ASMR
AUSTRALIAN SOCIETY
FOR MEDICAL RESEARCH

CONFERENCE BOOKLET

65th ASMR National Scientific Conference

16 - 18 November 2026 | Melbourne, Victoria

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PRESIDENT'S STATEMENT

Dear 2026 ASMR NSC Delegate,

It is my great pleasure to welcome you to the 65th Annual National Scientific Conference. Since its founding in 1961, the ASMR has proudly championed Australia's health and medical research community, connecting researchers, fostering collaboration, and providing a vital platform to share discoveries that advance human health.

The ASMR's key priorities remain supporting career development, advocating for a strong and sustainable research sector, engaging with the wider community, and fostering a member-centric organisation.

We are delighted to host an outstanding line-up of keynote speakers and sessions showcasing the depth and diversity of Australian medical research. Alongside world-class scientific presentations, the conference also features professional development opportunities that address the evolving needs of researchers at every stage.

Your continued engagement with ASMR is essential to our shared mission. Together, we can strengthen the voice of research in Australia and ensure a thriving, innovative sector for generations to come.

I look forward to meeting many of you throughout the conference, and to the inspiring discussions and connections that will no doubt emerge from this year's program.

Yours sincerely,

Dr Razia Zakarya
Acting President, Australian Society for Medical Research

ORGANISING COMMITTEE

Thank you to the VIC State Committee for leading this year's NSC.

Co-Convenor	Natasha Letunica	MCRI
Co-Convenor	Suelyn Van Den Helm	MCRI
Treasurer	Patrick Bajan	Burnet Institute
Sponsorship Lead	Jordyn Thomas	Baker Institute
Sponsorship Deputy	Jason Paxman	La Trobe University
NSC Lead	Bhavana Nayer	ARMI
NSC Lead	Wenyi Hu	CERA
NSC Deputy	Jessica Borger	Monash University
Gala Dinner Lead	Kiymet Bozaoglu	MCRI
Gala Dinner Lead	Ankita George	MCRI
Gala Dinner Deputy	Ebony Monson	La Trobe University
Gala Dinner Deputy	Marina Yakour	Doherty Institute
Communications Lead	Sohinee Sarkar	MCRI
Communications Lead	Solomon Guyler	University of Melbourne

DELEGATE HOUSEKEEPING INFORMATION

Conference etiquette

ASMR is committed to honouring the rights of copyright owners and to respectful sharing of scientific research and data. Attendees at ASMR events are expected to adhere to this policy.

The research content of these sessions is confidential and must not be shared. It is prohibited to **record** any of the presented information **without permission.** Photography is permitted (for personal use only).

Social engagement

Follow @TheASMR1 on X (formerly Twitter) and Instagram, and Australia Society for Medical Research (ASMR) on LinkedIn for updates during the conference. Use social media to share your thoughts on ideas and the NSC, and to connect with other researchers.

65th ASMR National Scientific Conference

Day 1: 16th November 2026

Time	Event	In parallel
08:00 – 08:45	Registration desk open	Poster set up
08:45 – 09:00	Opening ceremony	
09:00 – 09:45	**Plenary talk – Distinguished Professor Madhu Bhaskaran** "Bridging the Gap: Cross-Sector Partnerships to Translate Soft Electronic and Biosensor Technologies"	
09:45 – 10:05	Morning tea	
10:05 – 11:40	**Oral presentations session #1** *Bioengineering, devices & digital health* (9 talks x 10 min)	
11:40 – 12:15	**Invited MCR talks** — Dr Anna Wang, Assoc Prof Alisa Glukhova	
12:15 – 12:30	**Peter Doherty Leading Light award** Announcement + presentation	
12:30 – 13:15	Lunch	Trade displays
13:15 – 15:20	**Oral presentations session #2** *Infection, immunity & vaccines* (12 talks x 10 min)	**Oral presentations session #2B** *Cardiovascular, metabolic & cell biology* (12 talks x 10 min)
15:20 – 15:45	Afternoon tea	
15:45 – 17:15	**Panel: Career pathways in Research** Chaired by: Dr Ebony Monson and Assoc Prof Jessica Borger Panelists: Dr Goh Kai Lyn, Dr Petra Graves, Dr Ekaterina Woods, Dr Alice West and Prof Nicholas Opie	

65th ASMR National Scientific Conference

Day 2: 17th November 2026

Time	Event	In parallel
08:30 – 09:00	Registration desk open	
09:00 – 09:45	**Plenary talk – Dr Fernando Gordillo Altamirano** "Phage therapy in Victoria, the good, the bad, and the ugly"	
09:45 – 10:05	Morning tea	
10:05 – 11:10	**Oral presentations session #3** *Neuroscience* (6 talks x 10 min)	
11:10 – 11:45	**Invited MCR talks** — Dr Hui-Fern Koay, Assoc Prof Joshua Wiley	
11:45 – 12:30	**Workshop: Science Communication** Delivered by: Dr Shane Huntington	
12:30 – 13:15	Lunch	Trade displays
13:15 – 14:15	**Poster session**	
14:15 – 15:20	**Oral presentations session #4** *Public health, clinical & health services* (6 talks x 10 min)	**Oral presentations session #4B** *Maternal health, brain & mental health* (6 talks x 10 min)
15:20 – 15:45	Afternoon tea	
15:45 – 17:15	**Panel: AI in Research** Chaired by: Dr Emerson Keenan Panelists: Assoc Prof Lisa Zhu, Assoc Prof Rahul Rane, Assoc Prof Sonika Tyagi, Dr Rosita Shishegar and Dr Sahar Shahali	

65th ASMR National Scientific Conference

Day 3: 18th November 2026

Time	Event	In parallel
08:30 – 09:00	Registration desk open	
09:00 – 09:45	**Plenary talk – Professor Yugeesh Lankadeva** "Impact of integrating academic, clinical, and industry partnerships to improve health outcomes for critically ill patients"	
09:45 – 10:05	Morning tea	
10:05 – 11:20	**Oral presentations session #5** *Cancer & cell biology* (7 talks x 10 min)	
11:20 – 11:55	**Invited MCR talks** — Dr Brooke Patterson, Dr Patrick Lelliott	
11:55 – 12:40	**Fireside chat on Research Funding** Chaired by: Dr Shane Huntington With: Prue Torrance (NHMRC Acting CEO) and Rosie Strickleton (Helen Macpherson Smith Trust)	
12:40 – 13:25	Lunch	Trade displays
13:25 – 14:55	**Grant Writing Workshop: Consumer and Partner Engagement and Co-Design** Delivered by: Professor Devanshi Seth (The GrantEd Group)	
14:55 – 15:20	Afternoon tea	Posters to be removed
15:20 – 16:20	**Workshop: Science for social media** Delivered by: Dr Veronique Paris	
16:20 – 17:00	Awards + Closing Ceremony	

ORAL PRESENTATIONS BY SESSION

#	Time	Presenter	Affiliation	Title
Session 1 — Bioengineering, devices & digital health *Monday 16 November · 10:05–11:40 · Forum 1+2*				
S1-01	10:10–10:20	**Ganganath Perera**	RMIT University	Saliva-based Conductometric Multiplex Biosensor for Rapid Point-of-Care Cardiac Risk Assessment
S1-02	10:20–10:30	**Sreekanth Srirangam Prathivadibayankaram**	RMIT University	Chronic kidney disease detection and management through swift detection of biomarkers using HR-Si conductometric biosensor
S1-03	10:30–10:40	**Akila Hewa Thondilege**	Queensland University of Technology	Markerless Ground Reaction Force Estimation for Clinical Biomechanical Assessment Using Dynamic Hypergraph Neural Networks
S1-04	10:40–10:50	**Romana Nasrin**	Monash University	Moldable microchanneled polyHIPE scaffolds: a novel biomimetic approach to cranial defect reconstruction
S1-05	10:50–11:00	**Sadjad Khosravimelal**	Monash University	A Hybrid Biofabrication Approach for Developing Human-Cell-Based 3D Skin Models
S1-06	11:00–11:10	**Bhavana Nayer**	Monash University	Treg-derived IL-10 suppresses inflammatory macrophage states during muscle regeneration and enables an immunocytokine-based therapy
S1-07	11:10–11:20	**Vincent Yuan**	UNSW Sydney	The evidence gap in AI-enabled medical devices in Australia: a cross-sectional study
S1-08	11:20–11:30	**Amany Gouda-Vossos**	Australian Research Data Commons	Discover, Access, Analyse: Enabling Secondary Use of Health Data
S1-09	11:30–11:40	**Dina Pogrebnoy**	La Trobe University	Co-design, development and delivery of a digital application to deliver a self-management intervention in an inpatient setting after stroke.
Session 2 — Infection, immunity & vaccines *Monday 16 November · 13:15–15:20 · Forum 1+2 (Room A)*				
S2-01	13:20–13:30	**Sindew Mekasha Feleke**	La Trobe University	Tracking Persistent and Resurgent Onchocerciasis Transmission Using Genomic, Ecological and Epidemiological Analyses
S2-02	13:30–13:40	**Veronique Paris**	University of Melbourne	Autodissemination stations to suppress Aedes notoscriptus in urban Victoria
S2-03	13:40–13:50	**Ebony Monson**	La Trobe University	Lipid droplets as natural, engineered vehicles for antiviral therapy
S2-04	13:50–14:00	**Nadia Mazarakis**	Murdoch Children's Research Institute	Persistence of IgG4 skewing over 12 months following a fourth dose of a bivalent mRNA or protein-based COVID-19 vaccine
S2-05	14:00–14:10	**Christie Noble**	Murdoch Children's Research Institute	BCG vaccination induces age-dependent changes in responses to Mycobacterium tuberculosis
S2-06	14:10–14:20	**Georgia-Rose Gilmore**	Monash University	Antibiotics: A Double-Edged Sword - Linking Antibiotic Sensing to Hypervirulence and Persistence in Clostridioides difficile
S2-07	14:20–14:30	**Garry Chahal**	La Trobe University	Can lipid droplets be delivered to the cytoplasm to prime antiviral immunity in neighbouring cells?
S2-08	14:30–14:40	**Justin Boxuan Zhang**	Monash University	Studying T Cell Ectosomes In T Cell Surveillance
S2-09	14:40–14:50	**Bridget E. Walker**	University of Melbourne	A simple model for studying a neglected tropical disease and the importance of host signals for fungal pathogenesis.
S2-10	14:50–15:00	**Jiaqi (Albert) Shi**	Burnet Institute	Development of next-generation mRNA vaccines against malaria
S2-11	15:00–15:10	**Alysha Literski**	Burnet Institute	Improving the capacity of vaccine-induced antibodies against RH5 to arrest the growth of Plasmodium falciparum.
S2-12	15:10–15:20	**Rina Wong (Fu)**	Curtin University	Virucidal and Bactericidal Effects of a Nano-formulation of Australian Melaleuca alternifolia (Tea Tree) Oil against Human and Bovine Respiratory Pathogens
Session 2B — Cardiovascular, metabolic & cell biology *Monday 16 November · 13:15–15:20 · Forum 3 (Room B)*				
S2B-01	13:20–13:30	**Jacob Ellis**	WEHI	Regulation of transposable elements by mRNA export machinery in embryonic progenitor models
S2B-02	13:30–13:40	**Sanuri Liyanage**	SAHMRI	Yolk Sac-Derived Endothelial-Macrophage Progenitors in Skin: Drivers of Wound Healing and Tumour Growth

#	Time	Presenter	Affiliation	Title
S2B-03	13:40–13:50	**Shannen Walker**	Baker Heart and Diabetes Institute	Single-cell Transcriptome Identifies Novel Genes Associated with Hepatic Recovery Pathways in Metabolic Associated Steatohepatitis
S2B-04	13:50–14:00	**Yuyang Song**	Baker Heart and Diabetes Institute	mRNA Platforms Enable Spatiotemporal Control for Safer Thrombosis Prevention
S2B-05	14:00–14:10	**Brooklyn Hutton**	La Trobe University	Strain- and sex-dependent differences in PCSK9-induced atherosclerosis reveal the translational value of outbred models
S2B-06	14:10–14:20	**Caitlin Vella**	La Trobe University	Enhancing Efferocytosis with BELMO Reduces Atherosclerotic Disease Burden
S2B-07	14:20–14:30	**Maya S Bishop**	Florey Institute	Therapeutic benefits of megadose sodium ascorbate for reversing sepsis-induced cerebrovascular and cardiovascular dysfunction
S2B-08	14:30–14:40	**Roop Bhangu**	Monash University	Glucose-Responsive Nano Sugar with Kidney Tropism Enable Multi-Day Therapy in Diabetic Mice
S2B-09	14:40–14:50	**Haoyun Fang (Alexx)**	Baker Heart and Diabetes Institute	Dynamic Subcellular Remodelling of Heart Revealed by Multi-Omics from Early Myocardial Ischemia Reperfusion Injury
S2B-10	14:50–15:00	**Maria Jelinic**	La Trobe University	Senescent fibroblast-like vascular smooth muscle cells are associated with coronary artery plaque vulnerability and immune activation
S2B-11	15:00–15:10	**Sarah Brooke**	Florey Institute	Cardiopulmonary Bypass-Induced Blood-Brain Barrier Disruption in a Clinically Relevant Ovine Model
S2B-12	15:10–15:20	**Nchafatso Obonyo**	Baker Heart and Diabetes Institute	Restarting the Brain After Refractory Cardiac Arrest: Extracorporeal Cardiopulmonary Resuscitation Restores Perfusion and Uncovers Novel Therapeutic Targets
Session 3 — Neuroscience *Tuesday 17 November · 10:05–11:10 · Forum 1+2*				
S3-01	10:10–10:20	**Alayna Carmina Caruso**	Florey Institute	Polyanionic peptibody ameliorates tau pathology and improves synaptic function in tau transgenic mice
S3-02	10:20–10:30	**Dylan Kiltschewskij**	University of Newcastle	Disentangling Epigenetic Heterogeneity in Schizophrenia
S3-03	10:30–10:40	**Joshua Saito**	Florey Institute	Investigating the synaptic pathophysiology of a neurodevelopmental disorder in human neurons
S3-04	10:40–10:50	**Jenna White**	Florey Institute	Characterisation of a Novel Mouse Model of PURA Syndrome
S3-05	10:50–11:00	**Owen Jones**	Florey Institute	Investigating the role of zinc in potassium-mediated cerebral functional hyperaemia
S3-06	11:00–11:10	**Sujan Kumar Sarkar**	Florey Institute	Blocking P2X7R-Mediated Signalling Confers Central and Peripheral Therapeutic Benefits in a Mouse Model of Huntington's Disease
Session 4 — Public health, clinical & health services *Tuesday 17 November · 14:15–15:20 · Forum 1+2 (Room A)*				
S4-01	14:20–14:30	**Sarah Lampard**	La Trobe University	Understanding concussion knowledge, reporting intentions and behaviours in community women's and men's Australian Football
S4-02	14:30–14:40	**Chilot Desta Agegnehu**	La Trobe University	Past-week injecting frequency among culturally and linguistically diverse people who inject drugs in Melbourne, Australia
S4-03	14:40–14:50	**Alexandra R Davidson**	Bond University	Self-management program for people with chronic obstructive pulmonary disease (COPD): The Activating Primary Care COPD Patients with Multimorbidity (APCOM) Trial – Early Findings
S4-04	14:50–15:00	**Jordan Lim**	Monash University	Clinical tools for assessment of plaster cast quality in patients with limb fractures in the Emergency Department: a systematic review of radiological indices
S4-05	15:00–15:10	**Marianne Piano**	Monash University	A case study of how eyecare needs are identified, understood and met in residential aged care.
S4-06	15:10–15:20	**Tan Minh Nguyen**	Monash University	Assessing Cost-Effectiveness on Oral Health Preventive Interventions (ACE-Oral Health Prevention)
Session 4B — Maternal health, brain & mental health *Tuesday 17 November · 14:15–15:20 · Forum 3 (Room B)*				
S4B-01	14:20–14:30	**Jianing Xu**	Burnet Institute	Impact of different diagnostic definitions of pre-eclampsia: a systematic review and meta-analysis
S4B-02	14:30–14:40	**Alanna Gillespie**	Murdoch Children's Research Institute	Congenital cytomegalovirus infection and infant hearing loss in Australia: the Screen cCMV study
S4B-03	14:40–14:50	**Kanika Mehta**	Baker Heart and Diabetes Institute	Dementia mortality in the context of diabetes: age- and sex-specific time trends across seven jurisdictions

#	Time	Presenter	Affiliation	Title
S4B-04	14:50–15:00	**Erin Harcourt**	Federation University	Development and Validation of the Critical Care Memory Tool in Post-Intensive Care Patients
S4B-05	15:00–15:10	**Lauren T Ursich**	Florey Institute	Why Sex Matters: Exploring Neurobiological Differences Driving Binge Drinking
S4B-06	15:10–15:20	**Adelaide Bernard**	Baker Heart and Diabetes Institute	Leveraging elasticity scores to uncover diet-induced shifts in hypothalamic lipid
Session 5 — Cancer & cell biology *Wednesday 18 November · 10:05–11:20 · Forum 1+2*				
S5-01	10:10–10:20	**Yining Tian**	WEHI	Genomic Alterations in TNF-Related Cell Death Pathways as Potential Biomarkers for Personalized Therapy in Oral Squamous Cell Carcinoma
S5-02	10:20–10:30	**Brenda Briones Miranda**	Monash University	From clinical observations to an in vivo model of clonal haematopoiesis: Investigating BCL2–BAX-mediated clonal dynamics in zebrafish
S5-03	10:30–10:40	**Mackenzie Lighton**	University of Western Australia	Low-Dose Radiotherapy Alters Macrophage Polarisation in a Murine Mesothelioma Model
S5-04	10:40–10:50	**Olivia Rose Comito**	University of Notre Dame Australia	The interaction between the human gut microbiome and pancreatic ductal adenocarcinoma (PDAC): A prospective study correlating microbiome composition with anti-cancer treatment and tumour response.
S5-05	10:50–11:00	**Emily Cross**	University of Newcastle	Genetic relationships between metabolic traits and breast cancer: identifying shared biology
S5-06	11:00–11:10	**Winnie Tan**	WEHI	Nucleosome recognition and DNA compaction by the MORC2 remodeller
S5-07	11:10–11:20	**Nicole Sze Yong Nga**	Centre for Eye Research Australia	Increasing FGF7 levels promote corneal endothelial functions via NRF2-mediated response

POSTER SESSION

Board	Presenter	Affiliation	Title
Poster session *Tuesday 17 November · 13:15–14:15*			
P01	**Agustiningsih**	Burnet Institute	Investigating primary and recall humoral immune responses in malaria and the role of type I interferon signalling.
P02	**Akila Hewa Thondilege**	Queensland University of Technology	Improving Clinical Biomechanical Assessment Through Mesh-Based Virtual Markers
P03	**Assia Comella**	Royal Children's Hospital	Thirty Years of Paediatric Colonic Motility Assessment Modalities: A Systematic Review
P04	**Brianna Kline**	Murdoch Children's Research Institute	Mitochondrial fusion dynamics implicated in premature ovarian insufficiency
P05	**Chalie Marew Tiruneh**	University of Technology Sydney	Clinical outcomes of children and adolescents with type 1 diabetes mellitus in Ethiopia: evidence on glycaemic achievement and diabetic ketoacidosis
P06	**Deborah Hilton**	Independent (Deborah Hilton Statistics Online)	Injury prevention workplaces that perform statistical analysis related to health; words describing artificial intelligence from workers – is it a help or hinderance?
P07	**Dilan Bozanoglu**	Centre for Eye Research Australia	Unraveling the role of STING-RFC1 and RFC1-SMAD2/3 interactions in inner blood retina barrier integrity
P08	**Erin Harcourt**	Federation University	The efficacy of interventions for the psychological impacts of post-intensive care syndrome (PICS): a systematic review
P09	**Fern Ee Caryn Koo**	Murdoch Children's Research Institute	Beyond the Child: A Systematic Review of Parental Wellbeing and Family Functioning in Paediatric Colorectal Conditions
P10	**Habib Eichoue**	University of Sydney	Characterising the molecular response to protein restriction in prostate cancer using integrated plasma proteomics and single-cell datasets.
P11	**Imogen Samuels**	University of Melbourne	BAM-Boozled: Pyocin L1 Disrupt Outer Membrane Protein Assembly in Pseudomonas aeruginosa
P12	**Jacob Andrew Dye**	The George Institute for Global Health	Long-term outcomes of out-of-hospital cardiac arrest patients and their caregivers in the Targeted Temperature Management 2 (TTM2) trial
P13	**Jean Pierre Ndabakuranye**	RMIT University	Wearable ambulatory ECG platform for accessible cardiac monitoring
P14	**Jiawei Tang**	WEHI	Optimising CAR-T Cell Therapies Through CD4/CD8-Specific Signalling Programs
P15	**Joshua John Voger**	Florey Institute	Investigating the effects of physical manipulation of the vagus nerve on the inflammatory response in both male and female rats undergoing sepsis
P16	**Jude Oluwapelumi Alao**	Auckland University of Technology	Clinical response and systemic immune profiles following acoustic nasal therapy in chronic inflammatory nasal disease
P17	**Laura McKinley**	Northern Health	Routine prophylactic carbetocin following vaginal birth: a retrospective non-inferiority cohort study
P18	**Marcus Camilleri**	University of Melbourne	RNA isoforms provide cell-type-specific insights into human neurodevelopment
P19	**Nchafatso Obonyo**	Baker Heart and Diabetes Institute	A Case Report of a Preclinical Model of Cardiac Trauma and Haemorrhagic Shock
P20	**Nicholas Glatz**	Florey Institute	Changes to a Thalamocortical microcircuit in the Primary Somatosensory Cortex from Goal Directed Learning
P21	**Ryan M. Clarke**	University of Sydney	Establishing Small Molecule-Based Neuronal Transdifferentiation as a Tool for Modelling Age-Dependant Phenotypes in Amyotrophic Lateral Sclerosis
P22	**Sam Combes**	Florey Institute	The influence of glioma on interneurons in-vivo
P23	**Sarah Fraanje**	Hudson Institute of Medical Research	Investigating the therapeutic potential of herbal extract-infused hydrogel for tissue regeneration in rat birth injury model.
P24	**Sarah Mele**	La Trobe University	Investigating Treatments and Mechanisms in Short-Chain Enoyl-CoA Hydratase 1 (ECHS1) Deficiency
P25	**Theodore Lam**	St Vincent's Hospital Melbourne	Therapeutic Potential of Adipose-Derived Stem Cells in Peripheral Nerve Injury: A Systematic Review

Board	Presenter	Affiliation	Title
P26	**Vatsal Ved**	Monash University	Coronary plaque burden, composition and progression in young adults versus risk-factor-matched older adults: a serial computed tomography coronary angiography study
P27	**Vivian Tran**	La Trobe University	Integrating human and experimental models to identify immune mechanisms underlying cardiovascular complications in Long COVID
P28	**Yashna De Silva**	Monash University	Is Childhood Adversity Associated with Worse Disability Outcomes in Multiple Sclerosis?
P29	**Yingxue He**	WEHI	MLKL-Dependent Necroptotic Signalling Regulates Keratinocyte Differentiation and Epidermal Repair
P30	**Zoe Whitehouse**	La Trobe University	Parkinson's disease and calcium signalling beyond the brain
P31	**Zoriana Novosiadla**	La Trobe University	Dietary Tyrosine restriction rescues Drosophila model of HIBCH deficiency

AWT EDWARDS MEMORIAL ORATION

AWT (Tony) Edwards was a director of ASMR from 1962 to 1966. He died on Friday, 9th of December 1966, a week after becoming President of ASMR. He was regarded as a tireless worker for medical research and was a Senior Lecturer in the School of Physiology, University of NSW. Dr Robin Pavilliard of WA proposed an annual Oration after Tony's. death.

Professor CRB Blackburn (Dept of Med, Uni Sydney) gave the first AWT Edwards Oration in 1967 and said of Tony Edwards:

"I was fortunate to have Tony Edwards with me in the Clinical Research Unit when he first explored medical research. It was apparent in his early days at RPAH that research meant joy and excitement, work and responsibility. His subsequent career, brief though it was, showed that these early reactions were the mark of the man. His enthusiasm for everything - medicine, for research, for this Society, for painting, for his family, was the characteristic that remains most firmly with me. This Society will always have reason to be grateful for his contributions to its welfare; its high standing and continuing contribution to research will be the best memorial we can offer him – Tony, the research worker, Tony, the man"

His obituary is in the Medical Journal of Australia, January 21, 1967. A distinguished number of individuals have given the Edwards Oration over the years.



PAST EDWARDS ORATORS

1968	Professor Charles RB Blackburn “Excitement and Responsibility”
1969	Professor Austin E Doyle “Research and the Medical School”
1970	Professor Barry G Firkin “The University Teaching Hospital”
1971	Professor Paul I Korner “Medical Speculators and Accumulators”
1972	Dr Bryan Hudson “Clinical Departments in Teaching Hospitals – A Graft versus Host Reaction?”
1973	Dr Derrick Rowley “Motivations in Medical Research”
1974	Prof I Maddocks “Home Thoughts from Abroad”
1975	Professor David Maddison “What's Wrong with Medical Education?”
1976	Professor NF Stanley “Medical Research and Tropical Ecololgy - Global and Australian Scenes”
1977	Sir Gustav Nossal “Priorities in Scientific Research During a Troubled Age”
1978	Dr Chev Kidson “Medicine and Man: Challenges in Several Worlds”
1979	Professor Charles RB Blackburn “Perceptions of Research: People, Projects and Priorities”
1980	Sir Geoffrey M Badger “Australian Science and Technology Council's Attitudes to and Concepts of the Future of Medical Research in Australia”
1981	Professor Gordon L Ada “The Sage of Recombinant DNA”
1982	Professor Roger V Short “Contraceptive Effects of Breast Feeding”
1983	Professor Bede Morris “Unnatural Selection and the Destiny of Humanity”
1984	Dr Bob Brown “Space Age Society - Should We Go Back to the Wilderness”
1985	Mr Robyn Williams “What is Science For - Does Anyone Here Know?”
1986	Professor Barry G Firkin “The Clinical Investigator”
1987	Professor Frank Fenner “The Life and Times of Sir Macfarlane Burnet”
1988	Professor David G Penington AC “The Politics of Scientific Research in Australia in 1988”
1989	The Hon Dr Neal Blewett “Medical Research - Contributing to Australia's Prosperity”
1990	Professor Anthony J Wicken “The Clever Country and the Phantom of the Opera”
1991	Professor John Shine “Medical Research - Basic or Applied”
1992	Prof Lawrie Powell, AC “Fantasies, Fallacies and Facts in Australian Medical Research”
1993	Professor Donald S Coffey “Science, Creativity and Human Destiny”
1994	Professor Peter Goodfellow “The human genome project: the spectre of the past and the promise of the future”
1995	Professor Anne Woolcock “Asthma: What do we know in 1995”
1996	Professor John Mattick “The impact of genome projects on medical research and the future of medicine”
1997	Professor Grant Sutherland “The genetics of intellectual disability”
1998	Professor Suzanne Cory “How cells live and die”
1999	Professor M von Itzstein “Caroigtdrates; new directions in drug discovery”
2000	Professor Rob Moodie “Life, leisure and longing; public health in 2050”
2001	Professor Peter Andrews “Medical Research – from bench to business”
2002	Professor Peter Doherty “Cell mediated immunity in virus infections”
2003	Professor John Funder “Through a glass darkly – reflections from the back of the mirror”
2004	Dr David Vaux “Regulation of inhibitor of Apoptosis Proteins by RINGs”

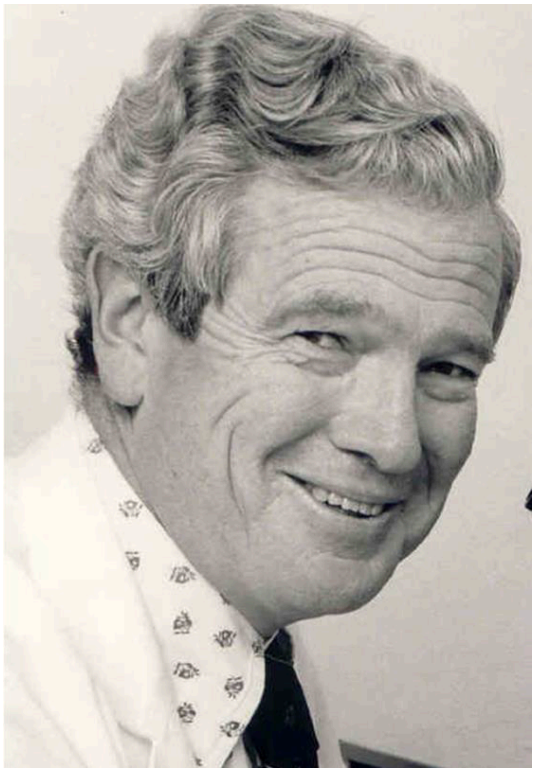
2005	Professor David de Kretser “The roles of the inhibins, activins and follistatins: A thirty year journey from reproduction to inflammation and beyond”
2006	Professor Chris Goodnow “Translating the genome sequence into health: how many genes protect us from autoimmune disease and which are they?”
2007	Professor Julie Campbell “Regeneration of smooth muscle organs”
2008	Professor Fiona Wood “The quest for scarless healing”
2009	Professor Charles Watson “Genes that build the brain”
2010	Professor Alan Cowman “An old enemy, a new battle plan: Combating the global scourge of malaria in the genomic era”
2011	Professor Robyn McDermott “Making every effort count: How we can ensure the best of our medical research gets to those who need it?”
2012	Professor Sarah Robertson “Male to female seminal fluid signalling – intersexual war and peace”
2013	Professor Stephen Simpson “Older but Wiser: The Science of Healthy Ageing”
2014	Professor Caroline McMillan “The early origins of obesity: The embryo, environment and Epigenetics”
2015	Professor Nicholas Talley “Chronic unexplained dyspepsia: A new disease model”
2016	Professor Alan Trounson “Pushing the boundaries of biology and technology: A non-linear model is rewarding but can create tensions”
2017	Professor Chennupati Jagadish “Nanotechnology and Medicine: Opportunities and Challenges”
2018 2019	Professor Paul Torzillo “Is there role for evidence in Indigenous health?” Professor Christobel Saunders AO “From discovery…to practice: Lessons learned from trying to move research ideas into practice and policy”
2020	Dr James Muecke, AM “Harnessing your passion to change the world”
2021	Professor David Craik “A journey of discovery on the trail of peptides and proteins”
2022	Professor Jenny Graves “Sex, genes and chromosomes - a life in comparative genomics”
2023	Professor Emily Banks, AM
2024	Professor Marguerite Evans-Galea AM
2025	Emeritus Professor Paul Young, “A Biomedical Translation Story: Lessons from the Molecular Clamp Journey”

FIRKIN ORATION

Born in Newcastle, NSW in 1930, Prof Barry G Firkin enrolled in Medicine, graduating with honours in 1954. In 1960 Prof Firkin, Director of the Clinical Research Unit at Royal Prince Alfred Hospital in Sydney drew together some like-minded people (Prof Alan Skyring, Prof Jim McRae and Prof Ruthven Blackburn) who had been influenced by the American Federation for Clinical Research to establish the Australian Society for Medical Research.

