVIRONMENTAL HEALTH

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The application of nanoparticles (NPs) has been rapidly growing as they are being used in a broad range of industries. Among those NPs, nanosilver (NAg) are the most popular advertised ones due to their antimicrobial properties, and hence they have been used in medical devices and a wide range of consumer products, including heath care products. The widespread use of NAg has led to the release of the NPs into the environment, and furthermore may lead to the accumulation of silver in the environment due to its inability to be degraded. The uncontrolled NAg release to natural environments may affect microbial communities, facilitating the development of antibiotic resistant microbes through the co-selection of antibiotic resistance genes (ARGs), as well as the disruption of biogeochemical processes (e.g. nitrogen cycle). The current on-going research aims to investigate the ecological implication of NAg to facilitate the spread of ARGs and disrupt nutrient cycles in marine environments. Our current result indicated the potential capabilities of NAg to co-select for ARGs and even mobile genetic elements (MGEs) in marine microcosms (Sydney's stormwater discharge), where the treatment of 0.5 mg/L NAg led to increasing *sul1*, *tetB*, and *intI1* gene abundances. At least 20-fold higher toxic 'background' silver levels in the samples relative to the recommended trigger values (0.8 to 2.6 µg/L silver for 99 to 80% species protection level, respectively) were detected. Metagenome sequencing and analysis will be done for both microcosm and field experiments (Lake Macquarie, NSW) to obtain the complete profile of ARGs, MGEs, and nutrient-cycle relevant genes. Synergistic or antagonistic effect with other heavy metals in real marine environments will be elucidated through multivariate analyses. The research findings are expected to contribute in the development of strategies for managing the use and disposal of NAg-containing products which are currently ineffective.

Poster Number 39 15th Nov

PERIVASCULAR MACROPHAGES MEDIATE LEUKOCYTE RECRUITMENT DURING STERILE INFLAMMATION.

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Background: Perivascular macrophages (PVM) represent a functionally distinct subset of macrophages that reside along post-capillary venules. PVM have been implicated in the recruitment of immune cells during bacterial-induced inflammation. However, little is known about their function in leukocyte trafficking during sterile inflammation.
Aim & Objectives: We aim to investigate the role of perivascular macrophages in mediating the recruitment of leukocytes during sterile inflammation.
Methods: Utilising intravital multiphoton microscopy, we have analysed the migratory dynamics of immune cells within the vasculature of the mouse cremaster muscle during tumour necrosis factor-α (TNF-α) induced inflammation.
Results: Flow analysis of TNF-α treated cremaster tissues show a significant influx of neutrophils and monocytes at 4h and 7h post-intrascrotal injection, respectively. Our findings from intravital microscopy demonstrate that the majority of neutrophil and monocyte transmigration and diapedesis occur in close proximity to perivascular macrophages.
Conclusion: Our study indicates that perivascular macrophages have an important role in guiding the homing of leukocytes during sterile inflammation. Further studies will be focused on identifying the molecular players involved in chemotaxis and cellular transmigration in this inflammatory setting, providing further insight into new therapeutic strategies for the treatment of TNF-driven inflammatory diseases.

AWARDS AND PRIZES

Awards and prizes include:

Honours Students:
- Best Oral Presentation by an Honours Student ($500 cash prize)
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- Josephine Anderson Award for Best Oral Presentation ($500 cash prize)
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Note: Travel grants can be claimed back (with valid receipts) from the conference committee within one calendar year from the date of the 2019 New Horizons conference. The travel grant can be used to support any costs related to airfare, accommodation and registration for presenting (oral or poster) at a national or international conference.

GENERAL INFORMATION

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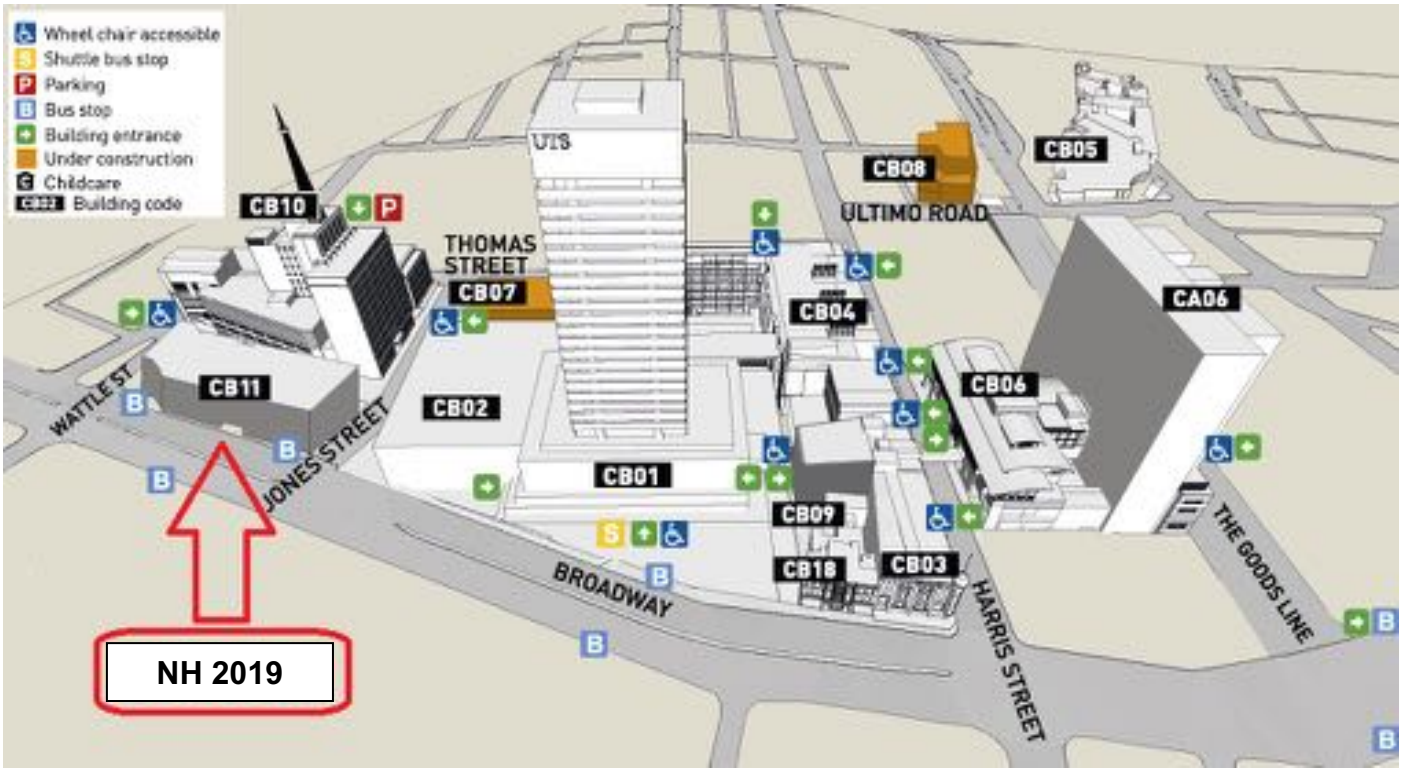

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