Barry became the first President of ASMR and also its first financial member. The annual scientific meeting (National Scientific Conference) has been held every year since 1961.

Barry passed away in 2001. The ASMR owes a debt of gratitude to Barry for his pivotal role in the establishment of ASMR. His vision, courage and tenacity in those early years set the groundwork for the growth and progress of a vigorous organisation which has successfully maintained its ideals while pursuing its goals. Barry was appointed a Life Member in 1983 with the oration in his honour commencing in 1993.



PAST FIRKIN ORATORS

1993	Professor Y H Tan “Building a Biotech Frontier in Asia”
1994	Dr Harvey Alter “Serendipity in medicine: the unexpected payoffs of non-directed research”
1995	Professor Albert Osterhaus “Problems with the development of an Aids vaccine”
1996	Professor Ralph Bradshaw “Dancing to the big band: the role of government in the support of basic research”
1997	Dr Keith Godfrey “Foetal programming and adult disease”
1998	Professor Sir Richard Doll “Tobacco: a medical history”
1999	Professor David Botstein “Genomic-wide patterns of gene expression in cancer”
2000	Dr Peter Goodfellow “From bench to bedside, from genomes to drugs”
2001	Dr Edison Liu
2002	Professor Ed Harlow “DNA tumour viruses and cancer”
2003	Dr Peter Jones “The fundamental role of epigenetic events in cancer”
2004	Professor Jeff Robbins “Modeling human cardiomyopathies via genetic manipulation in animal models”
2005	Professor Kenneth S Korach “Loss of estrogen receptor activity: Consequences in Endocrine histology”
2006	Professor Richard Flavell “Dynamic modulation of interchromosomal interactions during T cell differentiation”
2007	Professor Mina Bissell "From models to therapy: putting the Mammary Gland & Breast Cancer in Context’
2008	Professor Michael Karin
2009	Professor Jonathan Flint “Candidate gene studies in psychiatric disorders”
2010	Professor David Sinclair “The Sirtuins: Defence enzymes that counteract diseases”
2011	Professor Sir Mason Durie “Transforming Mental Health Services: Indigenous Pathways”
2012	Professor Colin Sibley “Placenta Not After Birth”
2013	Professsor Rafael de Cabo “Dietary interventions for healthy aging”
2014	Professor Josef Penninger “Haploid stem cells”
2015	Professor Eran Elinav “Host microbiome interactions in health and disease”
2016	Professor Alim-Louis (Ben) Benabid “From Bench to Bedside, from Physics to Medicine,from Electrons to Photons”
2017	Dr Bon-Kyoung Koo “CRISPR/Cas-assisted genetics in intestinal organoids”
2018 2019	Dr Honor Harger “Curating science: The mutual symbiosis of art and scientific exploration” Professor Daniel J Drucker “Translational biology and mechanistic insights from the glucagon-like peptide system”
2020	Professor Kanta Subbarao “COVID-19: A virologist’s view”
2021	Professor Jane E Harding “Caring for newborn babies for life”
2022	Professor Matt Brown “An Adventure in Translational Medicine”
2023	Professor Ian Reid
2024	Professor Frank Lin
2025	Professor Jo Brown, “Integrative approaches to improve outcomes in at risk pregnancies: a journey from physiological mechanisms to clinical utility”

2026 AWT EDWARDS ORATION

Distinguised Professor Madhu Baskaran

RMIT University



Distinguished Professor Madhu Bhaskaran is multi-award-winning electronics engineer and innovator. She is a Fellow of the Australian Academy of Technological Sciences and Engineering. She co-leads the Functional Materials and Microsystems Research Group at RMIT University which she established in 2010. She is the Director of the Discovery to Device Medtech Prototyping Facility at RMIT University. Her work on electronic skin and wearable sensors has been patented, and her group now works collaboratively with multiple industry and design partners to commercialise the technology for healthcare and aged care. She is a passionate advocate for equity and diversity and she proudly co-leads Women in STEMM Australia.

2026 FIRKIN ORATION

Professor Yugeesh Lankadeva

The Florey



Yugeesh Lankadeva is a Professor in the Florey Department of Neuroscience and Mental Health (The Florey), Department of Critical Care at the University of Melbourne and Department of Anaesthesia at Austin Hospital. Professor Lankadeva is Head of Stroke and Critical Care Priority Research Area, and Head of Translational Cardiovascular and Renal Research at The Florey. Professor Lankadeva is a NHMRC Emerging Leader [Level 2] Fellow, has over 110 publications, is an inventor on 6 patents, and has secured over $30 million in competitive research funding, including $15 million as Chief Investigator A. His discoveries in sepsis and heart surgery have translated into 10 clinical trials across USA, Europe, Asia, and Australia. Professor Lankadeva is CEO of Medtech start-up company, PanAscea Pty Ltd, with the aim of advancing a breakthrough therapy for sepsis worldwide.

PLENARY SPEAKERS



Day 1 · Monday 16 November · 09:00–09:45

Distinguished Professor Madhu Bhaskaran

RMIT University

"Bridging the Gap: Cross-Sector Partnerships to Translate Soft Electronic and Biosensor Technologies"

Distinguished Professor Madhu Bhaskaran is a multi-award-winning electronics engineer and innovator. She is a Fellow of the Australian Academy of Technological Sciences and Engineering. She co-leads the Functional Materials and Microsystems Research Group at RMIT University which she established in 2010. She is the Director of the Discovery to Device Medtech Prototyping Facility at RMIT University. Her work on electronic skin and wearable sensors has been patented, and her group now works collaboratively with multiple industry and design partners to commercialise the technology for healthcare and aged care. She is a passionate advocate for equity and diversity and she proudly co-leads Women in STEMM Australia.



Day 2 · Tuesday 17 November · 09:00–09:45

Dr Fernando Gordillo Altamirano

Alfred Health and Monash University

"Phage therapy in Victoria, the good, the bad, and the ugly"

Fernando Gordillo Altamirano, originally from Ecuador, graduated as a medical doctor from the Pontificia Universidad Católica del Ecuador (2014). Taking a career pivot towards biomedical research, he moved to Australia where he completed a Masters in Infection and Immunity at The University of Sydney (2017) and a PhD in Microbiology at Monash University (2021). Integrating his clinical background, he now runs the wet lab component of The Alfred Hospital's VICPhage program, Victoria's first clinical service offering phage therapy, the use of viruses that kill bacteria, to patients with antibiotic-resistant infections. His research has been published in journals including Nature Medicine, Nature Microbiology, and Clinical Microbiology Reviews. Fernando is a passionate science communicator, with appearances on documentaries, radio, podcasts and television, including the recurring segment Health Check on ABC News Breakfast.



Day 3 · Wednesday 18 November · 09:00–09:45

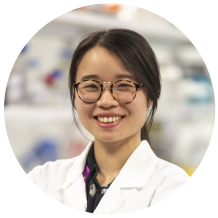
Professor Yugeesh Lankadeva

The Florey

"Impact of integrating academic, clinical, and industry partnerships to improve health outcomes for critically ill patients"

Yugeesh Lankadeva is a Professor in the Florey Department of Neuroscience and Mental Health (The Florey), Department of Critical Care at the University of Melbourne and Department of Anaesthesia at Austin Hospital. Professor Lankadeva is Head of Stroke and Critical Care Priority Research Area, and Head of Translational Cardiovascular and Renal Research at The Florey. Professor Lankadeva is a NHMRC Emerging Leader [Level 2] Fellow, has over 110 publications, is an inventor on 6 patents, and has secured over $30 million in competitive research funding, including $15 million as Chief Investigator A. His discoveries in sepsis and heart surgery have translated into 10 clinical trials across USA, Europe, Asia, and Australia. Professor Lankadeva is CEO of Medtech start-up company, PanAscea Pty Ltd, with the aim of advancing a breakthrough therapy for sepsis worldwide.

INVITED MID-CAREER RESEARCHER TALKS



Day 1 · Monday 16 November · 11:40–12:15

Dr Anna Wang

Centre for Eye Research Australia

"Investigating pericytes and IPTNTs in the human retina"

Dr Anna Wang is an Early Career Research Fellow at the Centre for Eye Research Australia with a decade of experience studying how disease affects the retina's neurons and blood vessels. During her PhD at the University of Melbourne, she investigated retinal ganglion cell function under disease stress, and this work led her to a postdoctoral position at UC Berkeley, where she discovered a previously unknown type of retinal ganglion cell, published in Nature. Her research combines cutting-edge imaging techniques with human and mouse tissue models to understand retinal disease, and has been recognised through competitive funding, an Early–Mid Career Researcher Achievement Award and a fellowship.



Day 1 · Monday 16 November · 11:40–12:15

Associate Professor Alisa Glukhova

WEHI

"Structural basis for inefficient G protein coupling in Class F GPCRs"

A/Prof Alisa Glukhova is a Snow Medical and NHMRC Fellow. She earned her PhD in Chemical Biology in 2014 from the University of Michigan, where she worked on solving structures of lipid-modifying enzymes. During her postdoctoral training at Monash Institute of Pharmaceutical Sciences, she used X-ray crystallography, cryo-electron microscopy, and pharmacology to study G protein-coupled receptors. Since 2020, she has led a lab at WEHI focused on understanding the structural and biochemical aspects of the Wnt signalling pathway, an important pharmacological target for treating many cancers.



Day 2 · Tuesday 17 November · 11:10–11:45

Dr Hui-Fern Koay

Peter Doherty Institute for Infection and Immunity

"Beyond the textbook T cell: Exploring and exploiting unconventional T-cell lineages"

Dr Fern Koay is an NHMRC Investigator Fellow and laboratory head at the Peter Doherty Institute for Infection and Immunity, University of Melbourne. Her research focuses on unconventional T cells, including MAIT, NKT and γδ T cells, and their roles in tissue and tumour immunity. Her work helped define key foundations of MAIT cell biology, including their functional heterogeneity, thymic development and transcriptional programming. Her laboratory investigates how unconventional T-cell populations adapt and interact as an immune network, alongside new approaches to manipulate MAIT cells and the MR1 antigen-recognition axis for immunotherapy. She serves on the executive committee of the international CD1-MR1 Society.



Day 2 · Tuesday 17 November · 11:10–11:45

Associate Professor Joshua Wiley

Monash University

"SLEEP AND CANCER: WHAT IS DISRUPTED, AND WHAT WE CAN FIX"

Associate Professor Joshua Wiley is an NHMRC Emerging Leadership Fellow and Director of Graduate Research in the School of Psychological Sciences at Monash University, where he leads the Behavioural Medicine Lab in the Turner Institute for Brain and Mental Health. He completed his PhD in health psychology at UCLA. His research combines sleep science, behavioural medicine, digital health and advanced statistical methods to understand how sleep, stress and mood change in daily life, and to develop personalised, scalable interventions, with a focus on people affected by cancer.



Day 3 · Wednesday 18 November · 11:20–11:55

Dr Brooke Patterson

La Trobe University

"Female, woman, and/or girl athlete injury prevention: Integrating evidence into practice to promote safer sport"

Dr Brooke Patterson is a physiotherapist and a current Australian Research Council Research Fellow at the La Trobe Sport and Exercise Medicine Research Centre. Her PhD investigated posttraumatic osteoarthritis after ACL reconstruction, while her post-doctoral program focusses on reducing knee injuries and concussion in women's collision sports. She has published 68 peer-reviewed articles and obtained >$14M in competitive research funding. She co-created and evaluated Prep-to-Play, an injury prevention program now embedded in community women's and girls' Australian Football, and her work has been recognised by multiple awards, including the 2026 Victorian Premier's Health & Medical Research Excellence Award. A former elite Australian Football player and current youth girls coach, Brooke brings credibility spanning research, clinical practice, and the playing field.



Day 3 · Wednesday 18 November · 11:20–11:55

Dr Patrick Lelliott

Baker Heart and Diabetes Institute

"Investigating the health impacts of micro and nanoplastics: models, measurement and modes of toxicity"

Dr Patrick Lelliott is a group leader in the Cardiac Cellular Systems lab at the Baker Heart and Diabetes Institute. He leads a research program generating standardised, real world relevant micro and nanoplastics, ways to detect and characterise these minute particles in human tissues, and mechanisms underlying their potential health impacts.

WORKSHOPS & PANELS

PANEL: Career Pathways in Research

Day 1 · Monday 16 November · 15:45–17:15

Explore career opportunities beyond academia and hear from researchers working across biotech, industry, clinical research, policy-making, teaching and start-ups, sharing how they built their careers.



CHAIR

Dr Ebony Monson

La Trobe University

Dr Ebony Monson is an NHMRC research fellow and lab head within the department of Biochemistry and Chemistry at La Trobe University. Her research focuses on developing novel antiviral therapies, using lipid droplets as a model. In her spare time, she also runs the not-for-profit science communication event, Nerd Nite!



CO-CHAIR · FROM RESEARCH TO A TEACHING-FOCUSED CAREER

Associate Professor Jessica Borger

Monash University

Professor Jessica Borger is an immunologist, educator, author and advocate for diversity and inclusion in STEMM. She is Director of Education at Monash University's School of Translational Medicine, where she leads undergraduate, graduate and PhD education across 18 departments, following an extensive academic and research career. She is also an editor for Immunology & Cell Biology and the best-selling author of Beyond the Pipeline, advocating for gender equity and inclusive careers in STEMM. Her contributions to immunology education and diversity have been recognised through several prestigious awards, including the 2024 ASI Cheers-Buchan Education Award.



BIOTECH SECTOR

Dr Goh Kai Lyn

Kiora Pharmaceuticals

Kai Lyn is an optometrist with a PhD in Ophthalmology from The University of Melbourne. She has worked in private clinical practice and optometry education, and coordinated clinical trials. She is now an Associate Clinical Project Manager at a small biotech company that develops treatments for diseases of the back of the eye.



CONTRACT RESEARCH ORGANISATION (CRO) SECTOR

Dr Petra Graves

ClinChoice

Dr Petra Graves is Senior Director, Clinical Operations at ClinChoice, where she leads clinical operations teams across Australia and New Zealand. With more than 15 years' experience across biotechnology, pharmaceutical development and CROs, including Australian and US-based biotech start-ups and global CROs, she has built a career spanning operational delivery, quality oversight and leadership in clinical research. She is passionate about patient-centred research and enjoys mentoring the next generation of clinical research professionals.



POLICY AND GOVERNMENT

Dr Ekaterina Woods

Victorian Department of Health

Ekaterina Woods, MD, PhD, is a Senior Policy Officer in the System Reform team at the Victorian Department of Health, where she has worked for seven years across major health reforms, using evidence to inform policy development, budget submissions, and implementation. Originally trained as a medical doctor in Russia, Ekaterina specialised in ophthalmology and completed a PhD in the field. After moving to Australia and completing a Master of Public Health, she worked in health economics research and health technology assessment at the University of Melbourne, with a focus on food allergy and eye disease, before transitioning into government.



PATENTS AND INTELLECTUAL PROPERTY

Dr Alice West

IP Australia

Dr Alice West is a Biotechnology Patent Examiner with IP Australia. After completing her PhD in biomedical science at Monash University in 2023, investigating innate immune regulators in gastric cancer, she gained experience in research commercialisation before moving into intellectual property. She enjoys working at the intersection of science and law, assessing the patentability of cutting-edge biotechnology inventions, and supporting researchers and the next generation of STEM professionals to translate discoveries into real-world impact.



RESEARCH COMMERCIALISATION · START-UP FOUNDER AND LAB HEAD

Professor Nicholas Opie

The University of Melbourne

Professor Nicholas Opie is a biomedical engineer and world expert in neural bionics and brain–machine interfaces. He founded brain–computer interface company Synchron Inc., whose Stentrode was named in Time Magazine's Top 100 Inventions of 2021, and is founding CEO of Ultra Bionics Pty Ltd and Honorary Professor and Head of the Vascular Bionics Laboratory in the Department of Medicine at the University of Melbourne. He has taken multiple medtech devices from concept to clinic, published over 70 peer-reviewed articles and filed over 100 patents, and was elected a Fellow of the Australian Academy of Technological Sciences and Engineering in 2026.

WORKSHOP: Science Communication

Day 2 · Tuesday 17 November · 11:45–12:30

Learn how to communicate your research with impact, whether the audience is a grant panel, a conference room or the public.



DELIVERED BY

Dr Shane Huntington OAM

Australian Society for Medical Research

Dr Shane Huntington OAM is the Chief Executive Officer of the Australian Society for Medical Research. A physicist by training (PhD in photonics and imaging), he spent a decade in research before moving into strategy and leadership roles at the University of Melbourne, including in the Faculty of Medicine, Dentistry and Health Sciences and the Melbourne Academic Centre for Health. A long-time broadcaster and science communicator, he has trained thousands of researchers in communication skills, and was awarded the Medal of the Order of Australia in 2020 for service to science as a communicator.

PANEL: AI in Research

Day 2 · Tuesday 17 November · 15:45–17:15

Explore how AI is being used across the research workflow, from experiment design and data analysis to scientific writing. Hear perspectives on emerging tools, practical applications, opportunities and challenges, and how AI can be used responsibly to support research.



CHAIR

Dr Emerson Keenan

The University of Melbourne

Dr Emerson Keenan is a biomedical engineer working at the intersection of artificial intelligence and medical technology research. He is an Honorary Research Fellow within the Department of Obstetrics, Gynaecology and Newborn Health, and is leading the AI for Research Innovation program within Melbourne Medical School, which is exploring how emerging AI tools can help accelerate scientific discovery. Emerson is also co-founder and CEO of Kali Healthcare, a University of Melbourne spin-out developing an AI-powered wearable platform for maternal and fetal monitoring.



PANELLIST

Associate Professor Zhuoting (Lisa) Zhu

Centre for Eye Research Australia

Associate Professor Zhuoting (Lisa) Zhu is Head of the Ophthalmic Epidemiology Unit at the Centre for Eye Research Australia (CERA), The University of Melbourne, and Director of the WHO Collaborating Centre for Prevention of Blindness and Deafness (Australia). Her research focuses on oculomics, the concept that “the eye is a window to overall health”, and the application of artificial intelligence in ophthalmology. She has published more than 200 peer-reviewed papers, secured more than $8.6 million in competitive research funding, and her awards include the Victoria Fellowship.



PANELLIST

Associate Professor Rahul Rane

Macquarie University

Associate Professor Rahul Rane is an evolutionary computational biologist and researcher in Applied AI and Genomics at Macquarie University. Previously, he led the sovereign Applied Genomics Initiative and served as Lead Scientist and Product Owner for CSIRO's flagship Artificial Intelligence for Science 'co-scientist' platform. His work spans AI for science, genomics, synthetic biology, biosecurity and health, with a focus on accelerating scientific discovery and translating research into real-world impact.



PANELLIST

Associate Professor Sonika Tyagi

RMIT University

Associate Professor Sonika Tyagi leads the Digital Health and Bioinformatics research lab at the School of Computing Technologies, RMIT University, and is an affiliate machine learning scientist at Monash University and Alfred Health. She develops machine learning tools and applies them to biological and clinical research questions, with a focus on integrative approaches to digital health and genomics, from AI models for the diagnosis of preterm birth to the SuperbugAI flagship project. She was a finalist in the Women in AI Awards (Australia–New Zealand, 2022), received a Healthcare Innovator Award in the “AI in Health” category (2024) and was named a Brilliant Woman in Digital Health (2023).



PANELLIST

Dr Sahar Shahali

The University of Melbourne and Monash University

Dr Sahar Shahali is a Research Fellow in the O’Bryan Lab, School of BioSciences, Faculty of Science at the University of Melbourne, and the Faculty of Engineering at Monash University. She completed her PhD in Mechanical Engineering at Monash University, focusing on the application of artificial intelligence in reproductive biology and assisted reproductive technologies. Her research develops AI-based methods, particularly deep learning and computer vision, to analyse biological images and videos, including automated semen analysis, embryo assessment, and broader applications in biomedical imaging and health monitoring.



PANELLIST

Dr Rosita Shishegar

RMIT University

Dr Rosita Shishegar is a Lecturer in Artificial Intelligence and Digital Health in the School of Computing Technologies at RMIT University. She also holds appointments as an Adjunct Research Fellow in the Department of Electrical and Computer Systems Engineering at Monash University and an Honorary Scientist at Austin Health. Before joining RMIT, she was a Senior Research Scientist at CSIRO's Australian e-Health Research Centre. Her research brings together artificial intelligence, machine learning, biostatistics and neuroimaging to advance digital health and personalised medicine. She develops computational methods for analysing complex biological and clinical data, with a particular focus on understanding the onset and progression of neurodegenerative diseases, including Alzheimer's disease, Huntington's disease and Friedreich's ataxia.

FIRESIDE CHAT: Research Funding

Day 3 · Wednesday 18 November · 11:55–12:40

Hear insights and perspectives from representatives of the research funding sector through a fireside chat with the NHMRC Acting CEO Prue Torrance about traditional grant funding and a representative from the Helen Macpherson Smith Trust on broader funding options.



CHAIR

Dr Shane Huntington OAM

Australian Society for Medical Research

Dr Shane Huntington OAM is the Chief Executive Officer of the Australian Society for Medical Research. A physicist by training (PhD in photonics and imaging), he spent a decade in research before moving into strategy and leadership roles at the University of Melbourne, including in the Faculty of Medicine, Dentistry and Health Sciences and the Melbourne Academic Centre for Health. A long-time broadcaster and science communicator, he has trained thousands of researchers in communication skills, and was awarded the Medal of the Order of Australia in 2020 for service to science as a communicator.



GUEST

Prue Torrance

National Health and Medical Research Council

Prue Torrance (she/her) is the Acting Chief Executive Officer of the National Health and Medical Research Council (NHMRC), Australia's leading agency for health and medical research. She provides strategic leadership for NHMRC and works across government, the research sector and international partners to strengthen Australia's health and medical research system. Her responsibilities span research funding, health advice, ethics, research integrity and national research stewardship.



GUEST

Rosie Strickleton

Helen Macpherson Smith Trust

Rosie Strickleton is the Program Manager at Helen Macpherson Smith Trust. She has more than a decade’s experience across the not-for-profit and philanthropic sectors in Australia and the UK, managing funding programs for private and public funders. Her experience includes grant making, strategic innovation, and supporting organisations to develop and fund work that responds to complex challenges.

WORKSHOP: Grant Writing: Consumer and Partner Engagement and Co-Design

Day 3 · Wednesday 18 November · 13:25–14:55

Consumer and partner engagement is a critical component of most health and medical research projects (including NHMRC and MRFF-funded projects). This session will help researchers to better understand:

- the importance of consumer, community and partner involvement in their project planning, execution and translation
- the spectrum of consumer engagement processes and practices including co-design
- how to embed consumer and partnerships within their projects and grant applications
- what genuine co-investment by partner organisations looks like, including co-contribution of funds, and tangible and intangible in-kind contributions.



DELIVERED BY THE GRANTED GROUP

Professor Devanshi Seth

GrantEd Health & Medical Research Stream Lead

For almost two decades, award-winning medical geneticist Devanshi Seth has been turning cutting-edge genomic science into real-world health impact. She has built and led international research teams, pioneered work in liver disease genomics, and founded Australia's Genetics of Liver Disease Research Program and the multinational GenomALC Consortium. Her expertise stretches from precision medicine and research leadership to governance, equity and diversity. She knows great research when she sees it, and more importantly, knows how to help make its importance impossible to miss in a competitive grant funding environment.

WORKSHOP: Science for Social Media

Day 3 · Wednesday 18 November · 15:20–16:20

Learn how to build your presence online, increase the visibility of your research, and expand your reach using social platforms to share your science.



DELIVERED BY

Dr Véronique Paris

The University of Melbourne

Dr Véronique Paris is a medical entomologist and science communicator at the University of Melbourne, where she researches mosquitoes, disease transmission and One Health. Alongside her research, she shares science online, where she has built a community of more than 40,000 followers, with her posts reaching more than 50 million views. She uses social media to connect research with the public, build communities, and create research and science communication opportunities. In this workshop, she'll share what she has learned from using social media as both a scientist and communicator.

ASMR PETER DOHERTY LEADING LIGHT AWARD

The ASMR Peter Doherty Leading Light Award recognises the outstanding contributions of Australian mid-career researchers (5 – 12 year post-doctoral). The name of this award the ASMR Peter Doherty Leading Light Award is in recognition of Professor Peter Doherty's career achievements, scientific accomplishments, and his ongoing support and mentoring of up and coming researchers.

This award will be presented annually for the best scientific paper by a mid-career researcher.

Australia's mid-career health and medical researchers represent the future leadership of the sector, and the "ASMR Peter Doherty Leading Light Award" will be one important initiative to foster this future leadership.

ORAL PRESENTATION ABSTRACTS

Session 1 — Bioengineering, devices & digital health

S1-01 · Session 1 · Monday 10:10 · Presenter: Ganganath Perera

Saliva-based Conductometric Multiplex Biosensor for Rapid Point-of-Care Cardiac Risk Assessment

Ganganath Perera[1], Jean Pierre Ndabakuranye[1], Madhu Bhaskaran[1], and Sharath Sriram[1]

[1]Functional Materials and Microsystems Research Group and the Micro Nano Research Facility, RMIT University, Melbourne, VIC 3000, Australia.

Background and Aims: Cardiovascular diseases remain a major heath burden, while conventional cardiac biomarker testing generally required blood collection, laboratory infrastructure, and specialised instrumentation. Saliva offers an attractive non-invasive alternative for point-of-care assessment. The main aim of this work is to develop a multiplex high resistivity silicon (HR-Si) conductometric biosensor for rapid salivary cardiac risk assessment.

Methods: RMIT-patented HR-Si conductometric biosensors were designed and functionalised with custom-made molecularly imprinted nanoparticles (nanoMIPs) specified for targeted salivary biomarkers (C reactive protein (CRP), cardiac troponin I (cTnI), brain natriuretic peptide (BNP), and N-terminal proBNP (NT-proBNP)). The electrical signal responses were measured before and after immobilisation of salivary biomarkers. The sample incubation time was 10 minutes, and signal measurement time was 1 minute The signal responses were wirelessly monitored via a mobile app.

Results: Linear signal responses were obtained for all four biomarkers with increased concentrations. All four biomarkers were selectively detected with a detection limit ×100 lower than the reported healthy levels in saliva. Detection of two additional biomarkers in saliva (cardiac troponin T (cTnT) and D-dimer) and development of multiplex sensor for detection of all six biomarkers are in progress.

Conclusions: High-sensitive HR-Si conductometric biosensor was developed for rapid detection of four cardiac biomarkers in saliva with the future development towards a multiplex point-of-care platform to detect six cardiac biomarkers and followed by clinical validation. This significance of this technology is to reduce pressure on emergency departments and enable cardiac screening in settings where laboratory testing is less accessible.

S1-02 · Session 1 · Monday 10:20 · Presenter: Sreekanth Srirangam Prathivadibayankaram

Chronic kidney disease detection and management through swift detection of biomarkers using HR-Si conductometric biosensor

Sreekanth S P[1], Ganganath S Perera[1], Jean Pierre Ndabakuranye[1], Madhu Bhaskaran[1], Sharath Sriram[1].

[1]Functional Materials and Microsystems Research Group and the Micro Nano Research Facility, RMIT University, Melbourne, VIC 3001, Australia.

Background and Aims: Chronic kidney disease (CKD) is a non-communicable chronic disease, identified as a hidden epidemic and which is increasing the load on the dialysis care and kidney transplantation. The current clinical methods for CKD detection are widely based on the urine albumin-to-creatinine ratio (UACR) test or proteinuria in urine, which inherit longer processing time. The unmet early detection of different aetiologies of CKD and medical interventions lead to end stage kidney disease (ESKD). The renal replacement via regular dialysis or by kidney transplantation, the only options available for ESKD. For a successful kidney transplant, regular drug monitoring to maintain immune suppression within therapeutic window is mandatory. Hence, the management of CKD involving detection, treatment, and renal replacement is critical. This research work focused on developing precision biosensors that function as point-of-care (PoC) screening and aid in the management of CKD.

Methods: HR-Si conductometric biosensors was fabricated on a high-resistive silicon wafer following photolithography process of micro-fabrication technology. The biosensor houses the antibody molecules specific to a target biomarker on its surface though chemical bonding and the interaction of the biomarker present in any of the bodily fluid with antibody molecules produce change in electrical resistance proportional to the concentration of the biomarker.

Results: The fabricated HR-Si conductometric biosensor was employed for the sensitive PoC detection of CKD biomarkers UACR, beta-2 microglobulin (β2MG), epidermal growth factor (EGF), and CD163 in urine, aimed at CKD detection and management of two diseases autosomal dominant polycystic kidney disease (ADPKD) and antineutrophil cytoplasmic antibody-associated vasculitis (ANCA-AAVs). To support the PoC therapeutic drug monitoring in kidney transplant patients, biosensor was utilised for accurate measurement of tacrolimus and mycophenolic acid.

Conclusions: This research work successfully demonstrated the employment of HR-Si conductometric biosensor in sensitive detection of CKD biomarkers, which can function as PoC screening.

S1-03 · Session 1 · Monday 10:30 · Presenter: Akila Hewa Thondilege

Markerless Ground Reaction Force Estimation for Clinical Biomechanical Assessment Using Dynamic Hypergraph Neural Networks

Surachat Dolayanukloh[1], Alexander Mewis[1], **Akila Hewa Thondilege**[2], Ethan Goan[2], Glen Lichtwark[3], Luke Kelly[4], Alina Bialkowski[1].

[1]School of Electrical Engineering and Computer Science, The University of Queensland. [2]School of Electrical Engineering & Robotics, Queensland University of Technology [3]School of Exercise and Nutrition Science, Queensland University of Technology. [4]School of Allied health, Sport and Social Work, Griffith University.

Background and Aims: Ground reaction forces (GRFs) are important biomechanical indicators for assessing gait, balance, mobility, and lower-limb function, supporting clinical decision-making in rehabilitation and musculoskeletal healthcare. However, their measurement typically requires specialised laboratories equipped with force plates and marker-based motion capture, limiting accessibility in clinical and community settings. This study aims to develop an accurate, interpretable, and efficient markerless system for estimating vertical GRFs from multi-view video, facilitating more accessible biomechanical assessment.

Methods: Synchronised multi-view videos were processed using Pose2Sim to detect and triangulate 3D body keypoints. These trajectories were used to fit an anatomically plausible musculoskeletal model, derive body-segment kinematics, estimate centre-of-mass dynamics, and generate a Hunt–Crossley physics-based force prior. Inputs were transformed into a pelvis-centred canonical coordinate frame. The proposed architecture combines a graph-transformer for surface keypoints with a dynamic hypergraph encoder for segment-level kinematics. Bidirectional cross-attention integrates pose, kinematic, anthropometric, and dynamic features to estimate per-foot vertical GRF trajectories. The keypoint encoder was pretrained on large-scale motion data using V-JEPA-based self-supervised learning.

Results: Evaluation on held-out BioCV subjects performing jumps, hops, running, and walking achieved per-trial Pearson correlation coefficients of 0.9436–0.9762 against force-plate measurements, with the highest accuracy observed for jumping and hopping. Ablation studies demonstrated the contributions of dynamic hypergraph learning, self-supervised pretraining, and physics-based simulations. Hyperedge analysis revealed movement-specific relationships, with locomotor activities emphasising trunk and core connections and ballistic movements showing greater upper-limb involvement.

Conclusions: The proposed approach demonstrates the potential of combining dynamic hypergraph learning with physics-informed modelling for accessible, markerless vertical GRF estimation. With further validation in clinical populations and real-world settings, this technology could support objective mobility assessment, rehabilitation monitoring, and functional evaluation beyond specialised biomechanics laboratories.

S1-04 · Session 1 · Monday 10:40 · Presenter: Romana Nasrin

Moldable microchanneled polyHIPE scaffolds: a novel biomimetic approach to cranial defect reconstruction

Romana NASRIN[1], Stephen J GOLDIE[1,2], Mikäel MARTINO[1], Jessica E FRITH[1], Neil CAMERON[1,3,4]

[1]Monash University, Melbourne, Australia, [2]Eastern Health, Melbourne, Australia, [3]University of Warwick, Coventry, U.K., [4]Nanotechnology and Catalysis Research Centre (NANOCAT), Universiti Malaya, Kuala Lumpur, Malaysia.

Background: Traditional bone grafting and rigid implants are often limited by donor site morbidity, poor contour integration, and mechanical failure in complex segmental defects. There is a critical need for an "off-the-shelf," injectable solution that provides both immediate structural support and long-term osteoinduction.

Objectives: This study evaluates a novel, 3D-printed, microchanneled polyHIPE (polymerized high internal phase emulsion) scaffold designed to facilitate rapid bone regeneration in critical-sized cranial defects.

Methods: Microchanneled dipentaerythritol penta/hexa-acrylate (DPEHA) polyHIPE scaffolds were engineered with interconnected open-cell porosity. These scaffolds were processed into moldable particles and suspended in a fibrin gel carrier. *In vitro* performance was assessed via mesenchymal stromal cell (MSC) proliferation and differentiation. *In vivo* efficacy was validated using a murine critical-sized cranial defect model.

Findings: *In vitro* analysis demonstrated superior MSC viability and deep cellular infiltration. Notably, MSCs showed a spatial preference for differentiation along the microchannel curvatures, confirmed by alkaline phosphatase (ALP) staining and mineralization assays. Quantitative gene expression profiles confirmed robust osteogenic lineage commitment. In vivo application of the injectable polyHIPE-fibrin composite resulted in significant bone volume recovery within the host cranium.

Conclusions: These moldable polyHIPE scaffolds represent a versatile advancement in craniofacial and orthoplastic reconstructive surgery. By combining the precision of 3D printing with the ease of a moldable delivery system, this technology offers a promising, minimally invasive alternative for reconstructing complex bone voids and non-union fractures.

S1-05 · Session 1 · Monday 10:50 · Presenter: Sadjad Khosravimelal

A Hybrid Biofabrication Approach for Developing Human-Cell-Based 3D Skin Models

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The skin provides an essential barrier against physical damage, chemical exposure, and microbial invasion. When this barrier is disrupted, effective wound healing becomes critical to restoring tissue integrity and preventing infection. However, conventional animal models have limitations related to ethical considerations and differences between animal and human skin, highlighting the need for reliable human-relevant models. Three-dimensional (3D) in vitro skin constructs offer a promising alternative for investigating skin biology, wound healing, and potential therapeutic treatments. In this study, a biomimetic 3D skin model was developed by combining melt electrowritten polycaprolactone (PCL) scaffolds with gelatin methacrylate (GelMA) bioinks to support human foreskin fibroblasts (HFFs) and N/TERT-1 keratinocytes. The PCL framework provided mechanical support and separated the construct into dermal and epidermal compartments, while the cell-laden GelMA matrices provided a hydrated environment for cell growth. The dermal compartment was fabricated by depositing and photocrosslinking fibroblast-containing GelMA, followed by inversion of the construct and deposition of a keratinocyte-containing GelMA layer to establish the epidermal compartment. Material characterisation demonstrated that GelMA exhibited shear-thinning behaviour suitable for bioprinting and formed a hydrogel with a storage modulus of approximately 9 kPa following photocrosslinking. The PCL framework exhibited approximately 70% porosity and a tensile modulus of approximately 120 kPa, providing a porous yet mechanically supportive structure. Biological assessments demonstrated high cell viability over seven days following encapsulation. Barrier function was further evaluated using Lucifer Yellow, with restricted diffusion indicating the development of barrier properties. Histological analysis after 21 days of air–liquid interface culture revealed a stratified epidermal layer. Together, these findings demonstrate the feasibility of integrating a mechanically supportive polymer framework with cell-laden hydrogels to engineer a structured, human-cell-based skin model. By combining controlled scaffold architecture, bioprinting compatibility, and epidermal stratification, this platform provides a foundation for further development of reproducible in vitro models for studying skin physiology, wound healing, and the evaluation of therapeutic and cosmetic products.

S1-06 · Session 1 · Monday 11:00 · Presenter: Bhavana Nayer

Treg-derived IL-10 suppresses inflammatory macrophage states during muscle regeneration and enables an immunocytokine-based therapy

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Background and Aims: Regulatory T cells (Tregs) are among the most promising cellular drivers of tissue repair and regeneration, yet the mechanisms underlying their pro-regenerative effects remain poorly defined. This has limited efforts to translate their capabilities into scalable therapies. Here, we aimed to identify the dominant Treg-derived effector mechanism in tissue regeneration, combining *in vitro* screening with a mouse model of volumetric muscle loss (VML) injury.

Methods: Building on our previous finding that Tregs exert their regenerative effects through monocytes/macrophages (Mo/MΦ) in injured tissue, we screened Treg-derived candidate mediators in bone marrow-derived macrophages (BMDMs) *in vitro*. The leading candidate was further investigated *in vivo* using mice with a conditional, Treg-specific knockout, to assess muscle regeneration post-VML by microCT-based quantification of muscle volume, histology, and profiling the injury-site immune infiltrate by flow cytometry. This informed the development of a cell-free therapeutic strategy, ultimately tested in aged and diabetic models of impaired healing.

Results: IL-10 emerged as the dominant Treg-derived regulator of Mo/MΦ phenotype *in vitro*. *In vivo*, loss of IL-10 from Tregs significantly impaired muscle regeneration post-VML and drove excessive accumulation of pro-inflammatory Mo/MΦ, along with NK and T cells, at the injury site. Guided by this mechanism, we engineered an immunocytokine that simultaneously delivered IL-10 while neutralising pro-inflammatory signalling. Its local delivery post-injury promoted regeneration, dampened inflammatory immune cell accumulation, and rescued impaired healing in mice lacking Treg-derived IL-10. Its efficacy extended to aged and diabetic models, contexts marked by reduced Treg abundance.

Conclusions: We showed that Treg-derived IL-10 is a non-redundant component of the immune regulatory network during regeneration, restraining inflammatory immune cell accumulation at the site of injury. We also demonstrated that this mechanistic understanding could be translated to engineer an effective cell-free therapeutic, providing a generalisable strategy to develop next-generation immunotherapies for tissue repair and regeneration.

S1-07 · Session 1 · Monday 11:10 · Presenter: Vincent Yuan

The evidence gap in AI-enabled medical devices in Australia: a cross-sectional study

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Background and Aims: Artificial intelligence (AI)-enabled medical devices are increasingly being integrated into healthcare. However, international evidence suggests that many of these devices enter the market with limited regulatory oversight and publicly available evidence on their safety and effectiveness. We aimed to characterise the availability of clinical information on safety and effectiveness for AI-enabled medical devices listed on the Australian Register of Therapeutic Goods (ARTG).

Methods: This cross-sectional study included all AI-enabled medical devices listed on the ARTG as of 1 May 2026. For each device, two reviewers searched for publicly available clinical information that assessed the safety or effectiveness of the device on the United States Food & Drug Administration (FDA) list of AI-enabled medical devices, PubMed, Embase, Google Scholar, the World Health Organisation's International Clinical Trials Registry Platform and the device manufacturer's website.

Results: 146 unique devices were included. More than half (n=82, 56%) of devices had no publicly available study information on clinical safety or effectiveness. Where study information was available (n=64), it was located in FDA summary documents (n=38, 59%), publications (n=46, 72%) or trial registrations (n=7, 11%). Over three quarters of these devices had at least one study that reported participant's age (n=50, 78%) and a quarter that reported race/ethnicity (n=16, 25%). No devices publicly reported participants' socioeconomic position. Most devices were reliant on studies that used a retrospective observational study design (n=46, 72%).

Conclusions: Only a minority of AI-enabled medical devices approved for use in Australia have publicly available information on clinical safety and effectiveness. When this information did exist, it was predominantly based on retrospective study designs and contained limited reporting on age, race and socioeconomic data. Addressing these gaps is imperative for evidence transparency and integration into clinical practice.

S1-08 · Session 1 · Monday 11:20 · Presenter: Amany Gouda-Vossos

Discover, Access, Analyse: Enabling Secondary Use of Health Data

Amany Gouda-Vossos[1]

[1]Australian Research Data Commons

Background and Aims: Data sharing in health and medical research offers significant potential to uncover new discoveries and increase efficiency in the research process. However, health data is often difficult to discover, access, and reuse beyond it's original purpose. To address this challenge, the Health Studies Australian National Data Asset (HeSANDA) has developed national infrastructure, guidance and resources through a practical "Discover, Access, Analyse" approach to secondary data research.

Methods: Established through the Australian Research Data Commons (ARDC), HeSANDA has grown into a collaborative network of more than 100 organisations, including universities, medical research institutes, health services, and clinical trial networks.

To support researchers in finding data, HeSANDA launched Health Data Australia (HDA), a national discovery service enabling researchers to find and request access to health datasets, while data custodians retain control over access decisions.

To enable responsible access to health data, practical guidance to address legal, ethical and governance considerations for data sharing, informed by stakeholder consultation and benchmarking of ethics review practices was developed in collaboration with experts at CT:IQ.

To guide researchers to analyse data effectively, a secondary data use framework developed alongside the NHMRC Clinical Trials Centre (USyd), providing researchers with scenarios for identifying potential applications of existing data, including evidence synthesis, secondary analyses, reproducibility and validation, and education and methods development.

Results: Together, these initiatives establish a practical pathway for researchers to identify secondary research opportunities, discover relevant datasets, navigate access requirements and undertake responsible data reuse.

Conclusions: The "Discover, Access, Analyse" framework demonstrates how data reuse can be incorporated throughout the research lifecycle. By combining national infrastructure with practical guidance and resources, this work aims to increase researcher's capability to use existing datasets, expand research opportunities, reduce unnecessary duplication of data collection.

S1-09 · Session 1 · Monday 11:30 · Presenter: Dina Pogrebnoy

Co-design, development and delivery of a digital application to deliver a self-management intervention in an inpatient setting after stroke.

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Background/Aims: Stroke survivors, particularly those from culturally and linguistically diverse (CALD) backgrounds, face significant barriers accessing self-directed therapy during inpatient rehabilitation. Western Health developed a multilingual video library to support activity engagement, yet no purpose-built platform existed to deliver it meaningfully. This project aimed to co-design an accessible, culturally responsive application, aligned with survivor and clinician needs.

Methods: A three-phase co-design framework engaged stroke survivors, lived experience advisors, and a multidisciplinary team across nursing, medicine, physiotherapy, and occupational therapy. Phase 1 gathered accessibility needs, functional requirements, and workflow considerations through interviews and workshops (n=10 staff including lived experience representation; n=3 survivors). Phase 2 developed personas and user stories to guide interface design priorities. Phase 3 consolidated findings into design specifications for a minimum viable product.

Results: Survivor interviews revealed that larger fonts, colour, minimal navigation, and relatable images of real survivors performing exercises were critical to engagement. Clinicians prioritised keyword and component-based video search, goal-aligned prescribing, and opt-in exercise reminders. A shared theme was that technology-related frustration shapes a core design principle of minimal steps from login to video. These insights produced a minimum viable product with multilingual support and a clinician portal enabling remote monitoring of patient engagement to inform prescription.

Conclusion: Embedding lived experience and multidisciplinary collaboration produces digital rehabilitation tools that are clinically relevant and culturally responsive. This work forms the foundation for further co-design iterations before the application delivers a Phase 2 clinical trial intervention, advancing equitable access to self-directed stroke recovery.

Session 2 — Infection, immunity & vaccines

S2-01 · Session 2 · Monday 13:20 · Presenter: Sindew Mekasha Feleke

Tracking Persistent and Resurgent Onchocerciasis Transmission Using Genomic, Ecological and Epidemiological Analyses

Sindew M. Feleke[1, 2], Shannon M. Hedtke[1], Emily N. Hendrickson[1], Neha Sirwani[1], Bacha Mekonen[2], Kadu Meribo[3], Sashi Leff[4], Zerihun Tadesse[5], Jamie Tallant[4], Warwick N. Grant[1]

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Introduction: Human onchocerciasis remains a major neglected disease in Africa, which accounts for >99% of the global burden. Despite progress through long-term ivermectin-based mass drug administration, persistent and resurgent transmission threaten elimination gains. Climate and environmental change may alter vector habitats, transmission patterns, and connectivity, creating new challenges for health security. Conventional surveillance detects transmission but cannot distinguish persistent local transmission from parasite or vector reintroduction from neighbouring endemic regions.

Methods: We integrated genomics, ecological modelling, and 20 years of epidemiological data to investigate drivers of persistent and resurgent transmission in Ethiopia. Genome-wide data from 285 *Simulium damnosum s.l.* blackflies were analysed to characterise vector diversity, population structure, genetic connectivity, and environmental adaptation. Ecological niche modelling identified suitable vector habitats, while genotype–environment association analyses assessed relationships between genetic variation and environmental conditions. These findings were integrated with epidemiological evidence to delineate biologically meaningful transmission zones and connectivity among endemic areas.

Results: Genome-wide analyses identified four Ethiopian *S. damnosum s.l.* taxa with extensive, taxon-specific, genetic connectivity across distances of up to 200 km. Strong differentiation between ecologically disjunct regions indicated limited connectivity at greater spatial scales. Ecological modelling identified highly suitable vector habitats concentrated in southwestern and northwestern Ethiopia. Genetic variation was significantly associated with environmental factors including temperature, wind speed, and vegetation cover, suggesting that blackfly lineages may exhibit different ecological preferences. We propose two major transmission zones in western Ethiopia, with extensive vector movement and multiple hotspots within each, connected by a transitional region.

Conclusion: Integrating genomic, ecological, and epidemiological surveillance can strengthen African health security by identifying transmission connectivity, anticipating environmentally driven shifts, and distinguishing potential sources of persistent or resurgent transmission. Our findings highlight the importance of adaptive ecological surveillance to support targeted intervention and sustain onchocerciasis elimination under changing environmental conditions.

S2-02 · Session 2 · Monday 13:30 · Presenter: Veronique Paris

Autodissemination stations to suppress *Aedes notoscriptus* in urban Victoria

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Background and Aims: Buruli ulcer (BU), caused by *Mycobacterium ulcerans*, is an emerging public health concern in Victoria, Australia. Increasing evidence implicates *Aedes notoscriptus* mosquitoes in environmental transmission, highlighting vector control as a potential strategy for reducing disease risk. We investigated whether targeted mosquito control could reduce *Ae. notoscriptus* populations and BU risk in a high-incidence area

Methods: We conducted a randomised controlled field intervention across 12 zones in Melbourne's inner north-west, with six intervention and six control zones covering approximately 50 km². From January to March 2024, intervention zones received autodissemination mosquito traps containing pyriproxyfen and *Beauveria bassiana*, with approximately 600 stations deployed across all areas. Mosquito abundance was monitored using 480 ovitraps before and after intervention. We compared changes

in mosquito egg abundance between intervention and control zones and assessed the association between intervention and subsequent BU notifications.

Results: Mosquito abundance declined substantially following intervention. Mean *Ae. notoscriptus* egg counts decreased from 172.14 to 11.26 eggs per trap in intervention zones, compared with 138.93 to 31.09 in control zones, representing an estimated 70% reduction associated with the intervention. Following adjustment for relevant temporal factors, intervention was associated with an 83% lower likelihood of BU infection at the peak of the study period.

Conclusions: Targeted mosquito control substantially reduced *Ae. notoscriptus* abundance and was associated with lower BU risk, supporting vector control as a potential component of BU prevention. As this was a field intervention, the association between mosquito control and human disease risk should be interpreted cautiously and requires confirmation across additional settings and longer time periods. Community engagement supported implementation and participation in the intervention.

S2-03 · Session 2 · Monday 13:40 · Presenter: Ebony Monson

Lipid droplets as natural, engineered vehicles for antiviral therapy

Ebony Monson [1], Zahra Telikani [1], Irumi Amarasinghe [1], Abbey Milligan [2], Donna Whelan [2], Andy Hill [1,3], William Phillips [1], Eduard Willms [1], Kazu Okuda [1], and Karla Helbig [1]

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Background and Aims: Lipid droplets (LDs) are rapidly upregulated by the host following viral infection, driving antiviral cytokine production (IFN-β and IFN-λ) and restricting replication of Zika virus, dengue virus and herpes simplex virus 1. We recently demonstrated that LDs can also be secreted and taken up by neighbouring cells, conferring protection during infection. This study aimed to optimise an artificial LD (aLD) system for in vivo antiviral applications.

Methods: We characterised the lipid composition of virally induced LDs using liquid chromatography–tandem mass spectrometry. We developed aLDs containing a complex phospholipid membrane and triglyceride core using a liposome-based method. Uptake was assessed across 12 cell types in vitro by confocal microscopy. Biodistribution was evaluated following intravenous injection in mice and cardinal vein injection in zebrafish.

Results: Antiviral LDs showed significant shifts in lipid composition, including a global increase in long- and very-long-chain polyunsaturated fatty acids, such as docosahexaenoic acid and arachidonic acid, and modest but significant enrichment of phosphatidylinositol and phosphatidylethanolamine in the LD membrane. Recapitulating this antiviral LD lipidome, we developed aLDs incorporating a complex phospholipid membrane and triglyceride core. These aLDs were taken up by all 12 cell types tested, with the greatest uptake observed in brain cell types, including astrocytes and neurons. Following administration in vivo, aLDs showed broad biodistribution in mice and zebrafish, localising to the lungs, heart, liver, brain and facial region within six hours and persisting for more than 48 hours. aLDs also demonstrated antiviral activity, which was enhanced by adding selected long-chain fatty acids.

Conclusions: As small lipid particles with complex membranes, aLDs demonstrated broad organ delivery and may offer advantages over extracellular vesicles and lipid nanoparticles. Their flexible composition enables the incorporation of lipids and therapeutic cargoes, highlighting their potential as a platform for antiviral delivery, including to the brain.

S2-04 · Session 2 · Monday 13:50 · Presenter: Nadia Mazarakis

Persistence of IgG4 skewing over 12 months following a fourth dose of a bivalent mRNA or protein-based COVID-19 vaccine

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Background and Aims: Repeated mRNA vaccination (≥3 doses) skews IgG4 responses, raising concerns associated with impaired antibody functions and reduced protection. Our objective was to determine Spike-specific IgG4 skewing over a 12-month period post-vaccination and the impact on antibody function and breakthrough infections.

Methods: We conducted a randomised controlled trial (RCT) to compare immunogenicity of a bivalent mRNA (Moderna: mRNA-1273.214/mRNA-1273.222) or protein (Novavax: NVX-CoV-2373) COVID-19 vaccine given as a fourth dose in healthy adults (NCT05658523). We measured Spike-specific IgG (total) and subclasses IgG1, IgG2, IgG3, IgG4 to wild-type (WT), BA.5, XBB.1.5 and JN.1 Spike trimer at baseline (day 0), and at 1 month, 6 months and 12 months post-vaccination using an

established multiplex assay. Fc receptor dimer (FcγRIIa, FcγRIIIa) and C1q hexamer binding were measured as surrogate assessments for ADCC, ADCP and ADCD, respectively.

Results: A subset of total randomised study participants (N=353) was selected for the IgG4 analysis; Moderna (n=90) or Novavax (n=88) vaccine arm. Vaccinees with multiple mRNA doses had higher IgG4 which persisted for 12 months, although IgG1 remained the dominant IgG subclass. Vaccinees with higher IgG4:IgG1 ratios irrespective of vaccine arm had more rapid breakthrough infection and reduced FcγRIIIa binding. Vaccinees in the highest tertile of IgG4 with the low IgG1 had reduced neutralising antibodies.

Conclusions: In this RCT, repeated mRNA vaccination increased both IgG4 and IgG1 levels but was not associated with reduced FcγR binding. However, participants with an elevated IgG4:IgG1 ratio irrespective of vaccine arm had a shorter time to infection. **Significance:** These results have important implications for ongoing booster strategies using mRNA vaccines.

S2-05 · Session 2 · Monday 14:00 · Presenter: Christie Noble

BCG vaccination induces age-dependent changes in responses to Mycobacterium tuberculosis

Christie CA Noble[1,2], Susie Germano[1], Katie Gell[1], Rhian Bonnici[1], Melanie R Neeland[2,3], Nigel Curtis[1,2,4], Nicole L Messina[1,2].

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Background and Aims: In continuous use for over 100 years, Bacille Calmette-Guérin (BCG) remains the only licensed vaccine for tuberculosis (TB) prevention. It provides variable protection against TB in adults but consistent protection in infants, with the underlying mechanisms poorly understood. We aimed to compare the effect of BCG vaccination on *in vitro Mycobacterium tuberculosis*-induced cytokine and cellular responses in adults and infants.

Methods: This study used PBMC samples from participants in two randomised controlled trials of BCG vaccination, one in infants and one in adults. Samples taken 6 months post-randomisation (53 infants, 75 adults) were stimulated in vitro for 21 hours with M. tuberculosis or RPMI only (unstimulated). Induced cytokine responses were measured by multiplex assay and cells were evaluated by spectral cytometry, with a panel including the surface activation-induced markers (AIM) CD69, OX40 and CD25. The effect of BCG on cytokine responses was analysed by linear models, with rank-based regressions used to compare proportions of activated cell frequencies, both adjusted for the unstimulated value.

Results: Following M. tuberculosis stimulation, BCG-vaccinated infants had a higher frequency of CD69+ CD4 T cells than controls. No cytokine differences survived BH correction, although at uncorrected thresholds, BCG-vaccinated infants secreted more IL-2, MIP-1β and GM-CSF in response to stimulation. In adults, stimulation-induced activated cell frequencies did not differ between groups; however, among antigen-specific AIM+ (OX40+CD25+) CD4 T cells, a lower proportion showed a CCR7−CD45RA− effector memory phenotype in BCG-vaccinated adults than controls. Adult M. tuberculosis-induced cytokine secretion did not differ between groups.

Conclusions: BCG vaccination enhanced M. tuberculosis-induced responses in infants but not in adults, consistent with more effective priming of the developing, mycobacteria-naïve immune system. In adults, prior mycobacterial exposure or age may blunt this effect. These age-dependent patterns offer insight into the mechanisms underlying BCG's variable clinical protection.

S2-06 · Session 2 · Monday 14:10 · Presenter: Georgia-Rose Gilmore

Antibiotics: A Double-Edged Sword - Linking Antibiotic Sensing to Hypervirulence and Persistence in *Clostridioides difficile*

Georgia-Rose Gilmore [1], Sarah Revitt-Mills [1], Yogitha Srikhanta [1], Dena Lyras [1]

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Background and Aims: *C. difficile* infection (CDI) is the leading cause of hospital-acquired diarrhoea. Disease is mediated by toxins TcdA and TcdB, while spores contribute to recurrence. Antibiotic use is a key risk factor for CDI, traditionally attributed to gut microbiota disruption. We identified a regulatory system present in 87% of *C. difficile* strains, comprising a transcriptional repressor and an antibiotic sensor, and showed it is induced by antibiotics associated with increased CDI risk. Given its high conservation, we hypothesised this system links antibiotic exposure to *C. difficile* pathogenesis and aimed to characterise its role in virulence and sporulation.

Methods: The regulatory system was disrupted via TargeTron mutagenesis in an epidemic *C. difficile* strain. Toxin production in antibiotic-exposed WT and mutant strains was measured *in vitro* by toxin ELISA, and virulence was assessed *in vivo* using a murine CDI model. Transcriptomic responses were assessed by RNA sequencing. Spore formation and properties were assessed using sporulation assays, ATR-FTIR spectroscopy and proteomics.

Results: Antibiotic-mediated activation of this system significantly increased TcdA (p=0.0026) and TcdB (p=0.0058) secretion versus untreated cells. Similarly, mutation of the transcriptional repressor increased TcdA and TcdB production (p=0.0005 and p=0.0027, respectively) and induced a hypervirulent phenotype *in vivo*, with survival reduced from 60% in WT-infected mice

(n=5) to 0% in mutant-infected mice (n=10) at 36 h post-infection (p=0.01). Faecal TcdA was elevated at 36 h (p=0.002), while TcdB showed a non-significant increasing trend (p=0.19). RNA-seq revealed similar transcriptional shifts following antibiotic exposure and system disruption, across networks governing virulence, motility and sporulation. Antibiotic exposure also altered spore composition, proteomes and resistance properties.

Conclusions: Antibiotic exposure reprograms *C. difficile*, promoting toxin-mediated disease and altering spore biology. These findings identify a previously unrecognised mechanism linking antibiotic sensing to CDI pathogenesis and highlight a potential target to reduce CDI severity and persistence.

S2-07 · Session 2 · Monday 14:20 · Presenter: Garry Chahal

Can lipid droplets be delivered to the cytoplasm to prime antiviral immunity in neighbouring cells?

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Background and Aims: Lipid droplets (LDs) are rapidly upregulated following bacterial and viral infection and play critical roles in the pathology of some cancers and neurodegenerative diseases. We have shown they play a vital role in the early innate immune response to multiple viruses including Zika, Dengue, influenza and SARS-CoV-2. Here, we explore a novel role for LDs as extracellular communicators that can influence the outcome of viral infection.

Methods: To examine LD secretion and uptake, we established a contact-independent astrocyte co-culture system in which separate cell populations expressing PLIN2-mCherry or PLIN2-GFP (the main LD protein) are cultured with shared media but without cell-cell contact. To determine the functional consequence of LD transfer, LDs isolated from immune-activated astrocytes were placed on naïve recipient cells before ZIKV infection. To test whether uptake is dynamin-dependent, LDs were applied to recipient cells pretreated with the dynamin inhibitor Dynasore or a DMSO vehicle control; uptake was assessed by fluorescence microscopy and western blot. Intracellular fate was tracked by live-cell lattice light-sheet microscopy of labelled LDs.

Results: LD transfer between cells increased significantly following viral infection. Uptake of primed LDs significantly enhanced immune responses and reduced Zika virus replication by approximately 50% in recipient cells. Inhibition of multiple endocytic pathways with Dynasore reduced LD uptake by approximately 60%, indicating that uptake is substantially dynamin-dependent. Lattice light-sheet microscopy captured LD internalisation and their association with endogenous cytoplasmic LDs in recipient cells.

Conclusions: These findings highlight a previously unknown role for LDs as novel extracellular communicators. We hypothesise that early viral infection triggers LD release to influence the fate of neighbouring cells. Harnessing this natural delivery route could enable LD-based therapeutics that prime protection across tissues ahead of viral spread, a broadly applicable strategy against diverse and emerging viral infections.

S2-08 · Session 2 · Monday 14:30 · Presenter: Justin Boxuan Zhang

Studying T Cell Ectosomes In T Cell Surveillance

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Background and Aims: T cells recognise antigen-presenting cells by forming specialised interfaces called immune synapses, which coordinate activation and effector function. It was recently discovered that T cells release activated T cell receptors (TCRs) in membrane vesicles called ectosomes at the end of immune synapses. This challenges the prevailing view that TCR downregulation after stimulation occurs primarily through degradation, and suggests that T cells may transfer information to neighbouring cells. However, when ectosomes are produced and how they affect target cells remain poorly understood.

Methods: We combined high-throughput live-cell imaging and super-resolution confocal microscopy to track immune synapse formation and ectosome behaviour. Isolated ectosomes were characterised using cryo-electron tomography (Cryo-ET) and nanoparticle tracking analysis. RNA sequencing was performed on cell lines treated with ectosomes containing matching or non-matching TCRs to investigate their effects on target-cell signalling.

Results: The number of ectosomes released by individual T cells increased with stimulation strength. Unexpectedly, ectosomes were produced not only following mature immune synapse formation, but also during antigen scanning of antigen-negative cells and from membrane nanotube tethers. Ectosomes deposited during antigen scanning remained on target-cell surfaces for several hours, whereas those released at mature synapses were predominantly internalised. Isolated ectosomes had a median diameter of approximately 150 nm and varied substantially in size and internal cargo by Cryo-ET. RNA sequencing showed that ectosome treatment induced transcriptional changes associated with antigen presentation and cellular stress in a B cell line, but not in a melanoma cell line. These effects were independent of TCR engagement.

Conclusions: Our findings reveal that T cells release ectosomes in multiple contexts, including during antigen scanning before mature immune synapse formation. Ectosomes can persist on target-cell surfaces or be internalised and alter target-cell gene expression independently of TCR recognition, identifying ectosomes as a previously underappreciated mechanism of T cell communication.

S2-09 · Session 2 · Monday 14:40 · Presenter: Bridget E. Walker

A simple model for studying a neglected tropical disease and the importance of host signals for fungal pathogenesis.

Bridget E. Walker, Patricia R. Jusuf and Alex Andrianopoulos

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Background and Aims: *Talaromyces marneffei* is an emerging fungal pathogen which causes invasive infections in immunocompromised individuals that are often fatal. Whole organism infection models are critical for investigating *T. marneffei* pathogenesis and identifying therapeutic targets for urgently needed anti-fungal treatments; however, few are available to study this pathogen. A key challenge in developing a *T. marneffei* infection model is its morphological temperature dependence: the fungus exhibits an environmental hyphal form and a pathogenic yeast form in the host at 37□C. This study aimed to evaluate *Tenebrio molitor* larvae as a model host for studying *Talaromyces marneffei* infections.

Methods: *T. molitor* larvae were examined for thermotolerance and inoculated with *T. marneffei* conidia of various doses to determine appropriate conditions for virulence screening. The model was then applied to examine the influence of temperature on *T. marneffei* morphology and pathogenicity, using parallel infection temperatures at environmental and host temperatures coupled with histopathological analysis of infected larvae.

Results: Injection with *T. marneffei* resulted in reproducible, dose-dependent mortality at 37□C, and *T. marneffei in vivo* yeast cell development was observed in tissue sections of infected larvae, confirming their suitability for modelling the yeast-associated disease. We also found that infections could be established at environmental temperature (25□C) – although 10-fold higher doses were required before larval survival was significantly impacted. Surprisingly, some *T. marneffei* yeast cells (only previously cultured at 37□C), were also identified in tissue sections of 25□C/infected larvae, indicating that larval host cues can partially induce yeast cell development in the absence of a 37□C temperature signal.

Conclusion: This work demonstrates the utility of *T. molitor* larvae for *T. marneffei* virulence assays and improves understanding of its dimorphic switching. This model can be used in any lab already certified for *T. marneffei* work, lowering the barrier to research on this neglected tropical disease.

S2-10 · Session 2 · Monday 14:50 · Presenter: Jiaqi (Albert) Shi

Development of next-generation mRNA vaccines against malaria

Jiaqi (Albert) Shi[1,3], Adam Thomas[1,4], Liriye Kurtovic[1,2,4], Herbert Opi[1,2,4], Stewart Fabb[5], Chee Leng Lee[5], Rekha Shandre Mugan[5], Colin Pouton[5], James Beeson[1,2,4].

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Background and Aims: Malaria is primarily caused by *Plasmodium falciparum* and *Plasmodium vivax* and remains a major global health burden. Currently, only the RTS,S and R21 vaccines are approved for use, which both express the major *P. falciparum* surface antigen, circumsporozoite surface protein (*Pf*CSP), as adjuvanted virus-like particles. As this shares no sequence homology with *P. vivax* CSP, these vaccines are only efficacious against *P. falciparum*. This emphasises the urgent need for novel approaches to develop multi-species vaccines. The recent success of mRNA vaccines highlights the potential for highly efficacious next-generation malaria vaccines. The mRNA platform has shown to be more efficient and robust for construct design and multi-antigen formulation than conventional platforms, and could be used to target both major *Plasmodium* species. We aimed to validate the RTS,S/R21 malaria vaccine antigen using the mRNA platform as proof-of-concept, and to evaluate a novel multi-species mRNA formulation by combining the RTS,S/R21 antigen with a leading *P. vivax* vaccine candidate.

Methods: We vaccinated C57BL/6 mice (n=5) with mRNA expressing RTS,S/R21 alone, *P. vivax* vaccine candidate alone, and a combined multi-species formulation in a three-dose regimen administered at 28-day intervals. The induction of antigen-specific IgG as well as antibody functional responses that are clinically relevant for malaria immunity was examined.

Results: All three mRNA vaccines induced high IgG magnitude and functional responses against their respective antigens, including the novel multi-species mRNA formulation.

Conclusions: Our work has demonstrated that the mRNA platform can be used to combine antigens and generate functional immune responses against the two major *Plasmodium* species. Future studies will investigate other leading malaria vaccine candidates, as well as emerging mRNA technologies such as self-amplifying RNA. This work will inform the next-generation malaria vaccine design and contribute to the global malaria control and elimination goal.

S2-11 · Session 2 · Monday 15:00 · Presenter: Alysha Literski

Improving the capacity of vaccine-induced antibodies against RH5 to arrest the growth of *Plasmodium falciparum*.

Alysha H. Literski[1,2], Betty Kouskousis[1], Claudia B.G. Barnes[1], Adam Thomas[1], Barnabas G. Williams[3,4], Brendan S. Crabb[1,2,5], Simon J. Draper[3,4,6], James G. Beeson

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Background and Aims: *Plasmodium falciparum*, the deadliest malaria parasite, remains a major global health challenge. While pre-erythrocytic vaccines provide partial protection, breakthrough infections can progress to symptomatic blood-stage disease. PfRH5 is an essential parasite protein and the leading blood-stage vaccine target. Anti-PfRH5 antibodies block red blood cell invasion and induce a distinctive extracellular parasite morphology termed “pseudo-rings”; however, the mechanism behind this phenotype and its role in antibody-mediated protection remains unclear. This study aimed to improve RH5 antibody efficacy and investigate the mechanism and significance of pseudo-ring formation.

Methods: Bliss additivity assays and isobologram analyses were used to assess interactions between RH5 antibodies, vaccine-induced polyclonal RH5 IgG, and 12 invasion-inhibiting compounds. Live-cell and fixed-cell fluorescence microscopy were performed to investigate pseudo-ring formation and define its underlying mechanism.

Results: Early-acting invasion inhibitors, particularly heparinoids, synergised with RH5 antibodies and RH5 polyclonal IgG, enhancing parasite growth inhibition beyond that achieved by either intervention alone. Microscopy demonstrated that pseudo-rings formed following treatment with bivalent, but not monovalent, antibodies, indicating that PfRH5 crosslinking drives this phenotype. These findings suggest a previously unrecognised role for PfRH5 in signalling the transition from invasion to parasite development. Antibodies that enhanced pseudo-ring formation were also identified, providing another potential strategy to improve RH5-mediated protection.

Conclusions: RH5-targeting antibodies inhibit malaria parasites through multiple mechanisms, including invasion blockade and induction of pseudo-ring formation. These findings provide valuable insights into understanding RH5 biology and inform novel therapeutic interventions against blood-stage malaria.

Significance/Impact: This work identifies innovative strategies to enhance RH5 vaccine efficacy through synergistic combination approaches and antibody optimisation. By uncovering a previously unrecognised function of PfRH5 and mechanisms that strengthen antibody-mediated protection, these findings may support the development of more effective malaria interventions, contributing to reduced disease burden and improved global health outcomes.

S2-12 · Session 2 · Monday 15:10 · Presenter: Rina Wong (Fu)

Virucidal and Bactericidal Effects of a Nano-formulation of Australian *Melaleuca alternifolia* (Tea Tree) Oil against Human and Bovine Respiratory Pathogens

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Background: Bioactive molecules from natural sources with antiviral/bacterial properties can be applied to both human and animal health and alleviation of antimicrobial resistance. Bovine respiratory disease (BRD) is caused by a combination of viral and bacterial pathogens. Australian Tea Tree Oil (TTO) derived from *Melaleuca alternifolia* contains a range of active molecules.

Methods: A nano-emulsion of TTO (nTTO) was developed with characterisation by particle sizing, zeta potential and cryo-electron microscopy. Virucidal effects of purified TTO and nTTO [10%, 5%, 2.5%] against enveloped viruses (Bovine herpes virus-1 (BHV1), SARS-CoV-2, Influenza virus, Respiratory Syncytial virus (RSV)) and non-enveloped viruses (Echovirus-12, murine Norovirus) were assessed using the $TCID_{50}$ assay.

Results: TTO (10%) and nTTO (5%) completely inactivated BHV1, whilst TTO (5%) produced a 4-log reduction in titre. The mean $TCID_{50}$/ml of BHV1 after exposure to TTO and nTTO at 1% were ($3.0x10^5$ and $3.6x10^2$) compared to untreated control ($3.2x10^5$). TTO and nTTO were ineffective against non-enveloped Echovirus-12 and murine Norovirus. When applied to Influenza virus, TTO and nTTO at 10% resulted in a 96.7% and 69% reduction in viral titre. RSV titre was reduced by 70% and 99% respectively, using TTO and nTTO at 10%, 5% and 2.5%. A 10% TTO solution inactivated SARS-CoV-2 coronavirus after an incubation time of 30 – 45 mins, whilst the human coronavirus NL63 was inactivated in 15 mins. A novel micro-vapour assay showed that TTO volatile vapours were effective against both bacteria and viruses. Vapours from undiluted, 10% and 1% TTO and nTTO inhibited the BRD co-pathogen bacterium *Mannheimia haemolytica* together with BHV1.

Conclusions: The nano-formulation of TTO was effective in inactivating enveloped respiratory viruses showing its effectiveness as a virucidal agent. The novel micro-vapour assay demonstrated the potential of virucidal and bactericidal vapours generated from TTO/nTTO, which may be applied to other volatile plant extracts.

Session 2B — Cardiovascular, metabolic & cell biology

S2B-01 · Session 2B · Monday 13:20 · Presenter: Jacob Ellis

Regulation of transposable elements by mRNA export machinery in embryonic progenitor models

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Background and Aims: Transposable elements (TEs) such as Long Interspersed Nuclear Elements (LINEs) and Short Interspersed Nuclear Elements (SINEs) are viral-like genetic elements that self-replicate via RNA intermediates and accumulate in the genome via insertional mutagenesis. Given their potential for disrupting the genome, they are largely transcriptionally silenced, and their de-repression is a hallmark of many diseases such as cancer. Although TEs rely on RNA export pathways to shuttle their transcripts to the nucleus to produce functional protein for their own retrotransposition, whether there are TE-specific RNA export mechanisms has yet to be established. Furthermore, whether TEs have regulatory function in certain cell types or cellular contexts remains an open question. We hypothesise that mRNA export machinery serves as a mediator and regulatory control point for TE expression. This project explores the consequences of mRNA export disruption on TE expression and localisation in embryonic progenitor models, where TEs are largely de-repressed.

Methods: By titrating dosage of the mRNA export factor, ALYREF, in mESCs via dTAG-mediated degradation, I investigated functional consequences of disrupting mRNA export on multiple TE classes (ie. LINEs and SINEs). RNA-level dynamics were assessed via Fluorescent in-situ Hybridisation (FISH) imaging and qPCR. Furthermore, protein-level dynamics were assessed via western blot and Fluorescence-Activated Cell Sorting (FACS).

Results: ALYREF depletion in mESCs results in the formation of distinct SINE (B2 family) foci proximal to nuclear speckles which co-localise with oligoDT signal, suggesting TE polyadenylation. Foci are no longer present once mESCs have been differentiated into neural progenitor cells (NPCs), suggesting cell-type specificity. Furthermore, ALYREF depletion results in transcriptional increase of LINE RNA as well as elevated LINE protein.

Conclusions: Depletion of ALYREF has cell-type-specific consequences for TE dynamics at an RNA and protein level, positioning mRNA export as an important regulatory node for the control of TE expression, via as-yet-undiscovered mechanisms.

S2B-02 · Session 2B · Monday 13:30 · Presenter: Sanuri Liyanage

Yolk Sac-Derived Endothelial-Macrophage Progenitors in Skin: Drivers of Wound Healing and Tumour Growth

Sanuri R. Liyanage[1,2], Anna Williamson[1], Thalia Salagaras[1], Dang Tran[1,2], James Budd[1], Mohammadhossein Hassanshahi[3], Joanne T.M. Tan[1,2], Vashe Chandrakanthan[1,2], Claudine Bonder[3], Christina Bursill[1,2], Shiwani Sharma[1,4], Peter J. Psaltis[1,2].

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Background: We recently identified novel YS-derived bipotent endothelial-macrophage progenitors as a postnatal renewable source of macrophages (MΦ) and endothelial cells (EC) in arterial tissue. Here, we investigated analogous skin progenitors and their contribution to vasculogenic and inflammatory responses during wound healing and melanoma growth.

Methods and Results: FACS-isolated skin progenitors from postnatal mice were $Lin^{-}CD45^{+}CD11b^{-}F4/80^{-}Sca\text{-}1^{+}c\text{-}Kit^{+}$, expressed CX3CR1 and CSF1R, and generated 187±41 macrophage colony-forming units per 10^5 cells. These progenitors demonstrated finite self-renewal capacity, declining progressively with age (~1,000 per 10^5 cells at E15.5, ~300 neonatally, ~100 at 12w, ~20 at 52w; $p<0.001$). $Flt3^{Cre}$×$Rosa^{mT/mG}$ fate-mapping mice confirmed their independence from Flt3-dependent bone-marrow haematopoiesis. Tamoxifen-inducible lineage tracing driven by Cx3cr1 and Csf1r-loci demonstrated YS origin at E8.5, with subsequent seeding and persistence in skin postnatally. *In vitro* and *in vivo* differentiation studies confirmed their differentiation into MΦs and ECs, with vasculogenic cord forming capacity. Adoptive transfer into cutaneous wounds and melanoma yielded robust engraftment, clonal expansion, and generation of perfused neovessels.

In a streptozotocin-induced diabetes model, hyperglycaemia reduced progenitor clonogenicity, differentiation, angiogenic capacity, DNA integrity, and mitochondrial function. Combining hyperglycaemia with fate-mapping revealed that diabetes attenuated progenitor accumulation in early wounds and blunted MΦ and EC expansion during later repair. Notably, healthy progenitors transplanted into diabetic wounds engrafted and promoted healing, an effect impaired when using diabetic progenitors.

Conclusions: Skin harbours previously unidentified YS-derived clonogenic progenitors with MΦ and EC differentiation capacity. They contribute to wound repair, are functionally impaired by diabetes, and may possess therapeutic potential to rescue impaired diabetic healing, though their vasculogenic properties may accelerate tumour neovascularisation.

S2B-03 · Session 2B · Monday 13:40 · Presenter: Shannen Walker

Single-cell Transcriptome Identifies Novel Genes Associated with Hepatic Recovery Pathways in Metabolic Associated Steatohepatitis

Shannen Walker[1], Mitchell Hallam[1,2], Simon T Bond[1,3], Gabriella Farrugia[1,4], Malathi Imiyage Dona[1], Aowen Zhuang[1], Christine Yang[1], Yingying Liu[1], Michael F Keating[1,3], Alex R Pinto[1,4], Brian G Drew[1,2,3]

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Background: Metabolic associated liver disease (MASLD) involves excessive hepatic lipid accumulation and affects an estimated 40% of Australian adults, contributing to the development of obesity, type-2 diabetes, and increased cardiovascular risk. When left untreated, MASLD can progress to metabolic associated steatohepatitis (MASH), characterized by inflammation and fibrosis, resulting in the permanent remodelling of the hepatic microenvironment. Prior to this stage, however, the liver has a remarkable ability to repair itself and may even regenerate back to full size if part of the liver is removed. Despite this, there are limited effective treatments for MASLD and MASH which can be attributed to a lack of thorough understanding regarding the causative agents responsible for its initial onset, subsequent advancement and the liver's normal repair pathways.

Methods: To investigate this, we conducted single-cell transcriptomics on livers from mice fed an AMLN diet, an intervention known to induce MASH as observed in humans. This was performed across 3 time points (2, 8 & 24 weeks) in both male and female C57BL/6J mice (n = 4/treatment).

Results: Overall, we analysed 88,000 cells at a depth of >20K genes across all conditions and identified more than 30 distinct cell populations. In addition, chronic exposure to AMLN diet stimulated a regenerative response with a number of novel gene targets identified that are likely involved in this process. We validated one of these targets (Nrg1) by utilising CRISPR and Lipid Nanoparticle technology to knock this gene out both in vitro and in vivo (Sox2-Cas9 mice). Preliminary studies showed that when fed a diet that induces liver injury (3,5-Diethoxycarbonyl-1,4-dihydrocollidine), Nrg1 knockout mice had smaller livers suggesting a reduced capacity for regeneration.

Conclusion: This work proposes a regenerative role for NRG1 which may be manipulated for the treatment of MASLD.

S2B-04 · Session 2B · Monday 13:50 · Presenter: Yuyang Song

mRNA Platforms Enable Spatiotemporal Control for Safer Thrombosis Prevention

Yuyang Song[1,2,3], Hung Nguyen[1,2,3], Pengkai Shi[1,2,3], Ahmed Refaat[1,2,3,4], Cuong Pham[1,2,3,5], Bangyan Xu[1,2,3], Shulei Ren[1,2,3], Julia Skoraczynski[3,4], Anne Nguyen[1,2], Haikun Liu[1,2,3], Alexander Klesen[4,6], Sylvain Trépout[7], Mark Vidallon[1,2,3,5,8], Karlheinz Peter[2,3,4,5,9,10], Xiaowei Wang[1,2,3,5,9].

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Background and Aims: Blood clotting is essential to stop bleeding, but unwanted clot formation (thrombosis) can block blood flow and cause a heart attack or stroke. Current antithrombotic therapies have two drawbacks: 1) increased bleeding risk by interfering with normal clotting and 2) limited duration of action, necessitating frequent dosing or continuous infusion. We developed an mRNA-based strategy to selectively target harmful clot formation while providing sustained protection.

Methods: We used a therapeutic antibody that selectively recognises activated platelets involved in harmful clotting while sparing platelets required for normal blood clotting. Conventional mRNA and self-amplifying mRNA (samRNA) encoding this therapeutic were packaged into lipid nanoparticles for protection and delivery. Therapeutic functions were assessed *in vitro*, followed by evaluation of antithrombotic efficacy, bleeding and systemic safety in mice.

Results: Both RNA approaches generated a functional therapeutic that preferentially recognised activated platelets and reduced platelet aggregation. *In vivo*, one administration of conventional mRNA provided significant antithrombotic activity for up to 24 hours. Using samRNA prolonged this effect, with significant protection still observed 7-10 days after treatment ($P<0.05$). The normal clotting ability was preserved with both RNA approaches, whereas bleeding was significantly prolonged by a clinically used antiplatelet therapy ($P<0.05$). Treatment was well tolerated, with no major changes in blood parameters, liver or kidney function, tissue morphology, or evidence of major systemic toxicity.

Conclusions: Our results demonstrate that mRNA can be used to produce an activated platelet-targeted antithrombotic therapy *in vivo* without bleeding risk. Switching from conventional mRNA to samRNA extended the antithrombotic effect from approximately 24 hours to more than one week after a single dose, without compromising the normal ability to stop bleeding or causing major systemic toxicity. Different RNA platforms can therefore be selected to control the duration of therapeutic protein expression, thereby providing opportunities to develop safer, longer-acting antithrombotic therapies.

S2B-05 · Session 2B · Monday 14:00 · Presenter: Brooklyn Hutton

Strain- and sex-dependent differences in PCSK9-induced atherosclerosis reveal the translational value of outbred models

Brooklyn Hutton[1,2], Jake Robertson[1,2], Caitlin Vella[1], Amy Baxter[1], Andrew Murphy[3,4], Alex Bobik[1,3], Antony Vinh[1,2], Grant Drummond[1,2,3], Maria Jelinic[1,2,3].

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Background and Aims: Atherosclerosis remains a leading cause of death, highlighting the need for reliable tools to facilitate the development of better therapies. While inbred C57BL/6 mice are widely used in preclinical studies due to reproducible plaque development, outbred UM-HET3 mice may provide greater genetic diversity and translational relevance. However, PCSK9-driven atherosclerosis is poorly characterised in this strain. We therefore aimed to determine strain- and sex-specific differences in PCSK9-induced atherosclerosis.

Methods: At 5 weeks of age, male and female C57BL/6 and UM-HET3 mice received AAV-PCSK9 or control vector and were fed normal chow or a Western-type diet (WTD) for 20 weeks. Body weight, blood pressure, and fasting blood glucose was measured monthly. At endpoint, blood lipids & insulin, immune profiles (blood and spleen), and aortic atherosclerosis were assessed.

Results: PCSK9+WTD consistently increased LDL-cholesterol and aortic lipid deposition in both strains and sexes, confirming disease induction. However, PCSK9+WTD caused metabolic dysfunction in both sexes of UM-HET3 mice (increased body weight; insulin resistance), but these changes were largely restricted to males in C57BL/6 mice. Flow cytometry also identified distinct immune responses. In the spleen, PCSK9+WTD increased pro-inflammatory monocytes in males and CD8+ T cells in females, while pro-inflammatory monocytes increased in both sexes in UM-HET3 mice. Circulating immune changes only occurred in male C57BL/6 mice.

Conclusions: These findings demonstrate that while PCSK9+WTD induces atherosclerosis in both strains, metabolic and immune responses differ by strain and sex. The more consistent responses between sexes in UM-HET3, suggests this strain might be useful for exploring sex differences in atherosclerosis.

S2B-06 · Session 2B · Monday 14:10 · Presenter: Caitlin Vella

Enhancing Efferocytosis with BELMO Reduces Atherosclerotic Disease Burden

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Background and Aims: Atherosclerosis is a chronic inflammatory vascular disease and a leading cause of morbidity and mortality globally. Despite lipid-lowering therapies, significant residual cardiovascular risk remains, demanding improved understanding of mechanisms driving plaque progression. Efferocytosis, the phagocytic clearance of apoptotic cells, is essential for tissue homeostasis and resolving inflammation, but is defective within atherosclerotic plaques. During pathogenesis, increased cell death combined with impaired clearance contributes to necrotic core formation and plaque instability.

Methods: To assess the impact of enhanced efferocytosis, we utilised the transgenic 'BELMO-LysM-Cre' mouse model, which exhibits enhanced recognition of dying cells by myeloid-derived phagocytes through augmenting engulfment receptor expression. Atherosclerosis was induced using an adeno-associated virus-expressing PCSK9 (AAV8-PCSK9) system combined with Western diet feeding over 20 weeks to promote advanced lesion development. Aortic plaque burden was assessed by Oil Red O staining, while lesion morphology and necrotic core in aortic sinuses were evaluated by immunohistochemistry.

Results: Independent of sex, body weight or triglyceride levels, BELMO-LysM-Cre mice demonstrated significantly reduced aortic plaque burden compared with LysM-Cre controls (16.18% vs 9.07%, $p<0.001$). Aortic sinus analysis revealed decreased total plaque area and necrotic core size ($p=0.0062$). Lesions in BELMO mice were skewed towards mild and moderate phenotypes, whereas severe lesions predominated in controls. Systemically, enhanced efferocytosis was associated with reduced circulating MCP-1 levels.

Conclusions: Augmenting efferocytosis via enhancing engulfment receptor expression reduces plaque burden and increases plaque stability, supporting its potential as a clinically relevant therapeutic target in atherosclerosis.

S2B-07 · Session 2B · Monday 14:20 · Presenter: Maya S Bishop

Therapeutic benefits of megadose sodium ascorbate for reversing sepsis-induced cerebrovascular and cardiovascular dysfunction

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Background: Delirium is common in sepsis, and many survivors develop persistent cognitive impairment. Cerebral ischemia, hypoxia and edema are implicated, yet it is unknown whether intracranial hypertension contributes to the neurological sequelae of sepsis, and no therapies specifically target cerebrovascular dysfunction.

Aims and Hypothesis: To determine the effects of sepsis and intravenous megadose sodium ascorbate on plasma and cerebrospinal fluid (CSF) ascorbate concentrations, intracranial pressure (ICP), cerebral perfusion pressure (CPP), and vascular responsiveness to norepinephrine in an ovine model of live Gram-negative sepsis. We hypothesized that sodium ascorbate would reduce ICP, improve CPP, and restore vascular responsiveness to norepinephrine in septic sheep.

Methods: Adult Merino ewes were surgically instrumented with lateral cerebral ventricular catheters and carotid arterial and jugular venous catheters. Non-anesthetized sheep were infused with intravenous live *Escherichia coli* for 31-h. After 23-h of sepsis, animals were randomized to receive intravenous 3 g/kg of sodium ascorbate (n=7) or fluid-matched placebo (n=6), as a bolus followed by a 7-h infusion. ICP and mean arterial pressure (MAP) were measured continuously. Changes in MAP to escalating norepinephrine doses were recorded at baseline and 23-h of sepsis, and after treatment at 27.5 and 31-h of sepsis.

Results: At 23 h of sepsis, plasma and CSF ascorbate concentrations were significantly depleted (16±0.3 to 10±0.2 μmol/L and 144±4 to 104±2 μmol/L, respectively), accompanied by reduced MAP and CPP and increased heart rate and ICP (all $P<0.05$). By 31 h of sepsis, intravenous sodium ascorbate markedly increased plasma (14332±154 vs. 11±0.1 μmol/L) and CSF (4918±165 vs. 84±3 μmol/L) ascorbate concentrations compared with placebo (both $P<0.001$). Sodium ascorbate also improved MAP (75±5 to 87±11 vs. 69±11 to 66±7 mmHg; $P=0.020$), normalised ICP (17.0±3.4 to 9.3±1.9 vs. 20.6±3.7 to 19.3±5.0 mmHg; $P=0.024$), and increased CPP (61±11 to 75±5 vs. 48±16 to 49±12 mmHg; $P=0.046$) compared with placebo. Pressor responsiveness to norepinephrine, impaired at 23 h of sepsis in both groups, was fully restored at 27.5 and 31 h by sodium ascorbate but not placebo. Norepinephrine administration did not increase ICP in either group.

Conclusion: Intravenous megadose sodium ascorbate restored blood and brain ascorbate concentrations, normalised ICP, improved CPP, and reversed vasopressor hypo-responsiveness to norepinephrine. These findings identify elevated ICP as a modifiable contributor to sepsis-induced cerebrovascular and cardiovascular dysfunction and support sodium ascorbate as a potential therapy for both systemic and cerebral derangements in sepsis.

S2B-08 · Session 2B · Monday 14:30 · Presenter: Roop Bhangu

Glucose-Responsive Nano Sugar with Kidney Tropism Enable Multi-Day Therapy in Diabetic Mice

Amir Roointan[1#], Sukhvir Kaur Bhangu,[12#], Thirimadura V. H. Mendis[1], Haiyan Zhu[2], Jay Jha[1], Soraia Fernandes,*[2,3], Karly C. Sourris[1], Siqi Li[1], Ting-Yi Wang[1], Irena Carmicha[4], Jonathan E. Sha[6], Karin, Jandeleit-Dahm[1], Frank Caruso[2], Mark E. Cooper[1], Christoph E. Hagemeyer[1,6]* and Francesca Cavalieri[2,7]*, Rong Xu[1]**

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Background: Type 1 diabetes (T1D) occurs when the immune system destroys the insulin-producing beta cells, leaving the body with little or no insulin. People with T1D require lifelong insulin replacement. However, conventional insulin injections cannot automatically adapt to changing blood glucose levels, while automated insulin delivery systems combining an insulin pump and continuous glucose monitor can be expensive and inaccessible. We developed biocompatible, glucose-responsive insulin nanoparticles to provide longer-lasting and safer blood glucose control.

Methods: We assessed insulin-loaded nanoparticles for their ability to release insulin in response to changing glucose levels. Insulin activity and nanoparticle compatibility were also evaluated. Therapeutic efficacy was examined in two T1D mouse models: chemically induced diabetic mice and Akita mice, which develop diabetes because of an insulin-gene mutation. Mice received insulin-loaded nanoparticles, insulin alone or nanoparticles without insulin. Researchers monitored blood glucose after treatment and performed a glucose tolerance test to evaluate the response to a rapid rise in glucose similar to that after a meal. Treatment safety and indicators of diabetes-related kidney injury were also assessed.

Results: The nanoparticles preserved insulin activity and released more insulin as glucose levels increased. A single subcutaneous injection provided blood glucose control for up to 72 hours, substantially longer than insulin alone. Treated mice responded appropriately to a glucose challenge, demonstrating glucose-responsive activity in the body. No major treatment-related toxicity was observed. The findings also suggested that sustained blood glucose control may help reduce diabetes-related kidney injury.

Significance: This glucose-responsive insulin nanoparticle system may offer a safer and more convenient alternative to frequent insulin injections. By releasing insulin when the body needs it, the system could reduce high and low blood glucose, lessen the injection burden and potentially protect against long-term diabetic complications.

S2B-09 · Session 2B · Monday 14:40 · Presenter: Haoyun Fang (Alexx)

Dynamic Subcellular Remodelling of Heart Revealed by Multi-Omics from Early Myocardial Ischemia Reperfusion Injury

Haoyun Fang[1 2], Seyed Sadegh Eslami[2 3], Anita Thomas[2], Kevin Huynh[1 2 4], Alin Rai[1 2 3], Thy Duong[2], Alex Faulkner[2], Peter Meikle[1 2 3], Daniel Donner[1 2 4], David W Greening [1 2 3]

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Background and Aims: Myocardial ischemia-reperfusion injury (MIRI) occurs when the restoration of blood flow following myocardial infarction exacerbates cardiac damage. Early MIRI is associated with subcellular perturbations, including mitochondrial reactive oxygen species production, DNA damage, endoplasmic reticulum stress and extracellular matrix remodelling; however, the tissue-wide multi-omic landscape of native cardiac subcellular dynamics under MIRI remains underdefined. Here, we aimed to map protein and lipid redistribution during early MIRI and assess sex-dependent and sex-independent responses.

Methods: Here, we induced myocardial infarction surgically via coronary artery occlusion in male and female mice for one hour, followed by 4 hours of reperfusion. Heart samples from the MIRI and sham groups were subjected to centrifugation-based subcellular fractionation followed by dual protein-lipid extraction and mass spectrometry-based multi-omics analysis. We used supervised machine learning to infer the subcellular proteome and lipidome distributions and redistributions comparing the Sham and MIRI groups.

Results: Whole-tissue profiling identified shared neutrophil-associated proteomic responses while lipidomics revealed concordant triacylglycerol and lysophosphatidylcholine enrichment after MIRI. Sex-dependent MIRI-induced changes included mitochondrial respiration and translation, protein turnover, and inflammatory processes. Further, following subcellular profiling we resolved 14 cardiac subcellular niches, defining a conserved subcellular proteome and proteome-informed subcellular lipidome. While the subcellular lipidome remained relatively stable after MIRI, we identified MIRI-induced subcellular remodelling of neutrophil granule-associated protein network, including Ctsg, Elane, Prtn3, Mmp8 and Mmp9, and redistribution of Padi4, a key protein involved in neutrophil extracellular trap-related cell death.

Conclusions: This study provides a tissue-wide view of protein and lipid organisation during early MIRI and shows selective subcellular reorganisation beyond changes in molecular abundance. Future temporal and cell-resolved studies will determine how these changes, particularly Padi4-associated neutrophil responses, contribute to injury and inform targeted interventions.

S2B-10 · Session 2B · Monday 14:50 · Presenter: Maria Jelinic

Senescent fibroblast-like vascular smooth muscle cells are associated with coronary artery plaque vulnerability and immune activation

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Background and Aims: Coronary artery atherosclerosis (CAA) is a leading cause of myocardial infarction and death worldwide. Emerging evidence suggests that vascular smooth muscle cell (VSMC) phenotypic switching contributes to plaque rupture and myocardial infarction. Therefore, we aimed to define VSMC phenotype diversity across CAA progression and determine whether senescent VSMCs accumulate in advanced and vulnerable plaques.

Methods: Human coronary artery specimens spanning the full disease spectrum, from pre-atherosclerotic arteries to ruptured plaques (n=14), were analysed using single-cell RNA sequencing, spatial transcriptomics and immunohistochemistry. Histopathology was used to classify disease stage. Trajectory and cell-cell communication analyses were performed to define VSMC state transitions and intercellular signalling networks.

Results: VSMCs comprised ~55% of all sequenced cells and segregated into five subtypes, including contractile, transitional, fibroblast-like and macrophage-like phenotypes. CAA progression was characterised by loss of contractile VSMCs and expansion of fibroblast-like and macrophage-like populations. Pseudotime analysis revealed a previously unrecognised VSMC differentiation trajectory from contractile to fibroblast-like to macrophage-like states during CAA progression. Spatial mapping

showed enrichment of fibroblast-like VSMCs within fibrous caps, whereas macrophage-like VSMCs accumulated in vulnerable shoulder regions. Notably, fibroblast-like VSMCs expressed the strongest senescence-associated gene signature of all sequenced cells. Immunohistochemistry showed co-localisation senescence markers (β-galactosidase and p16) with stress ligands (MICA and BTN3A1) in fibrous-cap VSMCs from advanced CAA lesions. Cell-cell communication analyses predicted enhanced signalling between fibroblast-like VSMCs and immune cells through stress-response pathways.

Conclusions: These findings identify senescent fibroblast-like VSMCs as a previously unrecognised cell state associated with CAA vulnerability. This study defines a novel mechanism linking VSMC phenotypic switching, senescence and immune signalling during plaque progression. Expression of MICA and BTN3A1 by senescent fibrous-cap VSMCs highlights a potential therapeutic strategy to stabilise vulnerable plaques and prevent myocardial infarction.

S2B-11 · Session 2B · Monday 15:00 · Presenter: Sarah Brooke

Cardiopulmonary Bypass-Induced Blood-Brain Barrier Disruption in a Clinically Relevant Ovine Model

Sarah Brooke[1], Alemayehu Jufar[1], Emily Hadzajlic[1,2], Angela Connelly[1], Linda Cornthwaite[1], Song T. Yao[2], Yugeesh R. Lankadeva[1,3], and Lindsea C. Booth[1,2]

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Background and Aims: Up to 50% of patients undergoing cardiopulmonary bypass (CPB) develop postoperative delirium. The underlying mechanisms are not well understood, although blood-brain barrier (BBB) disruption is thought to be a contributing factor. Limited clinical studies have shown increased BBB permeability 2-5 days postoperatively; however, CPB-induced structural changes of the BBB have not been well characterised. This study investigated severity and time course of CPB-induced frontal lobe BBB disruption using a clinically relevant ovine model.

Methods: Merino ewes underwent CPB before termination at end of CPB (n = 7), following a 48-hour recovery period (48 h; n = 9), or following a 48-hour recovery period with pre-existing, experimentally induced heart failure (48 h HF; n = 7); naïve controls did not undergo any surgical procedures (n = 6). Brains were perfused using 4% paraformaldehyde and cryosectioned into 40µm thick samples. Immunohistochemistry was performed to measure occludin and aquaporin-4 expression within the frontal lobe and imaged at 40x using a confocal microscope. FIJI was used to quantify mean intensity and percentage area expression within a manual region of interest, using aquaporin-4 as a vessel marker.

Results: One-way ANOVA analysis found CPB significantly decreased occludin expression in both 48 h ($p = 0.0117$) and 48 h HF groups ($p = 0.0156$), indicating increased BBB permeability.

Conclusions: These findings provide evidence of CPB-induced structural changes indicative of BBB disruption 48-hours postoperatively. These changes were not seen at the end of CPB. It remains to be determined whether these changes persist beyond 48-hours after CPB.

S2B-12 · Session 2B · Monday 15:10 · Presenter: Daniel Donner

Restarting the Brain After Refractory Cardiac Arrest: Extracorporeal Cardiopulmonary Resuscitation Restores Perfusion and Uncovers Novel Therapeutic Targets

Candice Todd[1,2,3], Aidan Burrell[1,4,5,6], Sasha Migus[1], Scott Loh[1,2], Marcus Mohr[1,2], Brooke Riley[5], Aascha D'Elia[1], Riley Batchelor[1,3,7], Gabrijela Sutalo[1,2,3], Nchafatso Obonyo[1,2,7], Dion Stub[1,3,6,8], Jason Bloom[1,2,3,7], David Kaye[1,2,3,7], **Daniel Donner[1,2,3,6]**

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Background and Aims: Extracorporeal cardiopulmonary resuscitation (ECPR) effectively restores systemic circulation during cardiac arrest (CA), even when the heart cannot be restarted through classical resuscitation (i.e. chest compressions and defibrillation). Experimentally, ECPR allows for controlled and reproducible global resuscitation (reperfusion) post-arrest, enabling the novel investigations herein exploring the complex neurological injury and recovery mechanisms following CA**.**

Methods: A total of 13 Large White adult pigs (56±2 kg, female) underwent endotracheal intubation, mechanical ventilation (isoflurane), instrumentation, and stabilisation. A sub-cohort of n=10 underwent the CA/ECPR protocol. Briefly, electrical induction of CA resulted in 5min of absent circulation prior to commencing mechanical resuscitative compressions with intracardiac haemodynamic guidance and vasopressor (adrenaline) support for 15mins. Veno-arterial cannulation was performed by intensivists using ultrasound guidance, and ECPR was delivered for 60min. Clinical assessments included high-fidelity vital sign, invasive haemodynamic, and blood/breath gas monitoring, and multi-region brain tissue were collected for both histopathology and integrated proteomic, phosphopeptide, and kinase analyses.

Results: Following CA, compressions and extracorporeal support sufficiently restored >80% physiological mean arterial pressures (48 ± 6 and 44 ±6 vs 53 ±4 mmHg at baseline, respectively). Arterial pO2 was also immediately restored with ECPR (454±36 vs 165±31 mmHg post-CA, $p<0.05$) to baseline values (418±49 mmHg), but not with earlier compressions. Brain cortex and hippocampal proteome/phosphoproteome remodelling was consistent with severe ischemia-reperfusion injury, coagulopathy, and acute inflammatory cascades. Additionally, integrated analyses revealed previously unreported site-specific disruption of pathways associated with low-abundance plasma lipoprotein and phospholipid assembly. **Conclusions and Significance:** As observed in clinical refractory CA, ECPR effectively restored blood flow, pressure and oxygenation in this experimental setting. Integrated analyses of brain tissue both validated known mechanisms of injury and revealed new opportunities for lipid-based biomarkers and targets for resuscitative and post-resuscitative care.

Session 3 — Neuroscience

S3-01 · Session 3 · Tuesday 10:10 · Presenter: Alayna Carmina Caruso

Polyanionic peptibody ameliorates tau pathology and improves synaptic function in tau transgenic mice

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Background and Aims: Alzheimer's disease is the leading cause of death in Australia and remains incurable. In Alzheimer's disease, the tau protein self-aggregates within neurons, causing downstream synaptic dysfunction and neuronal loss. Tau's positively charged proline-rich and microtubule-binding mid-domains become exposed in disease to facilitate aggregation and other neurotoxic tau interactions. To prevent this, we developed a polyanionic peptibody (ACR12) that electrostatically targets the mid-domains of tau and characterised its efficacy in tau transgenic mice.

Methods: ACR12 comprises of a negatively charged peptide, for electrostatic interaction with tau's mid-domains, fused to an inert single-chain antibody for enhanced peptide half-life. Recombinant ACR12 and tau proteins were used in *in vitro* binding and aggregation assays. ACR12-encoding DNA was then transfected into mammalian cells to investigate intracellular expression and target engagement. The ACR12 gene was next packaged into brain-penetrant AAV-PHP.eB and injected intravenously into K369I tau transgenic mice (ACR12 vs saline-treated Sham; n = 12-13 per group). Four-months post-injection, tau pathology was quantified via immunoblotting and immunofluorescence microscopy, and brain-wide proteomics performed. Additionally, synaptic function was assessed by patch-clamp electrophysiology on brain slices obtained from seven-month-old PS19 tau mice following intracerebroventricular AAV-ACR12 injection (n = 10-14 cells, 4 mice per group). Data was analysed by t-tests, one-way ANOVA or mixed-effects modelling.

Results: ACR12 was stably expressed within the cytoplasm of human neuroblastoma cells and engaged intracellular tau. In K369I mice, ACR12 significantly reduced total tau by 25.7% ($P<0.0001$), decreased phosphorylated tau at multiple epitopes by 52.2-62.5% ($P<0.05$), and restored brain-wide proteostasis towards wild-type levels. In PS19 mice, ACR12 improved long-term synaptic activity ($P<0.05$).

Conclusions: Electrostatic tau targeting reduces tau pathology and improves synaptic function. Limitations include early endpoints, before cognitive decline could be assessed, and small PS19 sample size. Our findings highlight the therapeutic potential of electrostatic tau interactors in disease.

S3-02 · Session 3 · Tuesday 10:20 · Presenter: Dylan Kiltschewskij

Disentangling Epigenetic Heterogeneity in Schizophrenia

Dylan Kiltschewskij[1,2], Murray Cairns[1,2]

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Background and Aims: Schizophrenia is a debilitating psychiatric condition associated with psychosis, cognitive deficits and functional decline. Clinical heterogeneity remains a major barrier to consistently effective intervention, with individuals varying in onset, progression, severity and symptom combinations, thought to reflect differing genetic and environmental risk. DNA methylation (DNAm), an epigenetic system shaped by genetic and environmental influences, is known to be dysregulated in schizophrenia, but whether it maps onto dimensions of clinical heterogeneity remains poorly understood. To address this, we systematically characterised DNAm associated with specific symptoms, medications, risk factors, and other measures to determine whether DNAm maps onto clinical variability.

Methods: Blood DNAm was profiled in 338 individuals with schizophrenia from the Australian Schizophrenia Research Bank, using Illumina EPICv1 BeadChips. Epigenome-wide association studies were conducted across 47 traits spanning symptoms, cognition, childhood adversity, psychotropic medications, and substance addiction.

Results: We identified 15 epigenome-wide significant methylation sites ($P < 6.44\text{x}10^{-8}$) predominantly linked to psychotropic medication use. A further 2,592 sites were associated with at least one trait at a discovery threshold ($P < 6.44\text{x}10^{-5}$). Methylation profiles largely clustered within trait categories, with childhood adversity and medications exhibiting strong internal concordance, while cognitive performance was correlated with negative symptoms (e.g. asociality, avolition). Strikingly, several schizophrenia-associated methylation profiles also correlated with established signatures of cardiometabolic health, including body mass index, C-reactive protein and cholesterol, suggesting the well-documented physical health burden in schizophrenia may have an epigenetic component. Finally, 193 methylation sites were associated with nearby mRNA expression, linking schizophrenia-associated methylation to corresponding changes in gene expression.

Conclusions: Together, these results establish the largest trait-resolved methylomic resource for schizophrenia to date, offering a foundation for dissecting biological heterogeneity underlying this condition and prioritising candidates for mechanistic and translational study.

S3-03 · Session 3 · Tuesday 10:30 · Presenter: Joshua Saito

Investigating the synaptic pathophysiology of a neurodevelopmental disorder in human neurons

Joshua Saito[1], Erlina Mohamed Syazwan[1], Snezana Maljevic[1], Sarah Gordon[1]
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Background and Aims: Baker-Gordon Syndrome is a neurodevelopmental disorder caused by pathogenic variants in SYT1, which encodes synaptotagmin-1, the essential presynaptic calcium sensor for neurotransmitter release. Although the pathophysiology of SYT1 variants has been investigated in primary rodent neurons, their impact on human neuronal function and disease progression remains poorly understood, and no effective treatments are currently available.

Methods: We established a bespoke live-cell imaging platform using human induced pluripotent stem cell (iPSC)-derived cortical neurons to interrogate presynaptic disorder mechanisms. We then generated human neurons carrying the pathogenic *SYT1* I368T variant alongside an isogenic comparison line, establishing the first heterozygous knock-in model of Baker-Gordon syndrome. Combining live-imaging techniques with patch-clamp electrophysiology, we assessed the synaptic maturity and ability of these iPSC-derived neurons to sustain evoked neurotransmitter release.

Results: We have found that these variants impact the synaptic vesicle cycle, causing a reduction in synaptic vesicle exocytosis upon neuronal stimulation. Additionally, leveraging the unique properties of iPSC's, we determined that variant cultures have fewer synapses which are active under stimulus conditions, a novel phenotype of the disorder that could play a major role in the pathophysiology of Baker-Gordon syndrome. Finally, we assessed the efficacy of a therapeutic compound across developmental time points and concentrations, identifying conditions capable of ameliorating cellular disease phenotypes.

Conclusions: Together, this work provides new insights into disorder pathophysiology and establishes a human neuronal platform for investigating Baker-Gordon Syndrome and evaluating therapeutic efficacy.

S3-04 · Session 3 · Tuesday 10:40 · Presenter: Jenna White

Characterisation of a Novel Mouse Model of PURA Syndrome

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Background and Aims: Pathogenic mutation in purine-rich element binding protein alpha (*PURA*) is an established cause of PURA syndrome. Individuals present with developmental and epileptic encephalopathy (DEE), causing severe motor deficits, intellectual disability, and epilepsy. Around 67% of patients are resistant to multiple anti-seizure medications. As the underlying cause of PURA-related epilepsy remain unclear, we engineered a mouse model of PURA syndrome carrying the most common variant of the disorder (p.Phe233del). We aimed to characterise this model and identify the cellular mechanisms producing seizures.

Methods: To understand the underlying mechanism of epilepsy in this model, we utilised littermate-controlled behavioural assays, electrocorticography (ECoG), patch-clamp electrophysiology of cortical layer II/III, and immunohistochemical assays in both wild-type (Wt) and heterozygous Pura^{F232*} mice. Sholl analysis was used to assess neuronal morphology. Unpaired t-tests and Wilcoxon signed-rank tests were used.

Results: Pura^{F232*} mice recapitulated key patient phenotypes, including poor ambulation ($P<0.01$, n=10 Wt/12 Pura^{F232*}) and seizures. Patch-clamp electrophysiology recordings did not show changes in the firing properties of cortical neurons ($P>0.05$, n=6 Wt/8 Pura^{F232*}). However, immunohistochemical reconstruction of single-neuron morphology showed hyper-maturation of both pyramidal neurons and inhibitory interneurons of the somatosensory cortex (pyramidal $P<0.0001$, n=6 Wt/6 Pura^{F232*}; interneuron $P<0.0001$, n=5 Wt/5 Pura^{F232*}). No changes in total cortical GABAergic neuron number were found ($P=0.47$).

Conclusions: Our Pura^{F232*} mouse model is the first humanised mouse model of the condition and recapitulates many key patient phenotypes, reinforcing its pre-clinical utility. The excessive dendritic branching in heterozygous mice could lead to altered cortical activity and hyperexcitability, although further network-level electrophysiology is required. As this hyper-maturation is observed in mouse models of Rett syndrome, this may be an important point of convergence in epilepsy pathophysiology across the two DEEs. Understanding the pathomechanism of seizures in PURA syndrome could inform anti-seizure medication screening and development of precision therapies.

S3-05 · Session 3 · Tuesday 10:50 · Presenter: Owen Jones

Investigating the role of zinc in potassium-mediated cerebral functional hyperaemia

Owen Jones[1]
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Background and Aims: Zinc is the second most abundant transition metal in the brain. Zinc Transporter 3 (ZnT3) - the second most abundant synaptic vesicle membrane protein - packages zinc into vesicles within presynaptic terminals, where it is released from active neurons into the perivascular space. Yet, a functional explanation for the high abundance of ZnT3 remains unknown. We hypothesised that neuronally-derived zinc contributes to functional hyperaemia - the localised and temporary redistribution of cerebral blood flow to metabolically active neurons - by enhancing potassium-mediated cerebral vasodilation through inward rectifier potassium (KIR) channels, specifically by increased KIR2.1 channel sensitivity.

Methods: We used complementary in vitro and in vivo approaches. Rat middle cerebral, posterior cerebral and basilar arteries were studied using wire myography to determine the effects of intracellular zinc on potassium-mediated vasodilation. Cortical blood-flow responses to tactile stimulation were assessed using widefield fluorescence microscopy in ZnT3 knockout and wild-type mice.

Results: Increasing intracellular zinc significantly enhanced potassium-mediated vasodilation in cerebral arteries, but not non-cerebral arteries. This enhancement was blocked by barium, indicating dependence on KIR2.1 channels, and was consistent with zinc relieving magnesium-dependent channel inhibition. Conversely, intracellular zinc chelation reduced vascular sensitivity to potassium. Preliminary in vivo data showed reduced stimulus-evoked cortical blood-flow responses in ZnT3 knockout compared with wild-type mice.

Conclusions: These findings identify neuronally derived zinc as a potential regulator of neurovascular coupling by enhancing KIR2.1-dependent potassium-mediated vasodilation. The results provide a possible mechanism linking neuronal zinc signalling with cerebral blood flow regulation and may have implications for conditions characterised by neurovascular dysfunction.

S3-06 · Session 3 · Tuesday 11:00 · Presenter: Sujan Kumar Sarkar

Blocking P2X7R-Mediated Signalling Confers Central and Peripheral Therapeutic Benefits in a Mouse Model of Huntington's Disease

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Background and Aims: Huntington's disease (HD) is an autosomal dominant neurodegenerative disorder characterised by motor, cognitive, psychiatric and gastrointestinal dysfunctions. HD is caused by *huntingtin* gene mutation. The P2X7R is an ATP gated ion channel, could be activated by toxic huntingtin protein and could trigger inflammation. However, its association in HD gut and brain health together remains unexplored. This study aimed to test the therapeutic potential of P2X7R antagonism ubiquitously with brain-penetrant Brilliant Blue G (BBG) and peripherally with A740003 (limited-to-non permeable to brain) to evaluate the comparative anti-inflammatory efficacy of these two approaches to ameliorate HD gut and brain symptoms.

Methods: P2X7R antagonists BBG (45.5 mg/kg from 6–16 weeks of age), A740003 (30 mg/kg from 7–16 weeks of age) and their respective vehicles were administered intraperitoneally to R6/1 HD mice and their wild type (WT) counterparts. Motor and cognitive functions, body weight, food and water intake trajectories along with functional and structural alterations of gastrointestinal system have been evaluated.

Results: BBG demonstrated improvement of several of the HD endophenotypes including body weight, motor, cognition and gastrointestinal impairments in R6/1 HD mice. Correspondingly, A740003 demonstrated improvement of body weight loss, attenuation of altered food and water intake in female HD mice while it improved motor function and selective gastrointestinal measures in both sexes. Collectively, targeting P2X7R exhibits therapeutic benefits in R6/1 HD mice, with prominent antagonism effects by BBG improving HD gut-brain symptomology. The benefits of A740003 are restricted to the periphery, yet this drug had some central actions, including improved motor function, along with improved intestinal health.

Conclusions: The findings feature novel strategies linking the impact of P2X7R antagonism in both central and peripheral symptomatology of HD. This has implications for future clinical trials for HD, a fatal disorder for which there is no available disease-modifying therapy.

Session 4 — Public health, clinical & health services

S4-01 · Session 4 · Tuesday 14:20 · Presenter: Sarah Lampard

Understanding concussion knowledge, reporting intentions and behaviours in community women's and men's Australian Football

Sarah Lampard[1 2], Dana Wong[3], Andrea Bruder[1 2 4], Kay Crossley[1 2], Alex Donaldson[2 5], Marc-Olivier Dube[1 6], Libby Gracias[1 2], Michael Makdissi[7], Andrew Hughes[7], Catherine Willmott[7 8 9], Jonathan Reyes[7 8 9], Anik Shawdon[7], Caroline O'Brien[7], Jeff Caron[10 11], Carolyn Emery[12], Brooke Patterson[1 2]

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[11]*Center for Interdisciplinary Research in Rehabilitation of Greater Montreal*
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Background and Aims: Despite increased global awareness regarding concussion diagnosis and consequences, up to 60% of athletes continue to not disclose potential concussion symptoms, risking worse symptoms and recovery. We aimed to explore concussion knowledge, reporting intentions and behaviours among adult women and men playing community Australian Football.

Methods: A sequential mixed-methods study using a survey (anonymous nationwide survey to players aged ≥18) and focus groups. Concussion knowledge (e.g., symptoms/diagnosis, % correct), reporting intentions and behaviours (e.g. adherence to guidelines) were analysed descriptively by gender. Factors and potential strategies influencing concussion reporting behaviours were explored in focus groups, and data analysed using framework analysis.

Results: 348 players (43% women; median age=31; 64% lifetime concussion history [M;72%, W:53%]) completed the survey, and 22 participated in focus groups. Concussion symptom/diagnosis knowledge was high (W: 91% M: 93%). Knowledge of the minimum return-to-play duration was higher in women (W:64%, M:49%). More men reported previously underreporting potential concussion symptoms (M:47%, W:31%). Of those diagnosed with concussion in 2024–25 (n=79), many reported returning-to-play prior to the recommended minimum 21 days (M:41%, W:30%). More women reported following a return-to-play protocol (W:67%, M:45%) and obtaining medical clearance (W:70%, M:56%). Three qualitative themes were constructed with players either being (1) UNAWARE; of concussion symptoms/guidelines, (2) UNCERTAIN; of the care pathway or doubting the process or potential consequences/benefits, or (3) UNMOTIVATED to report symptoms, despite adequate knowledge, Individual, interpersonal, and sport system factors which may deter or facilitate reporting were identified.

Conclusions: Despite increased concussion awareness globally, education alone is not enough. Targeted behaviour change strategies may be needed enhance the sub-optimal concussion-related knowledge and behaviours in Australian Football. Strategies should combine education with mandates to eliminate premature return-to-play, campaigns to foster club cultures that prioritise health first, and clearer and accessible reporting pathways and medical processes.

S4-02 · Session 4 · Tuesday 14:30 · Presenter: Chilot Desta Agegnehu

Patterns and predictors of past-month injecting among people who inject drugs from culturally and linguistically diverse backgrounds: a 16-year Melbourne cohort study

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Background and Aims: Injecting drug use causes substantial illness and premature death. Despite Australia's cultural diversity, little is known about people who inject drugs from culturally and linguistically diverse (CALD) backgrounds. We compared injecting patterns and predictors of recent injecting between CALD and non-CALD participants.

Methods: We analysed SuperMIX, an ongoing longitudinal Melbourne cohort of people who inject drugs interviewed annually 2008–2024 (up to 14 follow-ups). CALD was defined by birth in a non-English-speaking country and/or speaking another language at home. Mixed-effects logistic regression, accounting for repeated interviews, identified predictors of past month injecting, reported as adjusted probability differences with 95% confidence intervals (CIs). Four sensitivity and nine interaction analyses assessed robustness.

Results: Of 1748 participants, 304 (17.4%) were CALD, more often male (84.5% vs 67.2%) and more likely to inject in the groin (13.9% vs 5.2%) and more likely to be stably housed (73.6% vs 60.5%). Injecting patterns differed by age, employment, income, housing and groin injecting. CALD status was not associated with injecting in the past month (difference −1.21 percentage points; 95% CI −4.67 to 2.23; p=0.49), and no association differed by CALD status (all false-discovery-rate-

adjusted p≥0.76). Less injecting was associated with employment, stable housing, better physical and mental health, and higher alcohol use; more injecting with older age, smoking, and longer follow-up. Age, employment, smoking and follow-up time were consistent across sensitivity analyses.

Conclusions: CALD participants showed a distinct injecting risk profile, notably groin injecting, but we found no evidence of differences in continued injecting. Confidence intervals couldn't exclude a modest effect, and findings should be interpreted considering self-reported measures and attrition. This longitudinal comparison of CALD people who inject drugs suggests harm reduction and treatment should address modifiable social and health factors across all groups, while responding to culturally specific injecting risks.

S4-03 · Session 4 · Tuesday 14:40 · Presenter: Alexandra R Davidson

Self-management program for people with chronic obstructive pulmonary disease (COPD): The Activating Primary Care COPD Patients with Multimorbidity (APCOM) Trial – Early Findings

Alexandra R. Davidson[1], Sameera Ansari[2, 3, 1], Amanda Tauber[1], Lisa Olsen[1], Ian Yang[4, 5], Helen Reddel[3, 6, 7], Elizabeth Halcomb[8], Hassan Hosseinzadeh[9], Sarah Dennis[10, 11], Mark Morgan[1], Lisa Collison[12], Harry Patsamanis[13], Marijka Batterham[14], Glenn Salkeld[15], Nick Zwar[1,2].

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Background and Aims: Self-management support for chronic obstructive pulmonary disease (COPD) can reduce exacerbations and hospital admissions. Evidence of effectiveness in primary care is scarce, especially accounting for multimorbidity. We tested a novel self-management program for COPD in the context of multimorbidity in general practice. We hypothesised that at 12-months' follow-up, intervention group patients will have improved COPD-related health status assessed by the COPD Assessment Test (CAT, primary outcome) compared to the control group. Secondary outcomes include COPD knowledge, patient activation and overall health-related quality of life.

Methods: A multicentre, pragmatic, single-blind, cluster randomised controlled trial was conducted in five Australian states. General practices were randomised 1:1 to usual care or intervention. Patient eligibility criteria: i) aged ≥40 years, ii) spirometry-confirmed COPD, iii) visited their general practice in last 12-months, iv) ≥1 comorbidity. Intervention patients received a tailored, self-management program delivered by general practice nurses in collaboration with General Practitioners (GPs) and allied health professionals. A qualitative process evaluation examined intervention acceptability, feasibility and sustainability.

Results: Twenty-nine practices participated in the trial. Of 220 patients who completed baseline data, 54% were female, mean age was 72 years, and 35% lived alone. Patients had 1-16 comorbidities, and average CAT score was 19.6 (SD±7.5). Participants were prescribed 0-6 COPD medications; only 5% reported prior pulmonary rehabilitation attendance. Twenty-four patients, 12 nurses, and 5 GPs participated in semi-structured telephone interviews and reported overall positive experiences with the program. At 12 months' follow-up, 176 patients completed the surveys, and quantitative outcome analysis is underway.

Conclusions: The study identified substantial impact of COPD and comorbidities in patients at baseline. It will evaluate if a COPD self-management program that recognises the existence and impact of multimorbidity can lead to improved health outcomes. Funding and workplace structures are needed for long-term implementation.

S4-04 · Session 4 · Tuesday 14:50 · Presenter: Jordan Lim

Clinical tools for assessment of plaster cast quality in patients with limb fractures in the Emergency Department: a systematic review of radiological indices

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Background and Aims: Limb fractures are common presentations to the Emergency Departments (ED). Effective fracture immobilisation depends on appropriate application and quality of plaster casts. Objective tools to assess cast quality are not

routinely used in clinical practice. The objectives of this systematic review were to: (i) collate indices developed to assess cast quality in limb fractures; (ii) summarise the radiological measurement components of these indices.

Methods: Three databases (OVID MEDLINE, EMBASE and SCOPUS) were searched up to April 2026. Inclusion criteria were English-language observational and interventional studies reporting indices used to assess cast quality in limb fractures. Two reviewers independently assessed eligible studies. Risk of bias was assessed using the Newcastle–Ottawa Scale. Results were synthesised descriptively, with random-effects proportion meta-analysis conducted to estimate the frequency of each index reported across studies.

Results: Forty-three studies were included; five cast quality indices were identified, including Cast Index, Gap Index, Padding Index, Three-Point Index and Canterbury Index. Twelve common variables were synthesised across these indices. Most studies were observational, predominantly involving paediatric upper limb fractures. Cast Index was most frequently assessed, included in 38 out of 43 studies (proportion 0.88, 95% CI 0.79–0.98). Canterbury Index was the least frequently reported index (proportion 0.30, 95% CI 0.17–0.44).

Conclusions: The five cast quality indices, incorporating twelve radiological measurement variables, provide a foundation for developing an objective checklist to evaluate cast quality in the ED. Further research is required to determine whether a "high-quality" cast based on these measurements correlates with clinically meaningful outcomes.

S4-05 · Session 4 · Tuesday 15:00 · Presenter: Marianne Piano

A case study of how eyecare needs are identified, understood and met in residential aged care.

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Background and Aims: People living with dementia are at increased risk of preventable sight loss from age-related eye diseases. This risk is doubled if living in residential aged care. Our study aimed to understand how eyecare is delivered for people in residential aged care, including people with dementia.

Methods: A single site observational case study was conducted in an Australian residential aged care facility. Various activities were observed: mealtimes, medication rounds, socialising, art/music therapy, physical activity, resident meetings and an optometrist visit. Micro-interviews were conducted with care staff, lifestyle team members, external activity providers and visiting allied health professionals.

Thematic analysis was performed on field notes/interviews using the Consolidated Framework for Implementation Research. Findings were reviewed by an expert reference group uniting hospital, community and long-term care perspectives on eyecare, and a project advisory group comprising people living with dementia and past/present carers.

Results: In total, 53 observation sessions were conducted. Many groups were involved in meeting eyecare needs, but nurses and the visiting optometrist had the best understanding of these needs. Some people with dementia had difficulties articulating, understanding and/or managing their eyecare needs. Principal barriers for redress were regulatory environment creating documentation burden, disparities in information access between staff and externals, and information gaps between external eyecare providers and the facility, or between facility floors. Facilitators for leverage included widespread use of large print, lifestyle team creativity in activities, the electronic care plan, toolbox training opportunities for staff members and existing feedback mechanisms such as residents and relatives meetings.

Conclusion: A dementia-friendly eyecare pathway in residential aged care should address information gaps through a systematic approach to communicating previous ocular history, current treatment and eyecare needs to the facility at intake and post-appointment. Staff training can increase understanding of eyecare needs by key people providing support in the facility, such as lifestyle team members and personal care workers.

S4-06 · Session 4 · Tuesday 15:10 · Presenter: Tan Minh Nguyen

Assessing Cost-Effectiveness on Oral Health Preventive Interventions (ACE-Oral Health Prevention)

Tan Nguyen[1-3].

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Background and Aims: Resource allocation investment by Australian governments to prevent oral disease is ad hoc and largely focused on oral healthcare service delivery, and limited focus on oral disease prevention. The aim of this study is to apply the Assessing Cost-Effectiveness (ACE) priority-setting approach on oral health preventive interventions to understand whether they are cost-effective, and to understand other implementation considerations criteria relevant to inform government policy decision-making.

Methods: A Project Steering Group (PSG) consisting of consumer representatives, academics, and policymakers was established. The PSG selected six preventive interventions for economic modelling: anticipatory guidance provided by oral health therapists, implementing a sugar-sweetened beverage (SSB) tax, targeted school-based fissure sealant/fluoride varnish programs, applying the Caries Management System protocol (a Minimally Invasive Dentistry approach), and tobacco cessation services. The study used disability-adjusted life years (DALYs) as the primary outcome, with the explicit willingness-to-pay (WTP) threshold of AUD$50,000 per DALY averted. Secondary outcome measures used decayed teeth prevented (DT-prevented) and quality-adjusted life years (QALYs), where appropriate. Costs and outcomes had a 5% discount rate applied.

Results: A valoric 20% SSB tax emerged as the only cost-effective intervention, resulting in modelled projected net cost-savings of AUD$64 million from a societal perspective and 98 DALYs averted over 10 years. All other interventions were not cost-effective. When ranked by the DT-prevented outcome, the SSB tax remained most cost-effective, which was followed by utilising non-dental professionals to implement a targeted school-based fluoride varnish program.

Conclusions: A universal intervention such as 20% valoric SSB tax, can promote oral health equity while generating cost-savings. Utilising non-dental health professionals can increase cost-effectiveness. Most clinical preventive interventions did not demonstrate value for money under the current WTP threshold, highlighting caution in designing oral health policy for resource allocation. Future research should incorporate broader health co-benefits from oral health preventive interventions.

Session 4B — Maternal health, brain & mental health

S4B-01 · Session 4B · Tuesday 14:20 · Presenter: Jianing Xu

Impact of different diagnostic definitions of pre-eclampsia: a systematic review and meta-analysis

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Background and Aims: Pre-eclampsia affects approximately 4.6% of pregnant women worldwide, but diagnostic definitions vary across international guidelines. The clinical implications of these differences are uncertain. We aimed to assess how different diagnostic definitions influence pre-eclampsia prevalence, maternal and neonatal outcomes, healthcare utilisation, and risk screening prognostic performance.

Methods: We conducted a systematic review and meta-analysis of studies comparing two or more diagnostic definitions of pre-eclampsia. Seven databases were searched from inception to 10 February 2026, without language restrictions. Prevalence differences and risk ratios with 95% CIs were pooled using random-effects meta-analysis when at least two studies reported the same comparison. Risk of bias was assessed using ROBINS-E.

Results: Of 3356 records identified, 23 studies were included, of which 15 contributed data to the analyses. Compared with the traditional hypertension plus proteinuria definition, broader definitions increased prevalence by 0.3–1.3 percentage points, with 6.0–43.8% of women meeting broader definitions not identified by the traditional definition. Women additionally identified by broader definitions had lower risks of preterm birth before 37 weeks (RRs 0.70–0.72), NICU admission (0.52–0.67) and caesarean delivery in some comparisons (0.85–0.89), whereas most maternal outcomes did not differ. Sensitivity analysis excluding one study at high risk of bias produced similar findings.

Conclusions: Broader diagnostic definitions identify additional women who would be missed by traditional proteinuria-based definition and should not simply be regarded as having milder disease. These findings support expanding definitions beyond proteinuria detection, to reflect the multisystem nature of pre-eclampsia. Prospective evaluation of different diagnostic definitions is needed, particularly in low-resource settings.

S4B-02 · Session 4B · Tuesday 14:30 · Presenter: Alanna Gillespie

Congenital cytomegalovirus infection and infant hearing loss in Australia: the Screen cCMV study

Alanna Gillespie[1,2], Daisy Shepherd[1,3], Melissa Wake[1], Cheryl Jones[4], Xinyang Hua[3], Margarita Moreno-Betancur[1,2,3], Lisa Hui[1,2,3,5], Zeffie Poulakis[1,2], Hayley Smithers-Sheedy[4,6,7], Jafri Kuthubutheen[8], Seilesh Kadambari[9,10], Kim Powell[1], Tony Frugier[1], Marc Ramsperger[11], Charlene Mackenzie[11], Georgina Papadakis[11], Preethi Chandrasekaran[1,3], Richard Saffery[1], Valerie Sung[1,2,3] *on behalf of the Screen cCMV Investigator Group.*

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10 Great Ormond Street Hospital, UK.
11 Victorian Infectious Diseases Reference Laboratory, Melbourne Health, Australia. Affiliations for the Screen cCMV investigator group are available online: https://www.mcri.edu.au/research/projects/screen-ccmv-project.

Background and Aims: Congenital cytomegalovirus infection (cCMV) is the leading infectious cause of hearing loss and neurodevelopmental disability. The Screen cCMV study aims to determine the 1) prevalence and 2) infant hearing outcomes of cCMV in an Australian population.

Methods: Screen cCMV partnered with GenV, a whole-of-state birth cohort recruited from Victoria, Australia between October 2021-October 2023. Screen cCMV tested saliva samples from newborns aged <3 weeks using viral nucleic acid extraction and real-time CMV polymerase chain reaction (PCR) in two steps: 1) eight-sample pooled CMV PCR testing, 2) individual CMV PCR retesting of samples from positive pools. Beta actin testing was completed on 192 samples to confirm genomic DNA in samples. cCMV results were linked with GenV-collected demographic data and state-wide hearing screening data in May 2026. Descriptive statistics describe cCMV and hearing loss prevalence. Adjusted cCMV prevalence accounts for the proportion of samples with no genomic DNA.

Results: GenV collected saliva from 33,309 infants aged <3 weeks (51.3% male, mean socioeconomic disadvantage score 1009 (SD: 59) similar to population norms, 76.2% living in a major city). PCR testing confirmed cCMV in 94 of 33,309 GenV newborns (prevalence: 0.28%, 95%CI: 0.23%, 0.35%). Beta actin was detected in 191/192 (99.5%) samples, resulting in an

adjusted prevalence of 0.28% (95%CI: 0.23%, 0.35%). Hearing loss was audiologically confirmed in 6 of the 94 cCMV positive infants (6.4%, 95% Clopper-Pearson CI 2.4–13.4%). All hearing loss was unilateral with varying severities reported (1 mild, 1 moderate, 1 severe, 3 profound).

Conclusions: This is the first large scale study to determine Australian birth prevalence of cCMV. Approximately 3 out of every 1000 babies in the GenV cohort had cCMV, with unilateral sensorineural hearing loss detected shortly after birth in 6.4%. Future studies will explore longer term developmental outcomes of this cohort as they age.

S4B-03 · Session 4B · Tuesday 14:40 · Presenter: Kanika Mehta

Dementia mortality in the context of diabetes: age- and sex-specific time trends across seven jurisdictions

Kanika Mehta[1,2], Jedidiah I. Morton[1,3,4], Lei Chen[1], Kaarin J. Anstey[5,6,7], Bendix Carstensen[8], Edward W. Gregg[9,10], Martti Arffman[11], Gillian L. Booth[12,13,14], Luan Manh Chu[15,16], Kelly Fleetwood[17], Archana Singh-Manoux[18,19], Sandrine Fosse-Edorh[20], Marie Guion[20], Padma Kaul[21,22,23], Calvin Ke[12,13,14,24], Ilmo Keskimäki[11], Susanne Boel Graversen[25], Tinne Laurberg[25,26,] Henrik Støvring[25,27], Sarah H. Wild[17], Jonathan E. Shaw[1,3,28] and Dianna J. Magliano[1,3]

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Background and Aims: People with diabetes are at increased risk of dementia, yet large-scale data on age- and sex-specific dementia mortality trends in this group remain limited. Therefore, we estimated age- and sex-specific time trends in dementia mortality among individuals with and without diabetes from high-income jurisdictions.

Methods: We analysed aggregated mortality and demographic data using registries and administrative sources in Australia, Canada (Alberta and Ontario), France, Denmark, Finland and Scotland from 2000 to 2023. Poisson regression was used to estimate mortality rates for dementia as the underlying cause of death in people with and without diabetes at 60, 70, 80 and 90 years of age.

Results: A total of 114,559 and 589,706 dementia deaths were identified in over 42 and 244 million person-years of follow-up for individuals with and without diagnosed diabetes, respectively. Dementia mortality trends varied by age and jurisdiction but were generally consistent for both sexes. At younger ages (e.g., 60 and 70 years), the dementia mortality trends did not suggest any meaningful increases or decreases except for Scotland, which reported increasing dementia mortality over time only for those with diabetes. At older ages (e.g., 80 and 90 years), however, increases in dementia mortality were observed in most jurisdictions, ranging from 7.6% to 42.4% per five years. The magnitude of the increases was generally greater for those with diabetes. Mortality from dementia subtypes (e.g., Alzheimer's disease and vascular dementia) also increased over time in individuals aged 40 to 89 years, with greater increases in mortality rates for individuals with diabetes, specifically in Australia and Scotland.

Conclusions and Significance/Impact: Increases in dementia mortality were observed for those aged 80 and above and were most marked for people with diabetes. These findings highlight the growing burden of dementia for health systems.

S4B-04 · Session 4B · Tuesday 14:50 · Presenter: Erin Harcourt

Development and Validation of the Critical Care Memory Tool in Post-Intensive Care Patients

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Background and Aims: Critical care survivors are often traumatised by their Intensive Care Unit (ICU) experience. Factual, feeling, and delusional memories are explored in ICU populations using the ICU Memory Tool. However, the evidence that the memories measured using this tool reflect patient experience is mixed. This study aims to improve the measurement of ICU-related memories by developing and validating an alternative measure, the Critical Care Memory Tool (CCMT).

Methods: We developed the CCMT using proxy measures modified and adapted, consisting of questions focusing on demographics and experiences of pain, hallucinations, surreal experiences, nightmares, and fear/anxiety, resulting in 127 items.

Results: The study included 138 ICU survivors aged 18 to 80 years (*M* = 52.31, *SD* = 14.30), predominantly women (64.5%). The EFA revealed a 40-item, four-factor structure, with four district subscales (Anxiety/Fear, Hallucinations, Surreal Experiences, and Pain). The validity and reliability of the CCMT were excellent. Bivariate correlation analysis revealed that the CCMT correlated in expected ways with measures of psychological outcomes and the feeling and delusion memories subscale of the ICU memory tool.

Conclusions and Significance/Impact: The CCMT 4-factor structure, measures ICU patients memories of hallucinations, surreal experiences, anxiety/fear, and pain. Relationships with existing scales provide evidence of scale validity. Practical implications include identification and quantification of the ICU memories experienced by survivors of critical illness and prediction of ongoing psychological impacts such as anxiety, depression, and PTSD. Future research should confirm results using a Confirmatory Factor Analysis (CFA) and investigate further the construct validity of this tool.

S4B-05 · Session 4B · Tuesday 15:00 · Presenter: Lauren T Ursich

Why Sex Matters: Exploring Neurobiological Differences Driving Binge Drinking

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Introduction: Sex differences in alcohol use disorder (AUD) are increasingly recognised, yet the neurobiological basis underlying these differences remains poorly understood. The neuropeptide-rich centrally projecting Edinger-Westphal nucleus (EWcp) is an emerging regulator of excessive alcohol consumption in a sex-dependent manner; however, its cellular landscape and alcohol-induced transcriptional adaptations have not been defined.

Objective: We aimed to generate a spatially resolved cellular atlas of the EWcp and define alcohol-induced transcriptional adaptations in male and female mice.

Methods and Results: Following voluntary binge drinking, EWcp tissue was profiled alongside alcohol-naïve controls (n=4–7/sex/group) using Xenium spatial transcriptomics with the mouse brain panel supplemented with a custom 50-gene panel spanning stress, arousal, feeding, reward and hormone-related signalling. We developed an integrated multi-sample spatial transcriptomic workflow to resolve EWcp cellular heterogeneity, enabling comparative analysis of baseline sex differences and alcohol-induced transcriptional adaptations through differential expression and spatial-based analyses. We identified 12 transcriptionally distinct EWcp cell populations displaying conserved spatial organisation across males and females. Despite conserved cellular architecture, sex-dependent transcriptional differences were evident across all cell populations at baseline. Alcohol exposure induced further sex-dependent transcriptional differences both globally and within specific cell populations, including peptidergic neurons.

Conclusions: This study provides the first spatially resolved characterisation of the EWcp cellular landscape across sexes, revealing sex- and alcohol-associated transcriptional adaptations within a conserved cellular architecture. These findings advance our understanding of cell-type-specific molecular responses to alcohol across sexes, and provide a foundation for identifying candidate molecular targets currently undergoing functional validation studies to support the development sex-informed therapeutic strategies for AUD.

S4B-06 · Session 4B · Tuesday 15:10 · Presenter: Adelaide Bernard

Leveraging elasticity scores to uncover diet-induced shifts in hypothalamic lipid metabolism

Adelaide Bernard[1], *Kevin Liu*[1], *Yingying Liu*[1], *Jen Xin Fach*[1], *Hanne Woo*[1], *Kevin Huynh*[1], *Natalie Mellet*[1], *Manika Singh*[1], *William Ho*[1], *Peter Meikle*[1], *Brian Drew*[1], *Yi Wang* [1]
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Background and Aims: The brain is the second-most lipid-rich organ, with lipids playing essential roles in membrane formation, signalling, inflammation regulation, neurogenesis, energy storage, and protection against oxidative stress. Dysregulation of lipid metabolism is a key factor in obesity-related diseases and neurodegenerative disorders, highlighting the importance of lipid homeostasis for brain function. Despite recent advances in lipidomics technology, how brain lipid metabolism is affected by diet and the energy status of an organism remains poorly understood. The hypothalamus regulates energy homeostasis by integrating nutrient and hormonal signals to control energy expenditure and feeding behaviour. While high-fat diets are known to disrupt hypothalamic function, whether and how they disrupt lipid metabolism in the hypothalamus remains unclear.

Methods: This study leveraged lipidomics (quantifying 750+ individual lipid species) and bulk RNA sequencing to examine the impact of short- (3 days) and long-term (8 weeks) high-fat diet on hypothalamic lipid metabolism. Obesity has recently been shown to reduce the "metabolic elasticity" of peripheral organs, i.e. their ability to respond to energy balance disturbances and return to baseline homeostasis. We applied this concept to the hypothalamus to assess its adaptability to metabolic challenges, such as cycles of fasting and refeeding, under different diet conditions. Originally developed for transcriptome data, we extended this concept to analyse lipidome elasticity.

Results: Our findings revealed that just three days of a high-fat diet already significantly altered hypothalamic elasticity, which was further impacted after 8 weeks of high-fat diet. We identified novel pathway perturbations not evident when comparing single metabolic state snapshots in high-fat diet versus chow-fed mice.

Conclusions: Understanding the interplay between obesity, lipid metabolism and brain function is essential for developing new therapeutic strategies. This study shows that metabolic elasticity scoring offers a promising approach to identify novel pathways involved in the neurological aspects of obesity-related metabolic disorders.

Session 5 — Cancer & cell biology

S5-01 · Session 5 · Wednesday 10:10 · Presenter: Yining Tian

Genomic Alterations in TNF-Related Cell Death Pathways as Potential Biomarkers for Personalized Therapy in Oral Squamous Cell Carcinoma

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Background and Aims: Oral squamous cell carcinoma (OSCC) remains a major health burden. Tumour necrosis factor (TNF) regulates inflammatory cell death through FADD and CASP8, while inhibitor of apoptosis proteins restrain this response. FADD amplification and CASP8 mutation are frequent in HPV-negative OSCC. We investigated whether these alterations modify responses to SMAC mimetics, small-molecule inhibitors of apoptosis proteins, and could therefore serve as treatment-response biomarkers.

Methods: H400 and H357 OSCC cell lines were used to model FADD-related alterations. HAP-1 cells were used to validate prime-editing guide RNAs and introduce CASP8 mutations before editing OSCC cells. Cell-death responses to TNF plus SMAC mimetic treatment, with or without low-dose cisplatin, were assessed alongside protein expression relevant to necroptosis.

Results: FADD amplification sensitised H400, but not H357, cells to SMAC mimetic-induced death, and this response was not further enhanced by chemoradiotherapy combination. The FL25GG FADD mutation, which impairs FADD-caspase-8 interaction, did not alter SMAC mimetic sensitivity. HAP-1 cells carrying CASP8 mutations showed reduced sensitivity to TNF/SMAC mimetic treatment and relative resistance when low-dose cisplatin was added. These cells also showed impaired necroptotic responsiveness, consistent with undetectable MLKL and RIPK3 protein expression.

Conclusions and Significance/Impact: Alterations in the TNF-cell death axis can reshape inflammatory cell-death responses in a context-dependent manner. FADD and CASP8 status are therefore candidate biomarkers for stratifying OSCC responses to SMAC mimetic-based therapies, although their predictive value requires validation across additional models.

S5-02 · Session 5 · Wednesday 10:20 · Presenter: Brenda Briones Miranda

From clinical observations to an in vivo model of clonal haematopoiesis: Investigating BCL2–BAX-mediated clonal dynamics in zebrafish

Brenda Briones Miranda[1,2], Vahid Pazhakh[2], Ing-Soo Tiong[2], Piers Blombery[2], Graham Lieschke[1,2]

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Background and Aims: Clonal Haematopoiesis (CH) occurs when an individual mutant Haematopoietic Stem Cell (HSC) and its clonal progeny gain a competitive advantage, leading to dominance of the HSC pool. This is often facilitated by somatic mutations conferring the mutant HSCs with an increased capacity for self-renewal and differentiation. Acquired BAX mutations associated with clonal haematopoiesis have previously been identified in after prolonged BCL2 treatment, but the long-term consequences of sustained BCL2 inhibition on HSC clonal dynamics remain poorly understood. We aim to investigate whether BAX favours clonal haematopoiesis in a BCL2 deficient model.

Methods: We analysed longitudinal next-generation sequencing (NGS) data from patients with follicular lymphoma treated with obinutuzumab, venetoclax and lenalidomide to investigate BAX mutation dynamics. To explore the underlying dynamics, we developed a zebrafish model combining TWISTR-based multicolour clonal tracking with somatic BAX mutagenesis in a BCL2-deficient background. Fluorescent colour overrepresentation enables the identification of potentially expanding haematopoietic clones for subsequent molecular characterisation by NGS.

Results: Longitudinal NGS analysis identified acquired BAX mutations in the follicular lymphoma cohort, motivating further investigation of treatment-associated clonal dynamics. We also characterised a BCL2 mutant with features consistent with impaired pro-survival function, supporting its potential as a genetic model of BCL2 inhibition. This model has been integrated with a multicolour clonal tracking and somatic BAX mutagenesis to investigate the relationship between BCL2 deficiency and haematopoietic clonal expansion. In vivo clonal analysis is ongoing.

Conclusions and significance: Our clinical observations and newly established zebrafish model provide a framework to investigate the relationship between BCL2 deficiency, BAX mutations and CH in vivo. This model will enable longitudinal assessment of clonal dynamics and help determine whether BAX mutations confer selective advantage to haematopoietic clones, advancing our understanding of treatment-associated clonal selection.

S5-03 · Session 5 · Wednesday 10:30 · Presenter: Mackenzie Lighton

Low-Dose Radiotherapy Alters Macrophage Polarisation in a Murine Mesothelioma Model

Mackenzie Lighton[1], Faith Hartley[1,2], Rebecca D'Alonzo[1,3], Tracy Hoang[1,4], Alistair Cook[1,4], Martin Ebert[3,5]

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Background and Aims: Mesothelioma is a fatal cancer caused by asbestos exposure, with immune checkpoint inhibitors (ICIs) the first-line treatment offered. However, many patients do not respond. Poor responses may reflect an immunologically 'cold' tumour microenvironment (TME), characterised by limited anti-tumour immunity and lymphocyte infiltration. 'Cold' TMEs are enriched in tumour-associated macrophages (TAMs), which adopt anti-tumour 'M1-like' or pro-tumour 'M2-like' phenotypes in response to surrounding stimuli. Low-dose radiotherapy (LDRT) may modulate the TME and enhance ICI efficacy. Preliminary murine gene expression data suggest LDRT influences TAM polarisation, shifting these cells towards an 'M1-like' phenotype. This study aimed to validate these findings at the cellular level. We hypothesised LDRT-treated tumours would express a higher proportion of 'M1-like' markers than sham-irradiated tumours.

Methods: Tumours were established in BALB/c mice (n=40) using the AB1-HA mesothelioma cell line and treated with LDRT or sham-irradiation. Mice were euthanised, and tumours were harvested at 1 or 6 days post-irradiation. Flow cytometry was used to analyse the expression of phenotypic macrophage markers. Unpaired t-tests were used for statistical analysis. P-values less than 0.05 were considered significant.

Results: Analysis revealed a shift in the relative proportions of immune cells in response to LDRT, with decreased macrophage levels ($p=0.00002$) and increased T-cells ($p=0.005$) and neutrophils ($p=0.001$) demonstrated in LDRT-treated tumours. Macrophages within irradiated tumours demonstrated increased expression of 'M1-like' markers and PD-L1 ($p=0.0001$), and decreased expression of the 'M2-like' marker CD9 ($p=0.00002$). Observed changes were more pronounced at 1-day post-irradiation, with a shift toward baseline levels demonstrated over time.

Conclusions: These findings suggest that LDRT shifts macrophage polarisation towards the anti-tumour phenotype, which may play a role in enhancing the efficacy of ICIs. This study will help guide future research exploring the combination of ICIs with LDRT and biomarker selection, with the aim of improving patient responses to ICIs.

S5-04 · Session 5 · Wednesday 10:40 · Presenter: Olivia Rose Comito

The interaction between the human gut microbiome and pancreatic ductal adenocarcinoma (PDAC): A prospective study correlating microbiome composition with anti-cancer treatment and tumour response.

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Background and Aims: Research has suggested bacteria in the gut microbiome, and their metabolites, may interact with pancreatic tumours and their treatments. As such, this study aimed to prospectively investigate the relationship between the human gut microbiome and pancreatic cancer.

Methods: 24 participants with PDAC received combinations of chemotherapy, immunotherapy and an iRGD peptide. Stool samples were collected pre- and post-treatment with gut microbial profiling completed using PacBio HiFi full-length 16S rRNA sequencing.

Results: 5 participants demonstrated a complete disappearance of their tumours. These participants had the highest baseline levels of Firmicutes (>95.0%) and lowest levels of Proteobacteria (<0.5%).

9 previously inoperable participants became eligible for surgery. 6/9 participants had Firmicutes levels >95.0% and Proteobacteria levels <0.5% after treatment.

4 participants had disease progression after coming off treatment and demonstrated the highest baseline levels of Proteobacteria (<27%), and the lowest levels of Firmicutes (>44%).

17/24 participants received immunotherapy, with 14/17 showing an increase in Firmicutes (<40.15%) and 12/17 showing a decrease in Proteobacteria (<28.43%). Average relative abundance was 80.93% and 6.03% pre-treatment vs 92.05% and 3.58% post-treatment for Firmicutes and Proteobacteria respectively.

7/24 participants did not receive immunotherapy. 4/7 had a decrease in Firmicutes (<41.17) and 5/7 had an increase in Proteobacteria (<42.72%). Average relative abundance was 86.76% and 2.30% pre-treatment vs 81.10% and 9.37% post-treatment for Firmicutes and Proteobacteria respectively.

Microbial profiling identified 24 species of bacteria (19 in the Firmicutes phylum) associated with the complete disappearance of tumours ($p<0.05$), 6 species (Firmicutes phylum) associated with surgical eligibility ($p<0.05$) and 8 species (7 in the Firmicutes phylum) associated with immunotherapy administration ($p<0.05$).

Conclusions: An association was observed between microbial composition, immunotherapy administration and treatment response, with higher Firmicutes and lower Proteobacteria correlating with an improved response. Future research should focus on manipulation of gut bacteria to improve patient response to treatment.

S5-05 · Session 5 · Wednesday 10:50 · Presenter: Emily Cross

Genetic relationships between metabolic traits and breast cancer: identifying shared biology

Emily Cross[1,2], Laura Greco[1,2], Murray Cairns[1,2], Dylan Kiltschewskij[1,2]

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Background and Aims: Observational studies have reported associations between breast cancer and metabolic traits ranging from circulating metabolites to metabolic disease. However, the biology underlying these relationships remains poorly understood. We aimed to map germline genetic relationships between metabolic traits and breast cancer to better understand the interplay between metabolic health and breast cancer liability.

Methods: Genetic variants associated with 249 metabolic traits and breast cancer (as well as estrogen receptor (ER)-positive and ER-negative subtypes) were obtained from genome-wide association studies. We quantified genome-wide genetic correlation to identify shared inherited influences between breast cancer and metabolic traits, then applied 2 independent causal analyses to further investigate these relationships. Traits with strong evidence for shared biology were examined using gene-level association, predicted gene and protein expression, and regional genetic effects. Genes supported by multiple approaches were prioritised for colocalisation, testing whether metabolic and breast cancer associations were driven by the same underlying genetic signal.

Results: We identified 194 significant genetic correlations involving overall and ER-positive breast cancer. We found no evidence for a direct causal effect; however, 3 metabolic traits with overall breast cancer and 5 with ER-positive disease showed strong evidence of shared biology. Across these 8 trait pairings, gene-level analyses prioritised 26 gene-trait signals representing 16 unique genes, including the *GSTM1-GSTM5* glutathione S-transferase gene cluster and breast cancer-related genes *CASP8* and *MAP3K1*. Colocalisation of prioritised loci further supported shared genetic signals, including at the *GSTM* region for small HDL particle concentration and breast cancer.

Conclusions: These findings identify specific genes and genomic regions that may underpin the shared biology between metabolism and breast cancer. By narrowing broad genetic overlap to specific biological signals, this work helps clarify mechanisms of breast cancer susceptibility and prioritise pathways that may be relevant to prevention and treatment.

S5-06 · Session 5 · Wednesday 11:00 · Presenter: Winnie Tan

Nucleosome recognition and DNA compaction by the MORC2 remodeller

Winnie Tan[1,2,3], Jeongveen Park[4], Hariprasad Venugopal[5], Jieqiong Lou[2], Prabavi Dias[6], Pedro Baldoni[1], Toby Dites[1], Kyoung-Wook Moon[4], Christine Keenan[1], Alexandra Gurzau[1], JoonYoung Lee[4], Timothy Johanson[1], Andrew Leis[1], Jumana Yousef[1], Vineet Vaibhav[1], Laura Dagley[1], Ching-Seng Ang[2], Laura Corso[1], Chen Davidovich[5], Stephine Vervoort[1], Gordon Smyth[1], Marnie Blewitt[1], Rhys Allan[1], Elizabeth Hinde[2], Sheena D'Arcy[6], Je-Kyung Ryu[4], Shabih Shakeel[1,2,3].

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Background and Aims: The way DNA is packaged into chromatin determines which genes are active or silenced in a cell. This packaging is controlled by ATP-dependent chromatin remodelling enzymes, including Microrchidia CW-Type Zinc Finger 2 (MORC2), a recently identified enzyme that promotes gene silencing. MORC2 mutations are linked to several cancers and neurological disorders, including early-onset Charcot-Marie-Tooth disease. MORC2 activity depends on phosphorylation by the PAK1 pathway and has been linked to gastric cancer progression, yet how phosphorylation controls its chromatin remodelling function remains unclear. Critically, how MORC2 physically engages the nucleosome — the basic unit of chromatin — was unknown. This project aims to directly visualise the MORC2-nucleosome complex to uncover the mechanistic basis of its function, informing future treatments for cancer and neuropathies.

Methods: We combine cryo-electron microscopy (cryo-EM), crosslinking and hydrogen-deuterium exchange mass spectrometry to solve the structure of MORC2 bound to nucleosomes and DNA. Chromatin immunoprecipitation followed by sequencing (ChIP-seq) and Fluorescence Lifetime Imaging Microscopy (FLIM) coupled with Förster Resonance Energy Transfer (FRET) reveal MORC2's co-localisation relative to chromatin. High-speed atomic force microscopy and magnetic tweezers provide the first single-DNA-molecule data on MORC2 activity.

Results: We report the first cryo-EM structure of MORC2 bound to a nucleosome, showing how its zinc finger domain engages the histone H3 acidic patch. ATP binding drives MORC2 dimerisation, reducing its nucleosome binding. Disease-associated mutations impair ATP hydrolysis, reducing both DNA compaction and nucleosome interaction. ChIP-seq and live cell FLIM-

FRET studies show MORC2 preferentially binds open chromatin near nucleosomes, while atomic force microscopy and single-molecule assays demonstrate that DNA compaction by MORC2 depends on both ATP hydrolysis and phosphorylation.

Conclusions: This study reveals the molecular mechanism by which MORC2 engages nucleosomes and compacts DNA, establishing a new model for MORC2-driven chromatin remodelling and transcriptional repression, with implications for cancer and neuropathy treatment design.

S5-07 · Session 5 · Wednesday 11:10 · Presenter: Nicole Sze Yong Nga

Increasing FGF7 levels promote corneal endothelial functions via NRF2-mediated response

Nicole Sze Yong Nga[1,2], Heng-Ai Chang[1,2], Guei-Sheung Liu[1,2,3], Mark Daniell[1,2,4,5] and Gink Nathan Yang[1,2]

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Background and Aims: Fuchs' endothelial corneal dystrophy (FECD) is a progressive blinding disease characterised by loss and dysfunction of corneal endothelial cells required to maintain corneal clarity. Advanced disease requires corneal transplantation, highlighting the need for non-surgical strategies to preserve corneal endothelial function. Our previous single-nucleus RNA sequencing identified increased *fibroblast growth factor 7* (*FGF7*) in FECD endothelium, but the significance of this response remains unknown. This study aimed to determine the role of increased FGF7 in human corneal endothelial cells and its relevance to FECD.

Methods: FGF7 localisation was assessed by immunocytochemistry in endothelium from healthy donors and patients with late-stage FECD (n=3/group). Immortalised human corneal endothelial HCEC-B4G12 cells were treated with recombinant FGF7 (rFGF7) or transforming growth factor-β1 (rTGF-β1), an inducer of endothelial-to-mesenchymal transition (EndMT). EndMT, endothelial-associated markers and NRF2-associated stress responses were assessed by RT-qPCR, western blot and immunocytochemistry. Cell migration and proliferation were assessed by scratch wound-healing and WST-1 assays, respectively. Ultraviolet-A (UVA) irradiation was used to model FECD-associated oxidative stress *in vitro*.

Results: FGF7 was detected in a subset of cells within late-stage FECD endothelium that retained functional ion-pump ATP1A1, but was not detected in healthy endothelium. Unlike rTGF-β1, rFGF7 did not induce a coordinated EndMT response or alter cell migration or proliferation. rFGF7 increased endothelial-associated markers *ALCAM/CD166*, *ZO-1* and *ATP1A1*. rFGF7 also increased NRF2, a key regulator of cellular stress responses, and its downstream target *NQO1*. NRF2 was significantly increased following FGF7 treatment ($P<0.05$). UVA-induced oxidative stress increased endogenous *FGF7* expression >1.5-fold at 24 h ($P<0.01$).

Conclusions: These findings suggest FGF7 acts as a stress-responsive regulator that promotes endothelial phenotype and function without inducing pathological EndMT, potentially through an NRF2-mediated response. Targeting FGF7 signalling may offer a novel approach to preserve endothelial function and provide a foundation for developing non-surgical therapeutic strategies for FECD.

POSTER PRESENTATION ABSTRACTS

Board P01 · Presenter: Agustiningsih

Investigating primary and recall humoral immune responses in malaria and the role of type I interferon signalling.

Agustiningsih[1,2], Rama Dhenni[1,2], Juliane Hamelink[1,3], Dean Andrew[3], Jessica Canning[1,2], Adam Thomas[1,2], Nick Dooley[1], Jessica Loughland[1], Damian Oyong[1], Amaya Ortega Pajares[1], Grace Wright[1], Mayimuna Nalubega[1,3], Luzia Bukali[3], Jessica Engel[3], Megan Soon[3], Teija Frame[3], Fabian de Labastida Rivera[3], Tim Wells[4], Stephan Chalon[4], Joerg Moerhle[4], Rebecca Webster[3], James McCarthy[5], James Beeson[1,2], Bridget Barber[3], Christian Engwerda[3], Michelle Boyle[1,2]

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Background and Aims: Protective immunity to malaria relies primarily on high level of circulating antibodies. However, individuals in high-endemic areas often fail to mount protective antibody levels following vaccination, with antibody levels declining after each subsequent booster. The mechanism by which the humoral and memory responses against the malaria parasite are developed and maintained is unclear. This study aimed to investigate the qualitative and quantitative differences between primary and recall anti-malarial humoral immune responses, and to determine how the malaria-induced immunoregulatory network via type I interferon (IFN) influences these responses.

Methods: We used plasma samples collected from healthy volunteers participating in controlled-human malaria infection study treated with ruxolitinib, a licensed orally bioavailable small molecule inhibitor of type I IFNs signalling. Using bead-based multiplex assay, we quantified the level of IgG and IgM against 35 antigens of the malaria parasite.

Results: We found not only prototypical recall responses to well-characterised antigens, including MSP1-42, MSP2, and AMA1, but also de novo responses to a limited number of antigens, including MSP9, GLURP, and P41 following secondary challenge with minimal impact from ruxolitinib treatment. However, using peptide array ELISA to MSP2, an immunodominant malaria antigen that contains many linear epitopes which allows us to study the antibody responses at the epitope level, we found that ruxolitinib increased the breadth of recall antibody responses.

Conclusions: This data provides important insights into how repeated malaria infection shapes the quality and breadth of humoral responses. Such insights are essential for development of more effective malaria vaccines.

Board P02 · Presenter: Akila Hewa Thondilege

Improving Clinical Biomechanical Assessment Through Mesh-Based Virtual Markers

Akila Hewa Thondilege[1], Ethan Goan[1], Alina Bialkowski[2], Luke Kelly[3], Clinton Fookes[1], Glen Lichtwark[4]

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Background and Aims: Markerless motion capture offers a promising alternative to conventional marker-based systems for biomechanical assessment, and clinical movement analysis. However, its evaluation commonly relies on manually placed physical markers as groundtruth, despite their dependence on subject-specific body morphology and operator interpretation. This can introduce uncertainty into marker-level accuracy measurements and downstream biomechanical outcomes, including joint angles and range of motion (ROM). This study investigates the subject specificity of physical marker locations and proposes a mesh-based, surface-feature-driven virtual marker method for more consistent biomechanical evaluation.

Methods: Multi-view video recordings were used to reconstruct three-dimensional body meshes. Physical markers were mapped onto reconstructed body surfaces using static poses to identify corresponding mesh locations. We compared this subject-specific representation with a common anatomical virtual marker library defined on the mesh surface and verified by biomechanical experts. The proposed method uses local surface features and neighbouring mesh vertices to represent anatomical landmarks, reducing dependence on individual vertex selection. The marker representation was evaluated through inverse kinematics and comparisons of joint angles, and Range of Motion values across repeated trials and participants.

Results: Analysis of marker-to-mesh correspondence demonstrated consistent relationships across repeated trials within individuals, but differences between individuals indicating manually placed markers do not necessarily provide universally transferable anatomical references. The mesh-based virtual marker method provides a common surface representation for anatomical landmarks while preserving individual body geometry. Evaluation of downstream kinematic measurements further investigates how the choice of marker representation influences joint-angle estimates and ROM, highlighting the importance of reference selection when assessing markerless motion capture systems.

Conclusions: Physical marker placement can introduce subject-specific uncertainty into markerless motion capture evaluation. A mesh-based, surface-feature-driven virtual marker approach offers an alternative for consistent anatomical

correspondence and downstream biomechanical assessment. This framework support reliable evaluation of markerless systems for clinical movement analysis.

Board P03 · Presenter: Assia Comella

Thirty Years of Paediatric Colonic Motility Assessment Modalities: A Systematic Review

Assia Comella [1,2,3], Hannah Evans-Barns [1], Phil Dinning [4], Mark Safe [1], Misel Trajanovska [2,3], Sebastian K. King [1,2,3]

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Background and Aims: Children post-surgical repair of congenital colorectal conditions, such as Hirschsprung disease and anorectal malformations, can be affected by faecal incontinence.

Management of such requires management requires several investigations, clinic appointments and treatment strategies. Different investigations are available to accurately describe gastrointestinal transit time. The authors aimed to assess the literature summarising paediatric colonic motility investigations available over the last 30 years, their uses, advantages, and limitations.

Methods: The authors completed a systematic review according to the PRISMA protocol by compiling an assessment of the used modalities.

Results: 1061 journal articles were screened and 122 included in the systematic review. Modalities vary globally, as different countries prioritise specific tools to objectively measure gastrointestinal transit time and inform personalised therapy.

Discussion: While each modality offers distinct advantages, they also possess limitations. No current colonic motility investigation is perfect, and availability varies by centre. Furthermore, several well-established methods involve radiation, which must be minimised in the paediatric population. The review found that evidence regarding colonic motility modalities in paediatrics is scattered compared to the adult population. Comparison and reproducibility of existing data is also complicated due to high rates of protocols and reporting variability.

Conclusions: It is vital to understand the characteristics of each modality to determine which is most appropriate for any given clinical indication. There is a need to develop a non-invasive, objective, world-wide reproducible and ambulatory method that can provide information on actual day-to-day physiological colonic motility. If such modality was achieved, this could allow measurement in control healthy cohorts to produce normative data for comparison and optimally target differences.

Board P04 · Presenter: Brianna Kline

Mitochondrial fusion dynamics implicated in premature ovarian insufficiency

Brianna L. Kline[1,2], Tanavi Sharma[3], Catherine Palmer[3], Yau Low[1], Eric Hanssen[4,5], Jaidah Fergus-Mackie[1,2], Xuebi Cai[1], Gorjana Robevska[1], Jocelyn van den Bergen[1], Philippe Touraine[4], Bruno Donadille[7], Hind Alsharhan[8], Alhaddad Bader[9], Fowzan Alkuraya[10,11], Daniella H. Hock[3,12], Svenja Pachernegg[1], Sylvie Jaillard[1,13] Diana Stojanovski[3], David A. Stroud[1,3,12], Katie L. Ayers[1,2], Andrew H. Sinclair[1,2,12], Sophie Christin-Maitre [7,] Elena J. Tucker[1,2]

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Background and Aims: Premature ovarian insufficiency (POI) impacts ~1-3.7% of women and is characterized by absence/loss of ovarian function before the age of 40. Oocytes have a high energy demand and previous research has identified an association between reduced mitochondrial count/poor mitochondrial function and reduced reproductive potential. Next-generation sequencing has allowed for the rapid detection of potentially causative variants in genes encoding mitochondrial proteins in patients presenting with POI.

Methods: Whole exome sequencing identified three unrelated POI patients with biallelic variants in Mitofusin -1 (*MFN1),* a critical mitochondrial fusion gene. We expressed tagged wildtype and mutant MFN1 in HeLa cells to investigate localization and mitochondrial network morphology via immunofluorescence. We interrogated this further in *MFN1* patient-derived lymphoblasts via western blot, proteomic analysis, electron microscopy, mitochondrial morphology analysis, and mitochondrial/glycolytic stress tests to determine the impact of identified variants.

Results: We identified *MFN1* variants as a novel mitochondrial-associated cause of POI. We have observed that patient variants decrease mitochondrial fusion. Proteomic and western blot analyses demonstrate that patient variants destabilise MFN1, resulting in reduced mitochondrial fusion in relevant disease models. This contributes to combined oxidative phosphorylation deficiency and glycolytic stress, mechanisms known to damage ovaries.

Conclusions: This work identifies *MFN1* as a novel human disease-associated gene, and a novel POI-associated gene in three unrelated individuals. It highlights the importance of mitochondrial dynamics in maintaining female reproductive potential and confirms that variants in genes encoding mitochondrial proteins should be searched for in patients experiencing infertility.

Board P05 · Presenter: Chalie Marew Tiruneh

Clinical outcomes of children and adolescents with type 1 diabetes mellitus in Ethiopia: evidence on glycaemic achievement and diabetic ketoacidosis

Chalie Marew Tiruneh[1,4], Muhammad Chutiyami[1] (Lecturer), Marilyn Cruickshank1,2 (Professor), Shannon Lin3 (Associate Professor), Sewagegn Yeshiwas5 (Lecturer), Bereket Fantahun6 (Associate Professor), Lin Perry[1] (Professor).

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Background and Aims: Type 1 diabetes poses significant challenges for children and adolescents, particularly in under-resourced settings. Clinical outcomes are key indicators of effective diabetes management; however, evidence from these settings remains limited, hindering the development of targeted interventions and policies to improve outcomes. This study aimed to determine the incidence of diabetic ketoacidosis (DKA), the rates of achieving recommended glycaemic levels, and the factors predicting this.

Methods: A multicentre study combining secondary document analysis and survey data was conducted among 411 children and adolescents with type 1 diabetes attending diabetes clinics at five hospitals in Ethiopia. Glycaemic status was assessed against recommended targets for HbA1c (<7%), fasting (80-144 mg/dL), and random blood glucose (70-180 mg/dL). DKA incidence was determined from clinical records. Multivariable logistic regression ($p \leq 0.05$) was used to identify factors associated with HbA1c.

Results: Of 411 participants (51.3% female; mean age 10.9±4.7 years), 405 had HbA1c records. Only 13.3% achieved the HbA1c target, with a mean HbA1c of 9.56±2.25%. Fasting and random glucose targets were met by 42.5% and 38.3% of participants, respectively, and 29.9% experienced hypoglycaemia. Better glycaemic status was associated with male sex, shorter diabetes duration, no recent hospitalisation, attendance at diabetes education, and higher quality of life. During 9,492 person-months of follow-up, 19.7% experienced at least one DKA episode, corresponding to an incidence of 8.53 per 1,000 person-months.

Conclusions: Low achievement of glycaemic targets and a high incidence of DKA were observed in an under-resourced setting, even among clinic attendees. Although the findings are based on clinic attendees, they highlight important gaps in diabetes management. Strengthening diabetes education, treatment adherence support, access to care, and psychosocial services may improve outcomes. These findings provide context-specific evidence to inform clinical practice, health service planning, and policy development for young people with type 1 diabetes in low-resource settings.

Board P06 · Presenter: Deborah Hilton

Injury prevention workplaces that perform statistical analysis related to health; words describing artificial intelligence from workers – is it a help or hinderance?

Deborah Hilton [1,2,3,4]

[4]Roy Morgan Research https://www.roymorgan.com/

Background and Aims: Artificial Intelligence [AI] is increasingly being incorporated into medical research with clearly astronomically positive yet concerningly detrimental repercussions. Hilton authored a manuscript [Journal of University College of Medicine and Dentistry titled; Infodemic and its Impact on the Mental Health of Researchers and Health Professionals: The COVID-19 Pandemic Aftermath]. The text of this manuscript was entered into wordart cloud generator to identify themes [https://wordart.com/].

Methods: Thirty-two people were approached randomly at the Workplace Health and Safety Exhibitor booths [Melbourne]. Regarding AI, they were invited to describe AI with five words relating to work practice after viewing the example, then advised that these descriptive words from booths approached would be thematically analysed utilising wordart.

Results: Twenty-four people provided words [minimum one, thirteen maximum]. Four people mentioned non-use at work yet still provided words. Another eight people didn't provide words [AI non-use]. Words provided included; predictive, consequence, analysis, historical, prediction, automation, future, help, digital, optimisation, streamlining, summarising, mitigating risk, safety, compliance, automation, future, efficiency, workload information, proactive, reliability, efficiency, proof,

audits, compliance, time-saving, expert, compliance, reporting, induction, licenses, overwhelming, abused, misunderstood, beneficial, opportunity, issue, public, quotes, solutions, specific, useful, cognitive load, focus, prototype, sense-making, empowerment, continuity, ideation, risk, fire, compliance, brand damage, litigation, insurance, pedestrian detection, protecting, worksafe, concise, sound better, confident, addictive, accessible, time to fill, success rates, candidate experience, conversion, return of investment, sets out data, interpretation layer, looking to AI, occupational therapy, clarifies/checks, 80% of the way quickly, effective, quick/speed, irritating, confusing, impersonal, scary, inevitable, compulsory, resourceful, futuristic, reframe, identifies, open to learning, corrects, opportunities, grounded, answer, simplification, optimization, capabilities, chatbox, identify/detect patterns and instant.

Conclusions and Significance/Impact: Four themes from the word cloud that were predominant included; predictive, compliance, automation and efficiency. The next level of themes related to; future, proactive, empowerment, simplification, reliability and optimization.

Board P08 · Presenter: Erin Harcourt

The efficacy of interventions for the psychological impacts of post-intensive care syndrome (PICS): a systematic review

Brittany Wadforth*[1,5], Erin Harcourt*[1,2,4,5], Naomi E Hammond[2,3], Joanne E Porter[4], Luka Saxena[2], Dixie Statham[1], George Van Doorn[1,4], Megan Youngson[5], Jacob Dye[2,4,6].

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Background and Aims: Psychological morbidity after intensive care unit (ICU) admission is common among survivors, family members, and carers. This systematic review evaluated the effectiveness of interventions used to reduce the psychological and psychosocial symptoms of Post-Intensive Care Syndrome (PICS) and PICS-Family (PICS-F).

Methods: PubMed, CINAHL, Scopus, PsycINFO, and Web of Science were searched in August 2025 and updated in January 2026. Eligible studies included randomised or quasi-experimental intervention studies published between 2010 and 2025 and written in English. They involved adult or paediatric ICU survivors, family members, carers, or bereaved relatives, with any and all psychological and psychosocial interventions being eligible. The comparison group comprised post-discharge ICU patients who did not receive an intervention, and the outcomes were symptoms of depression, anxiety, and Post-Traumatic Stress Disorder (PTSD). Two independent reviewers screened studies, extracted data, and assessed risk of bias using the Cochrane Risk of Bias tool. Narrative synthesis was used to identify and interpret patterns in the data.

Results: 36 studies involving 7,181 participants were included. Interventions included ICU or Neonatal ICU diaries, multicomponent psychosocial interventions, psychoeducation, CBT, mindfulness, EMDR, VR, exercise, and pharmacological treatments. Overall, most interventions were not effective at reducing anxiety, depression, PTSD, or improving Health-Related Quality of Life (HRQoL). Outcomes for PTSD interventions showed the most promise, with ~1/3 of relevant studies reporting benefits. Here, CBT-based approaches and ICU diaries were most effective.

Conclusions and: Significance/Impact: Evidence for psychological and psychosocial interventions for PICS and PICS-F remains mixed, and no single intervention can currently be recommended as the gold standard. Future studies should use adequately powered designs, standardised outcomes, and longer follow-ups.

Board P09 · Presenter: Fern Ee Caryn Koo

Beyond the Child: A Systematic Review of Parental Wellbeing and Family Functioning in Paediatric Colorectal Conditions

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Background and Aims: Families of children with anorectal malformation (ARM) and Hirschsprung disease (HD) often experience ongoing caregiving demands extending beyond the child's medical management. This systematic review aimed to synthesise quantitative literature examining parental wellbeing and family functioning outcomes among families of children with ARM or HD.

Methods: Using the PRISMA protocol, a systematic search was conducted across Ovid Medline, Embase, Web of Science, PsycINFO, and CINAHL. Eligible studies included quantitative studies evaluating psychosocial outcomes relating to parents

or families of children (aged <18 years) surgically treated for ARM or HD. Data extraction and quality appraisal using the Joanna Briggs Institute tool were completed independently by two reviewers.

Results: From 1205 records identified, nine studies met inclusion criteria and were synthesised without meta-analysis due to methodological heterogeneity. Across studies, families reported challenges relating to psychological wellbeing, parenting stress, caregiving burden, and family functioning, particularly in the context of ongoing bowel dysfunction and faecal incontinence. However, there was also considerable variability in resilience and adaptation among families.

Conclusions: Current evidence suggested that ARM and HD may have significant psychosocial impacts on the broader family unit. Future research should prioritise longitudinal and family-centred approaches to better inform integrated models of biopsychosocial care.

Board P10 · Presenter: Habib Eichoue

Characterising the molecular response to protein restriction in prostate cancer using integrated plasma proteomics and single-cell datasets.

Habib Eichoue[1], Patrick El Hage[1], Maria Lastra Cagigas[1,2], Luigi Fontana[1]

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Background and Aims: C-reactive protein (CRP) is strongly associated with Prostate-Specific Antigen (PSA), suggesting that inflammation might be fundamental in prostate cancer. CRP can be effectively reduced with dietary interventions; however, the influence of dietary protein on CRP levels remains unclear. This randomised controlled trial aims to examine the impact of animal protein consumption on CRP levels in adults with localised prostate cancer.

Methods: We report secondary analyses of a randomised feeding trial (NCT01692587) in 38 men. The intervention was an isocaloric animal protein-reduced (PR) diet in which participants received 0.8 g of protein kg-1 lean body weight per day (n=19) or continued their Western diet (n=19). Plasma samples were collected at baseline and after 4-6 weeks of intervention. CRP was measured by ELISA and plasma proteomics was performed with SomaSeq (Illumina). Correlation analysis between CRP and the proteome was performed in R. Genes encoding CRP-associated proteins were mapped onto a single-cell prostate cancer dataset. Ranked GSEA was employed to assess enrichment of GO and KEGG pathways.

Results: Reduced animal-protein intake was independently associated with decreased CRP after adjusting for weight change; specifically, the PR arm exhibited a 48% reduction in CRP levels. The change was correlated with 158 plasma proteins (FDR<0.05), encompassing key players in the acute-phase response, complement activation, and immune effector functions. Mapping the top 20 CRP-associated proteins onto a single-cell atlas of localised prostate cancer revealed that negatively correlated transcripts were abundant in glial cell clusters, whereas positively correlated proteins were expressed primarily in prostate epithelium, endothelium, and T-cells.

Conclusions: The findings implicate dietary protein, particularly animal protein, as a modifiable regulator of circulating CRP in patients with prostate cancer. CRP-associated molecular changes overlap with transcripts commonly expressed within the localised tumour microenvironment.

Board P11 · Presenter: Imogen Samuels

BAM-Boozled: Pyocin L1 Disrupt Outer Membrane Protein Assembly in *Pseudomonas aeruginosa*

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The emergence and global spread of antimicrobial resistance (AMR) is a significant problem threatening human, plant, and animal health. Central to the problem of AMR are Gram-negative bacteria, which exhibit intrinsic resistance to many antibiotics due to their impermeable outer membrane (OM). Lectin-like bacteriocins (Llps) represent a promising new class of protein antibiotics produced by Gram-negative bacteria to eliminate competitors. These bacteriocins target the β-barrel assembly machinery (BAM) complex through binding to the essential, surface-exposed protein BamA, disrupting OM protein assembly and compromising cell envelope integrity. Here, *Pseudomonas aeruginosa* (PAO1) is susceptible to the Llp Pyocin L1, and is used as a model to define the molecular consequences of Llp intoxication. Integrated proteomic and lipidomic analyses were performed to characterise how Llp treatment reshapes cellular homeostasis and activates envelope stress responses. These datasets identified candidate resistance-associated pathways, including alterations in lipid A composition and phosphatidylethanolamine in cell envelope remodelling. Building on these findings, current work investigates variation across clinical *P. aeruginosa* isolates to determine whether mechanisms identified in laboratory strains predict resistance phenotypes observed in hospital settings. By linking systems-level molecular changes with clinically relevant diversity, this work aims to define how Llps perturb bacterial physiology and how pathogens evade Llp-mediated killing, informing the development of next-generation therapeutics against drug-resistant Gram-negative infections.

Board P12 · Presenter: Jacob Andrew Dye

Long-term outcomes of out-of-hospital cardiac arrest patients and their caregivers in the Targeted Temperature Management 2 (TTM2) trial

Jacob Dye[1,2,3], Ashwani Kumar[1], Manoj Saxena [1,4], Gisela Lilja[5,6], Frances Bass[1,7], Niklas Nielsen[8,9], Luka Saxena[1], Alamgir Kabir[1], Katie Sweet[10], Leanlove Navarra[11], Paul Young[11,12,13,14], Naomi E Hammond[1,7], on behalf of the Australian TTM2 investigators and the TTM2 Trial PTSD-Substudy Group

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Background and Aims: Experiencing out-of-hospital cardiac arrest may result in persistent functional, cognitive and psychological morbidity and increased healthcare use, affecting survivors and caregivers. We evaluated 6- and 24-month outcomes in two substudies of the TTM2 trial.

Methods: A New South Wales substudy linked trial and administrative data, evaluating survival, function (Glasgow Outcome Scale Extended [GOS-E]; 1[dead]–8[upper good recovery]), cognition (Montreal Cognitive Assessment [MoCA]; 0[severe cognitive impairment]–30[normal cognition]), health-related quality of life (EQ-5D-5L Visual Analogue Scale [VAS]; 0[worst health imaginable]–100[best health imaginable]) and average hospitalisation costs.

A separate international substudy assessed post-traumatic stress disorder (PTSD) symptoms in survivors and caregivers using the PTSD Checklist for DSM-5 (PCL-5; range 0[no symptoms]–80[extreme symptoms]; PCL-5≥31 probable PTSD). Mixed-effects models compared changes between groups exploring moderation by caregiver event exposure and patient GOS-E.

Results: At 6 months, 23/54 New South Wales participants had died and six were lost to follow-up. All survivors lived at home, 38% returned to work, 96% had favourable GOS-E scores and 64% had cognitive impairment. Mean EQ-VAS was 79 and hospitalisation costs averaged A$45,173 per patient. At 24-months, no additional deaths had occurred. Return to work increased (52%), favourable functional status remained common, cognitive impairment also increased (88%), mean EQ-VAS was 73 and costs averaged A$47,111.

In the PTSD substudy, at 6-months mean PCL-5 scores were 10.41 among 103 survivors and 13.09 among 69 caregivers; probable PTSD in 7.8% and 10.1%, respectively. At 24-months, mean PCL-5 scores were 8.83 among 83 survivors and 10.63 among 52 caregivers; probable PTSD in 7.2% and 7.7%, respectively. PCL-5 differences were imprecise, with no evidence that event exposure or GOS-E moderated outcomes.

Conclusions: Functional outcomes and healthcare costs were broadly stable, but cognitive impairment was common and psychological symptoms persisted in survivors and caregivers, supporting long-term cognitive and psychological follow-up after cardiac arrest.

Board P13 · Presenter: Jean Pierre Ndabakuranye

Wearable ambulatory ECG platform for accessible cardiac monitoring

Continuous electrocardiogram monitoring can support the detection of intermittent cardiac abnormalities that may not be captured during short clinical assessments. However, conventional systems can be unsuitable for extended monitoring outside clinical settings because of cost, limited portability, bulky hardware and reliance on gel-based electrodes. Lubdub is developing wearable dry-electrode technology to make ambulatory cardiac monitoring more accessible.

This presentation describes the technical foundations of Lubdub's work and the progression from wearable ECG research towards a practical monitoring platform. The underlying investigations evaluated six gold thin-film dry-electrode geometries through skin-contact impedance measurements and ECG acquisition from the chest and neck. Measurements were performed across lying, sitting and standing postures under resting, physical, mental and combined stimuli. The selected hexagonal labyrinth electrode demonstrated consistent ECG acquisition across the evaluated locations and conditions. Its integration into a compact three-electrode prototype enabled wireless transmission to a smartphone, while comparison with expected ECG parameters and a commercial monitor supported the feasibility of the approach. The complete prototype weighed approximately 12 g, provided 12 hours of operation and caused no observable skin irritation during a seven-day wear assessment involving one participant.

These findings provide a technical basis for Lubdub's continued development of wearable ambulatory ECG technology. The presentation also discusses other challenges including electrode placement and geometry, stable signal acquisition, amplification, power management, hardware miniaturisation, fabrication, usability and validation. Addressing these challenges is essential for translating wearable ECG research into an accessible platform for longer-term cardiac monitoring.

Board P14 · Presenter: Jiawei Tang

Optimising CAR-T Cell Therapies Through CD4/CD8-Specific Signalling Programs

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Background and Aims: Chimeric antigen receptor (CAR)-T cell therapy has transformed blood cancer treatment by equipping T cells with synthetic receptors to identify and eliminate tumour cells. Calibrating CAR signalling is critical: insufficient signalling limits efficacy, while excessive signalling drives exhaustion and inflammatory toxicity. However, current CAR-T products deliver identical signals to CD4+ helper and CD8+ killer T cells, despite processing signals differently. We hypothesised that each subset requires different CAR signalling strengths for optimal function.

Methods: We previously showed that programmable CARs (proCARs) generate signalling strengths scaled to their clustering (oligomeric) state, isolating signal strength from antigen-binding and signalling domains. Here, we generated anti-CD19 proCARs spanning different signalling strengths, expressed them in primary human CD4+ and CD8+ T cells, and challenged them with NALM6 target cells expressing graded CD19 densities. CD19-knockout NALM6 and untransduced T cells controlled for antigen- and CAR-specific activity. ProCAR designs were ranked by cytokine production and proliferation.

Results: The two subsets responded differently to the proCAR panel. CD8+ cytokine production increased with CAR oligomeric state, whereas CD4+ T cells showed IFNγ, GM-CSF and TNF production peaking at different oligomeric states. These differences persisted across antigen densities, indicating a subset-intrinsic effect. Proliferation in both subsets initially increased with antigen density, but declined in CD8+ T cells at the highest density, while continuing to increase in CD4+ T cells.

Conclusions: The same signalling input therefore drove distinct output patterns in CD4+ and CD8+ T cells, suggesting that uniform signalling in current CAR-T products may not accommodate their distinct signalling requirements for optimal safety and efficacy. These *in vitro* findings, alongside ongoing *in vivo* validation, may inform strategies to tailor CAR signalling on distinct immune cell populations, potentially improving the safety, efficacy and accessibility of adoptive cell therapies.

Board P15 · Presenter: Joshua John Voger

Investigating the effects of physical manipulation of the vagus nerve on the inflammatory response in both male and female rats undergoing sepsis

Joshua Voger[1], Andrew Butler[2], Rachel Peiris[1], Angela Connelly[1], Jaspreet Bassi[3], Andrew Allen[1,3], Mariana Melo[3], Lindsea Booth[1,3]

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Background and Aims: Vagus nerve stimulation (VNS) has a powerful anti-inflammatory effect, through mechanisms that are not completely understood. Experimental VNS typically relies on the acute implantation of electrodes around the vagus nerve. However, evidence suggests that some anti-inflammatory effects may result from physical manipulation of the nerve itself. To investigate this, we developed a rodent sepsis model using E. coli, where rats received chronic or acute implantation of a vagal cuff. It was hypothesised that a chronic vagal cuff would avoid the potential anti-inflammatory effects of physical manipulation of the vagus.

Methods: Sprague Dawley rats (males/females) were anaesthetised with isoflurane, and a chronic nerve cuff was implanted around the left cervical vagus. Fourteen days later, animals were anaesthetised with isoflurane, and the femoral vein and artery were cannulated for urethane infusion (1.5g/kg) and blood pressure and heart rate recordings, respectively. A baseline blood sample was collected before intravenous administration of E. coli (4×10^9 CFU/mL, 1.25µL/g). Blood samples were collected 1h, 2.5h, and 4h post-infection. Animals were divided into stimulated (VNS; n=12) and unstimulated (sham; n=13) groups.

Results: The pro-inflammatory cytokine tumour necrosis factor alpha (TNFα), measured by ELISA, was lower in the VNS group (sham: 8.61 ± 3.10 ng/mL vs. stim: 2.68 ± 2.51 ng/mL, at 1h). In a separate cohort (n=12) the same cuff was implanted on the day of sepsis induction, without electrical stimulation. These rats showed reduced TNFα (2.91 ± 2.16 ng/mL, at 1h, vs. sham), indicating acute vagal manipulation alone can exert anti-inflammatory effects.

Conclusions and Significant Impact: This provides a critical insight into experimental design, as researchers must consider potential confounding effects in this model. These findings demonstrate that VNS studies in rodent sepsis models can use a chronic vagal cuff to avoid the anti-inflammatory effects of physical manipulation of the vagus.

Board P16 · Presenter: Jude Oluwapelumi Alao

Clinical response and systemic immune profiles following acoustic nasal therapy in chronic inflammatory nasal disease

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Background and Aims: Acoustic nasal stimulation is being explored as a non-pharmacological treatment for allergic rhinitis and chronic rhinosinusitis, but its clinical response and biological correlates are poorly characterised. We assessed whether four weeks of acoustic nasal therapy reduced symptom burden and whether clinical changes were accompanied by changes in circulating Type 2 cytokines. Nasal microbiota profiling was included to examine local microbial responses.

Methods: Thirty adults with allergic rhinitis and/or chronic rhinosinusitis completed a single-arm longitudinal study. SNOT-22 was measured at baseline (V1), after four weeks of twice-daily treatment (V2), and at follow-up (V3). Serum from 29 participants was analysed for IL-4, IL-5, IL-13, TNF-α, IL-6 and IL-1β. Nasal bacterial and fungal swabs were collected for microbiota profiling.

Results: SNOT-22 improved by 15.43 points from V1 to V2 ($p<0.0001$), with 20/30 participants (66.7%) achieving a clinically meaningful improvement. Scores increased by 11.97 points from V2 to V3 ($p=0.0003$), leaving V3 3.47 points below baseline ($p=0.242$); 10/30 participants (33.3%) remained responders. IL-4, IL-5 and IL-13 showed no overall visit effect or significant adjusted pairwise differences. TNF-α, IL-6 and IL-1β were below the quantitative range in all samples, preventing valid concentration-based longitudinal analysis. Microbiota sequencing is ongoing.

Conclusions and Significance: Four weeks of acoustic nasal therapy produced a clinically meaningful, but largely non-sustained, improvement in symptoms without detectable changes in the measured circulating Type 2 cytokines. These findings suggest that clinical response may not be reflected by systemic cytokine shifts. Integrating nasal microbiota data will test whether treatment response is better captured within the local nasal environment and may help identify biological features associated with response.

Board P17 · Presenter: Laura McKinley

Routine prophylactic carbetocin following vaginal birth: a retrospective non-inferiority cohort study

Laura McKinley[1]

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Background and Aims: Postpartum haemorrhage (PPH) causes substantial maternal morbidity. During the 2025 Australian oxytocin shortage, Northern Health introduced routine prophylactic carbetocin after vaginal birth. We assessed whether carbetocin was non-inferior to syntocinon for preventing PPH, using a prespecified 5% absolute risk margin.

Methods: This single-centre retrospective before-and-after study included consecutive vaginal births. Women received syntocinon 10 IU intramuscularly from November 2024 to April 2025 (n=1,005), or carbetocin 100 micrograms intramuscularly from May to October 2025 (n=985). The primary outcome was blood loss ≥500 mL; secondary outcomes were blood loss ≥1,500 mL and ≥2,000 mL. We calculated risk differences and 95% confidence intervals (CIs).

Results: Parity, induction and assisted-birth rates were similar between cohorts. Mean blood loss was 462 mL with syntocinon and 459 mL with carbetocin. PPH ≥500 mL occurred in 322/1,005 (32.0%) versus 313/985 births (31.8%), respectively (risk difference -0.3%, 95% CI -4.46% to 3.93%; p=0.938). Blood loss ≥1,500 mL occurred in 35 (3.5%) versus 31 (3.1%) births (risk difference -0.3%, 95% CI -2.01% to 1.34%; p=0.770), and ≥2,000 mL in 9 (0.9%) versus 12 (1.2%) births (risk difference 0.3%, 95% CI -0.68% to 1.32%; p=0.628). The upper CI bound was below 5% for each outcome.

Conclusions: Routine prophylactic carbetocin was non-inferior to syntocinon for preventing PPH after vaginal birth. The retrospective, single-centre design limits causal inference; prospective multicentre evaluation is required.

Significance/Impact: Carbetocin may provide an effective single-dose alternative during oxytocin supply disruption and support continuity of evidence-based maternity care.

Board P18 · Presenter: Marcus Camilleri

RNA isoforms provide cell-type-specific insights into human neurodevelopment

Gene regulation is notably complex in the brain, where processes like alternative splicing enable single genes to produce multiple distinct RNA products ("isoforms"). Isoform-switching is a well-established key regulator of neurodevelopment, shaping cell identity and function across the developing brain. However, our understanding of RNA isoforms during human

neurodevelopment remains limited, particularly at the cell-type level and beyond the first trimester. Addressing this knowledge gap is essential to understanding how RNA isoforms shape healthy brain development, and how their disruption contributes to disease.

We mapped the RNA isoform landscape of the developing human prefrontal cortex across an unprecedented range of timepoints, incorporating >100k cells and 18 samples spanning 22-weeks-gestation to 20-years-old with single-nuclei long-read RNA-sequencing using the 10x Chromium and Oxford Nanopore platforms. Data was analysed using Seurat and our custom FLAMESv2 pipeline.

We identified 19 major cell-types spanning excitatory neurons, GABAergic interneurons and non-neuronal cells. Isoform-level analyses identified many cell-type-specific features indiscernible at the gene-level, including activated microglia and improved resolution of CGE- and MGE-derived inhibitory interneuron subtypes, suggesting mature RNA/splicing can contribute to interneuron cell-state identity. Overall, glial cells expressed fewer isoforms than neurons, however we also discovered a non-canonical, truncated MBP isoform that outperformed the canonical MBP isoform as a marker of maturing oligodendrocytes across timepoints.

We've performed the first single-cell study of RNA isoforms spanning human brain development, revealing extensive isoform diversity and identifying age/cell-type specific marker RNA isoforms. These findings position RNA isoforms as a key underexplored layer shaping brain development and disease risk.

Board P19 · Presenter: Nchafatso Obonyo

A Case Report of a Preclinical Model of Cardiac Trauma and Haemorrhagic Shock

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Background and Aims: Penetrating cardiac injury remains a complex clinical challenge with high mortality. Platforms are needed to enable life-sustaining research into the safe and effective application of trauma guidelines and emerging resuscitative technologies. We describe a predictable model of cardiothoracic trauma with penetrating cardiac injury and haemorrhagic shock.

Methods: All experimental procedures were approved by the local animal ethics committee. This case presents the outcome of a large white adult pig having sustained an experimentally controlled penetrating injury to the heart resulting in massive haemorrhage. Briefly, in the setting of an experimental trauma theatre the animal was anesthetised and stabilised, prior to baseline point-of-care-ultrasound echocardiography. A thoracotomy was performed to initiate a controlled penetrating injury to the anterior wall of the left ventricle. Following the injury, emergency cardiorrhaphy was performed, during which permissive hypotension was maintained. Fluid and vasopressor support (noradrenaline) were used to restore blood pressures, prior to ultrasound-guided cannulation of the right femoral artery to place a 20Fr sheath and conduct resuscitative balloon occlusion of the aorta (REBOA).

Results: Baseline echocardiography confirmed normal cardiac structure and function. A total of 1.9L of whole blood was lost between the time of injury and successful cardiac wound closure. Approximately 2.5L of fluids (Hartmann's solution) and noradrenaline infusion (0.01ug/kg/min) were required to normalise central venous and arterial blood pressures (CVP and ABP, respectively). Following withdrawal from noradrenaline, REBOA with Zone 1 placement resulted in a 30mmHg elevation in ABP (59 vs 29mmHg) and 13mmHg elevation in CVP (13.9 vs 1.1mmHg). Following the predetermined post-operative period (~2hrs post-cardiorrhaphy), euthanasia was performed and postmortem findings revealed successful haemostasis had been achieved and maintained.

Conclusions: This case describes the feasibility of an experimental platform for research and training in the setting of penetrating cardiac injury and massive haemorrhage with emergency cardiac surgical repair.

Board P20 · Presenter: Nicholas Glatz

Changes to a Thalamocortical microcircuit in the Primary Somatosensory Cortex from Goal Directed Learning

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Introduction: Goal-directed learning transforms the way sensory information is represented within cortical circuits. Anatomical evidence and functional evidence increasingly suggests an important role for feedback pathways containing internally integrated information in learning. The higher-order thalamus in particular has been identified as an important feedback region

in goal directed learning. However, how higher-order thalamic inputs, such as the posteromedial thalamic nucleus (POm) and their downstream cortical targets, such as layer 2/3 pyramidal neuron tuft dendrites in primary somatosensory cortex (S1), are differentially modified during learning remains unclear.

Objective: To uncover this, we aimed to compare the activity of populations of POm axons and S1 dendrites in the same mice, before and after learning.

Methods and Results: Using two-photon calcium imaging, we first characterized POm axons in naïve mice and identified distinct subpopulations based on their responsiveness to different stimulus modalities. Although the POm projection is predominantly tactile-responsive, a small population of auditory-responsive axons was observed. Following auditory Go/No-Go learning, auditory-responsive POm axons were strongly recruited and altered their activity during correct auditory task performance. We then examined downstream layer 2/3 tuft dendrites and found a distinct pattern of learning-associated plasticity. Auditory-responsive dendrites were recruited following both auditory and tactile contingency learning, indicating broader learning-dependent changes than observed in the POm input. Learned Hit trials were also associated with prolonged dendritic activity across response populations.

Conclusions: Together, these findings demonstrate that goal-directed learning differentially reshapes higher-order thalamic inputs and downstream dendritic populations, revealing a transformation of sensory-related activity across the thalamocortical circuit.

Board P21 · Presenter: Ryan M. Clarke

Establishing Small Molecule-Based Neuronal Transdifferentiation as a Tool for Modelling Age-Dependant Phenotypes in Amyotrophic Lateral Sclerosis

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Background and Aims: Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disorder characterised by the progressive degeneration of motor neurons. Ageing is the strongest risk factor for ALS, however its contribution to disease progression is inadequately modelled in preclinical systems. Patient-derived motor neurons generated from induced pluripotent stem cells (iPSCs) have provided preliminary insights into ALS pathobiology; however, cellular reprogramming to pluripotency limits the relevance of these approaches to late-onset disease, as it removes age-associated epigenetic and molecular signatures. Our preliminary data shows that iPSC-derived motor neurons from sporadic ALS patients reveal limited disease phenotypes, emphasising the importance of this limitation. Direct cellular transdifferentiation offers a compelling strategy to surmount this limitation, by bypassing pluripotency and preserving donor age-related signatures. We therefore hypothesise that a transdifferentiation-based human neuronal model of ALS will better facilitate the modelling of age-related ALS disease signatures.

Methods: Tandem optimisation of small molecule-driven neuronal transdifferentiation methods to generate both cortical and spinal motor neurons was informed by existing literature. Conversion success was preliminarily validated qualitatively using phase-contrast microscopy. Molecular validation of neuronal identity will be confirmed using immunofluorescence cell surface and intracellular markers.

Results: Phase-contrast microscopy revealed that fibroblasts exposed to small molecule cocktails undergo significant morphological changes over time including the development of cellular processes. Higher concentrations of small molecules increased rate of morphological change as well as cell death.

Conclusions: Work is ongoing to further optimise the transdifferentiation approach. Future studies will transcriptomically characterise cellular identity and ageing of transdifferentiated neurons and patient-matched fibroblasts. If successful, this work will deliver a next-generation human neuronal model that more accurately captures age-dependent ALS pathobiology, providing a physiologically relevant platform for future mechanistic discovery and therapeutic development.

Board P22 · Presenter: Sam Combes

The influence of glioma on interneurons in-vivo

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Gliomas are highly invasive primary brain tumours that disrupt neural circuit function and contribute to cognitive decline. While tumour-neuron interactions have been increasingly characterised in excitatory populations, the impact of glioma on inhibitory interneurons remains poorly understood. Here, we investigated longitudinal changes in interneuron signalling during glioma infiltration using 2-photon calcium imaging in awake behaving mice in vivo. Human GFP-expressing MU035 glioma stem cells and the genetic calcium indicator GCamP were co-injected into the secondary motor cortex (M2) of immunocompromised

NSG mice. Repeated 2-photon calcium imaging of neuronal activity, tumour growth and glioma morphology was then performed in awake behaving mice over the course of disease progression (~15 weeks). Glioma infiltration progressed throughout M2 at ~35–40 μm/day and remained detectable for up to 120 days post-implantation. Interneuron activity was altered during tumour expansion, accompanied by widespread changes in local network dynamics. These findings demonstrate that glioma infiltration influences inhibitory interneuron activity in-vivo, which may contribute to the cognitive deficits associated with glioma progression. Characterising how gliomas remodel inhibitory networks may provide new mechanistic insight into tumour-induced neurological dysfunction and reveal novel neuroscience-based therapeutic targets for future therapies.

Board P23 · Presenter: Sarah Fraanje

Investigating the therapeutic potential of herbal extract-infused hydrogel for tissue regeneration in rat birth injury model.

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Background and Aims: Birth injury affects 1 in 3 women undergoing natural childbirth, with forceps-assisted delivery further increasing pelvic floor injury risk. These injuries can damage the pelvic floor and increase the risk of pelvic organ prolapse (POP), the herniation of pelvic organs into the vagina. Treatments are limited and focus on strengthening muscles, not wound healing. Traditional herbal medicines have long been used across cultures to heal injuries and illnesses. *Ocimum tenuiflorum*, or Tulsi, has been used in traditional Indian medicine to promote healing, with studies demonstrating wound-healing effects in diabetic foot ulcers. This study investigates Tulsi extract's effects on vaginal fibroblast viability and proliferation and explores its potential for promoting tissue repair after birth injury.

Methods: Vaginal fibroblasts from POP patients were treated with varying Tulsi concentrations. An MTS assay across three patient-derived cell lines and multiple time points determined cytotoxicity thresholds and assessed concentration- and time-dependent effects on viability. RT-qPCR examined Tulsi's effects on cellular fibrosis, informing its potential for wound healing *in vivo*. Simulated birth injury was induced in rats, followed by treatment with Tulsi-infused hydrogel (TIH). Vaginal tissue was collected at 1 and 6 weeks and analysed for extracellular matrix remodelling, immune response and angiogenesis using histological staining, immunofluorescence and RT-qPCR.

Results: TIH enhanced wound healing and angiogenic response. Histological analysis showed increased collagen deposition during the early response to treatment. Immunofluorescence analysis indicated a positive response to CD68 and CD206 for 1-week samples in comparison to the 6-week samples, with RT-qPCR providing key insight into genomic changes in wound healing.

Conclusions: Collectively, these findings highlight the effect that TIH has on wound healing and tissue regeneration following simulated birth injury in rats. This suggests its potential for application in wound regeneration following birth injury, reducing the risk of POP occurring later in life

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Board P24 · Presenter: Sarah Mele

Investigating Treatments and Mechanisms in Short-Chain Enoyl-CoA Hydratase 1 (ECHS1) Deficiency

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Background and Aims: Short-chain enoyl-CoA hydratase 1 deficiency (ECHS1D) is a rare genetic disorder caused by biallelic pathogenic variants in the ECHS1 gene. ECHS1 is a mitochondrial enzyme that plays important roles in both valine catabolism and fatty acid β-oxidation (FAO). ECHS1D is characterised by severe neurological and physical impairment that often leads to childhood mortality. Attempted therapies such as protein and single nutrient-restricted diets show variable efficacy, whereas the development of new treatments is hindered by the low prevalence of the disorder and a lack of model systems for treatment testing. Here, we report on the establishment of a *Drosophila* model of ECHS1D.

Methods: Flies carrying mutations in the *Echs1* gene were characterised for their physical and metabolic phenotypes, and dietary interventions to improve fly model health were explored. A genetic interaction study was conducted to elucidate the relative contributions of the valine and FAO pathways to disease pathogenesis.

Results: The Echs1 null larvae recapitulated human ECHS1D phenotypes including poor motor behaviour and early mortality and these phenotypes could be rescued by the expression of the human ECHS1 gene. We observed that neither the restriction

of valine nor a genetic block genetic block introduced upstream of the ECHS1 enzyme could enable development progression beyond the larval stage.

Conclusions: Our findings suggest that the ECHS1 protein has roles beyond both valine and fatty acid metabolism, alluding to an alternative pathogenic mechanism. This work provides underlying evidence supporting a shift away from nutrient modification as treatment for ECHS1D, potentially impacting how treatment discovery for this disease is approached in future work.

Board P25 · Presenter: Theodore Lam

Therapeutic Potential of Adipose-Derived Stem Cells in Peripheral Nerve Injury: A Systematic Review

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Background and aims: Peripheral nerve injuries can cause significant functional morbidity. Whilst direct repair, grafts and conduits can support axonal regeneration, their outcomes are often limited by regeneration distance and donor-site morbidity. Adipose-derived stem cells (ADSCs) are readily harvested, low-immunogenic mesenchymal cells that enhance nerve repair through multiple mechanisms. This study aims to examine the key regenerative components of ADSCs and evaluate the pre-clinical evidence in peripheral nerve repair.

Methods: Articles were extracted from Embase, Pubmed, and Medline, and from manual searches of reference lists. Results were collated and grouped according to exploration of ADSC's role in nerve regeneration, and pre-clinical evidence. Literature reviews, opinion articles, guidelines were excluded.

Results: ADSCs are thought to promote peripheral nerve repair by promoting axonal growth, re-myelination, angiogenesis and reducing inflammation through paracrine, and Schwann cell differentiation. Preclinical studies across repair, graft and conduit models show that ADSCs improve axonal regeneration, myelination, angiogenesis, and functional recovery.

Conclusion and impact: This review highlights the strong regenerative potential of ADSCs in peripheral nerve repair through paracrine signalling and Schwann cell differentiation, with preclinical studies demonstrating improved functional recovery. Whilst these findings highlight promising translational potential, clinical application remains in the early stages, and further research is required to optimise delivery, dosing and long-term safety.

Board P26 · Presenter: Vatsal Ved

Coronary plaque burden, composition and progression in young adults versus risk-factor-matched older adults: a serial computed tomography coronary angiography study

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Background and Aims: Premature coronary artery disease is rising, yet risk equations classify most young adults as low risk and calcium scoring misses non-calcified plaque. Using computed tomography coronary angiography (CTCA), we aimed to compare plaque burden, composition, progression and the baseline burden– progression association between young (18–50 years) and risk-factor-matched older adults.

Methods: This retrospective single-centre study (Monash Health, 2011–2022) included adults with clinically indicated serial CTCA ≥2 years apart. Young adults were matched 1:1 to older adults (51–75 years) on sex and five risk factors. Identical segments were quantified semi-automatically on both scans (Autoplaque v3.0). Primary outcomes were baseline total (TPB), non-calcified and calcified plaque burden (plaque volume/vessel volume ×100) and composition; secondary outcomes were annualised burden changes. Mann–Whitney U tests and statin-adjusted median regression compared groups; within-pair progression analyses also adjusted for baseline TPB.

Results: Among 61 matched pairs (median age 46.8 vs 61.8 years; 67% men; median follow-up 4.3 years), 40 young adults (66%) and all older adults had baseline plaque; the remaining 21 developed plaque by follow-up. Young adults had lower median TPB (3.80% vs 8.34%; statin-adjusted difference −4.50 percentage points [pp], 95% CI −6.98 to −2.02; p<0.001), non-calcified (−3.58 pp; p<0.001) and calcified (−0.41 pp; p=0.047) burden. Both groups had predominantly non-calcified plaque (median 92.3% vs 91.2%; p=0.618). Burden progression did not differ significantly between groups (TPB median 0.74 vs 0.61 pp/year; p=0.616) or within pairs (difference 0.23 pp/year; 95% CI −0.47 to 0.55). Higher baseline TPB was associated with slower progression (age interaction p=0.45).

Conclusions: Young adults referred for CTCA had approximately half the plaque burden of risk-factor-matched older adults, with similarly non-calcified composition and no detectable difference in burden progression, consistent with an earlier stage of the same disease. Earlier prevention may be warranted, pending larger outcome-linked studies.

Board P27 · Presenter: Vivian Tran

Integrating human and experimental models to identify immune mechanisms underlying cardiovascular complications in Long COVID

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Background & Aims: Long COVID is an emerging public health challenge characterised by persistent symptoms following SARS-CoV-2 infection. Cardiovascular complications, including chest pain, palpitations and exertional intolerance, are among its most debilitating manifestations, yet the immune mechanisms driving persistent cardiovascular injury remain poorly understood. Persistent immune activation has been implicated in Long COVID, but its contribution to chronic cardiovascular pathology has not been defined. To address this knowledge gap, we are integrating human and experimental models to investigate immune mechanisms underlying the cardiovascular symptoms of Long COVID. **Methods:** Peripheral blood mononuclear cells from individuals with Long COVID-associated cardiovascular complications and from individuals with pre-existing cardiovascular complications who have recovered from a SARS-CoV-2 infection have been immunophenotyped using flow cytometry, while circulating inflammatory mediators are quantified using cytokine bead array analysis. Additionally, a validated mouse model of Long COVID is being used to characterise the cardiovascular pathology, including immune cell infiltration, endothelial injury and cardiac remodelling. **Results:** Together, these complementary studies will identify immune signatures associated with cardiovascular complications of Long COVID and determine whether persistent cardiovascular pathology is accompanied by chronic immune activation and tissue injury. **Significance & Impact:** By integrating human immune profiling and experimental cardiovascular pathology in our mouse model, this study will provide one of the first comprehensive analyses linking adaptive immune responses in Long COVID with persistent cardiovascular pathology. This will advance our understanding of immunopathogenesis of cardiovascular complications in Long COVID and provide the foundation for future mechanistic studies and targeted therapies for post-viral cardiovascular complications.

Board P28 · Presenter: Yashna De Silva

Is Childhood Adversity Associated With Worse Disability Outcomes in Multiple Sclerosis?

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Background and Aims: Approximately 33,000 Australians live with MS. Factors that increase MS risk are well understood, but the factors that influence disease severity are now a field of growing interest. Childhood adversity has been shown to be predictive of long-term health outcomes across many diseases, however this association in people with MS is not well-explored. Therefore, this study aims to investigate if childhood adversity was associated with worse MS disability outcomes, and if this association was mediated by smoking status, overweight at 15 years of age, and timeliness of disease modifying therapy.

Methods: This was a cross-sectional single centre observational cohort study. Participants were adults with a diagnosis of MS seen at Alfred Health MS clinics between January 2026 and August 2026 consenting to participation. Childhood adversity was assessed in two ways: First, using the Adverse Childhood Experiences Questionnaire (ACE-Q) score; people reporting ≥4/10 ACEs were categorised as having adversity. Second, childhood Socioeconomic Status (SES) was estimated by matching participants' childhood postcodes to the respective area-based index of relative socioeconomic disadvantage; adversity was measured by decile of disadvantage. Primary outcome was disability severity, measured using the Age-Related Multiple Sclerosis Severity score. This is calculated using patients' disability scores assessed by neurologists during routine clinic visits. Bootstrapped linear regression and logistic regression models were used to investigate these associations. **Results:** 117 people with MS were enrolled in this study. No associations were seen between the two models of childhood adversity and MS severity. Experiencing ≥4 ACEs was significantly associated with ever-smoking (OR = 4.0, 95%CI 1.54-11.0). Childhood adversity was not associated with treatment timelines.

Conclusions: This single-centre study demonstrated that childhood adversity was not associated with worse MS disability outcomes, possibly due to equitable treatment despite socioeconomic disadvantage. However, these results warrant further investigation utilizing samples that are more representative of the broader Australian experience.

Board P29 · Presenter: Yingxue He

MLKL-Dependent Necroptotic Signalling Regulates Keratinocyte Differentiation and Epidermal Repair

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Background and Aims: Atopic dermatitis is characterised by impaired skin barrier function and inflammation. Necroptosis is a form of regulated cell death mediated by RIPK3 and MLKL, but its role in epidermal regeneration remains unclear. We investigated whether necroptotic signalling regulates keratinocyte differentiation and skin repair independently of cell death.

Methods: Skin repair was examined in RIPK3- and MLKL-deficient mice using excisional wound and toxic epidermal necrolysis models. Epidermis-specific MLKL-deficient mice were used to assess keratinocyte-intrinsic effects. Cultured keratinocytes were exposed to sublethal necroptotic stimuli to evaluate calcium responses and differentiation markers. Three-dimensional human skin equivalents lacking MLKL were used to assess epidermal stratification.

Results: RIPK3- and MLKL-deficient mice exhibited accelerated skin recovery, with histological findings suggesting altered epidermal repair dynamics. In cultured keratinocytes, sublethal necroptotic stimulation triggered MLKL-dependent calcium influx and promoted differentiation. Conversely, loss of MLKL impaired keratinocyte differentiation and epidermal stratification in three-dimensional skin equivalents.

Conclusions: These findings identify a non-lytic role for MLKL signalling in promoting keratinocyte differentiation, while demonstrating that disruption of this pathway can accelerate skin recovery in vivo. The contrasting outcomes suggest that MLKL has context-dependent functions during epidermal repair.

Significance/Impact: Defining how MLKL coordinates differentiation and tissue repair may uncover new approaches to restoring the skin barrier in conditions such as atopic dermatitis. Further work is needed to establish how these effects interact in inflammatory skin disease.

Board P30 · Presenter: Zoe Whitehouse

Parkinson’s disease and calcium signalling beyond the brain

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Background and Aims: Whilst the pathogenesis of Parkinson’s Disease (PD) is not fully understood, key pathological processes are mitochondrial dysfunction, and accumulation of misfolded proteins, both of which are closely linked to disruptions in calcium signalling. Calcium signalling is facilitated by via various channels, pumps, and receptors which move calcium from intracellular stores including the ER and mitochondria and from the extracellular environment. While PD has historically been viewed as a neuronal disorder, recent research reveals systemic changes. These findings include gene expression changes and accumulation of disease-related proteins in peripheral cells such as blood, but there is limited research into the role of calcium signalling in peripheral cells of PD patients. We aim to investigate calcium signalling in blood cells of PD patients.

Methods: To address this, non-neuronal calcium signalling was measured in PD lymphoblastoid cell lines (LCLs) derived from the blood of PD patients and controls using a fluorometric plate-based assay and a stimulus invoking a calcium response.

Results: PD LCLs displayed a significantly lower level of basal calcium compared to controls. Following stimulation there was no differences in calcium measurements and brings them in level with controls. Proteomic analysis identified a significant downregulation of calcium binding proteins, suggesting altered regulation of intracellular calcium, potentially involving calcium release from the ER.

Conclusions: These results suggest altered mechanisms regulating calcium signalling in PD LCLs. Future studies will dissect the calcium signalling pathways involved using specific ER inhibitors, investigate the contribution of calcium storage organelles, and determine whether these alterations are conserved across other peripheral cell types. This work will help define the mechanisms underlying altered calcium regulation in PD and support the development of peripheral biomarkers for early diagnosis and pre-clinical research, bringing us closer to solving the puzzle of PD.

Board P31 · Presenter: Zoriana Novosiadla

Dietary Tyrosine restriction rescues *Drosophila* model of HIBCH deficiency

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Background and Aims: Inherited disorders of amino acid metabolism (IMDs) result in toxic metabolite accumulation or deficiencies in essential metabolic products. Dietary interventions can mitigate symptoms, but systematic approaches to identify effective dietary treatments are lacking. HIBCH deficiency disrupts valine breakdown and is associated with mitochondrial dysfunction. This study aimed to identify dietary modifications that mitigate disease-associated phenotypes in a Drosophila model of HIBCH deficiency and explore the cellular processes underlying these effects.

Methods: A fully defined synthetic diet was used to generate a 51-diet array varying individual amino acid concentrations. Developmental timing and survival were measured to identify beneficial dietary modifications. Follow-up experiments included expanded nutrient concentration series, pharmacological interventions and transcriptomic analysis to further characterise the response.

Results: Systematic screening identified an unexpected dietary interaction in the HIBCH deficiency model. While modifying dietary valine did not improve mutant survival, reducing tyrosine to 50% of its concentration in the complete diet significantly increased survival. Rapamycin and salubrinal, known modulators of nutrient- and stress-sensing pathways, respectively, phenocopied the survival benefit of moderate tyrosine restriction suggesting that reduced tyrosine may modulate these pathways. Tyrosine restriction did not shift the HIBCH transcriptome, despite improved survival, suggesting the diet alters other aspects of HIBCH pathophysiology.

Conclusions: Our systematic approach identified tyrosine restriction as an unexpected dietary intervention that significantly improves survival in a Drosophila model of HIBCH deficiency. The benefits of dietary and pharmacological interventions suggest that nutrient- and stress-sensing pathways may contribute to this response. These findings demonstrate the value of screening beyond the affected metabolic pathway and provide a foundation for investigating new approaches to managing inherited metabolic disorders.