XXIIIrd INTERNATIONAL CONGRESS OF GENETICS

GENETICS AND GENOMICS

Linking Life and Society

16-21 July 2023

MELBOURNE CONVENTION AND EXHIBITION CENTRE
AUSTRALIA

www.icg2023.com.au

CONGRESS HANDBOOK

HOSTED BY:

iGF

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STOmics

Single-cell Stereo-seq axolotl brain paper, Science 2022

Stereo-seq mouse organogenesis paper, Cell 2022

WELCOME

It is with immense honour and joy that I extend a warm welcome to all participants in the XXIII International Congress of Genetics. I express my deepest gratitude to each one of you who is taking the time to join us at the Congress, which has been of paramount significance in the field of genetics since it was first held in 1899.

It is indeed a time to celebrate the return of in-person meetings that have not been possible for a significant portion of the five years since the last Congress held in 2018 in Brazil. The intervening years have been marked by profound sadness caused by the Covid-19 pandemic and have created challenges for the Organisers of the Congress. The Organising Committee has worked tirelessly to bring this Congress into being, driven by a shared passion to celebrate our understanding of genetics and its far-reaching implications.

The International Genetics Federation (IGF) has played a pivotal role in fostering the development of genetics on a global scale, collaborating with member societies across the world. Through its efforts, advances in genetics have been disseminated more widely. Countries with nascent research landscapes have been included, joining us all in contemplating how genetics can contribute to a more inclusive and equitable world. Representatives of IGF member societies will meet at the Congress to discuss how we can do more.

The Organisers take immense pride in presenting an inspiring scientific program, encompassing diverse themes within genetics and featuring eminent scientists who will share the latest advancements in their respective fields. The program has been created to embrace researchers from across the globe.

In addition to the exceptional scientific program, social events will enable truly unforgettable moments of connection. I urge you to attend a most creative Opening Ceremony and Reception and the Congress Social Evening – *Connection* will be unforgettable. On top of that there are several events designed to engage and inform the public, but they will be of equal interest to Congress delegates.

Surely, this Congress has been meticulously planned, with attention given to every detail. It is our genuine hope that the IGF will continue to inspire co-operation, foster scientific dialog, and emphasise the pivotal role of genetics in shaping a future that embodies equality among individuals, ensures health and food security, and equips us to face the pressing challenges posed by climate change and biodiversity loss with wisdom and efficacy.

Once again, I extend my warmest welcome and encourage you to make the most of the enriching days ahead.

Professor Marcia Margis-Pinheiro

President – International Genetic Federation

On behalf of the Organising Committee, I extend a warm welcome to all participants of the 2023 International Congress of Genetics in the vibrant city of Melbourne, Australia. We acknowledge with the deepest respect that this Congress will be held on the lands of local indigenous Australians, the Wurundjeri people of the Kulin nation. We pay our sincere respects to their elders past AND present, recognising their custodianship and faithful stewardship of the land on which we gather. We thank the International Genetics Federation for entrusting us as hosts of this Congress that has provided a global forum to discuss and celebrate advances in genetics since 1899.

We assemble in Melbourne to celebrate the remarkable progress made in genetics since the last Congress held in 2018 in Foz do Iguacu Brazil. Over the last five years there have continued to be extraordinary technological advances in genomics and gene editing. The Congress theme, ***Genetics and Genomics: Linking Life and Society*** recognises that this meeting is being held at an important moment in history, a time when the tools are available to do exhilarating fundamental research, and to address major issues in health, agriculture and environmental care.

The scientific program created by the Local and International Program Committees is exciting. There will be a feast of great talks across the breadth of genetics, but the Congress also affords the opportunity for conversations - the sharing of insights and ideas and the formation of collaborations in planned and serendipitous encounters. In an era defined and, at times, confined by digital connectivity, the benefits of coming together, and the joy and energy of face to face meetings, have become even more pronounced. In planning this Congress we have strived to create an event that blends science, culture and connectivity - from the beginning of the opening ceremony to the end of the last talk.

We hope that you will have an experience in Melbourne that is deeply meaningful and memorable.

Professor Kathryn North AC

Congress President

HOST ORGANISATIONS

The City of Melbourne is honoured to welcome in excess of 1600 participants from 50 countries for the International Congress of Genetics, which returns here for the first time in 20 years.

Melbourne is a proud knowledge city with a leading scientific edge. We have several state-of-the-art institutes respected globally for their expertise in delivering clinical trials and major health outcomes.

As a city, we have cultivated a passion for education, collaboration, and innovation. We're home to two of the world's top 100 universities and the birthplace of historic scientific breakthroughs, such as the cochlear implant and frozen embryo.

All this makes Melbourne the perfect destination for your congress.

We look forward to welcoming you to our city – not only for the official programming, but also to marvel at Melbourne's world-famous sights.

Catch a match of Aussie Rules at the globally recognisable MCG, sip coffee in one of the world's most liveable cities and snap a selfie among the street art in one of our iconic laneways.

Our City Ambassadors will be onsite for the duration of the congress to help you discover all that Melbourne has to offer.

I wish you all the best for your time here with us.

Lord Mayor Sally Capp

CITY OF
MELBOURNE

The International Genetics Federation (IGF) is an association of national genetics societies interested in promoting the advancement of the science of Genetics. It seeks to support the activities of national societies and foster cooperation between them. The IGF is the custodian of the International Congress of Genetics, an elite conference that is held once every five years in different cities around the world.

For more information visit:
www.geneticsfederation.com

AGTA Australasian Genomic Technologies Association

The Australasian Genomic Technologies Association (AGTA) is dedicated to advancing and promoting the field of genomics and genomic technologies in Australasia. AGTA is the principal body for the promotion of genomics research in Australasia and it draws on the breath of genomics research and technology development across Australasia.

For more information visit:
www.agtagenomics.org.au

GSA
GENETICS SOCIETY OF AUSTRALASIA INC.

The Genetics Society of Australasia (GSA) is the professional organisation for scientific researchers and educators in the field of genetics in Australia, New Zealand and the Asia-Pacific region. The Society is dedicated to promoting research and education in genetics and facilitating communication among geneticists and the broader public.

For more information visit www. genetics.org.au

HUMAN GENETICS SOCIETY OF AUSTRALASIA
... making sense of your genes

The Human Genetics Society of Australasia (HGSA) was formed in 1977 to provide a forum for the various disciplines collected under the title of Human Genetics. In our unified intent to support the genetic health of the Australian and New Zealand population HGSA members value communication with all our clinical and laboratory colleagues. The Society contributes to all major debates and advocates for the safe, ethical and effective use of genetic information in healthcare. The HGSA is regularly called upon as the expert body to contribute to national and international initiatives that involve human genetics.

For more information visit www.hgsa.org.au

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BUSINESS EVENTS
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SCIENTIFIC PROGRAM

A truly global forum as been developed to bring together the international genetics community to share ideas and the latest research under the overarching theme: **Genetics & Genomics: Linking Life & Society**.

Over the coming days, the Congress will cover the breadth of fundamental discoveries in genetics and genomics, the latest advances in technologies, and important and topical applications in areas such as health, agriculture and the conversation of species and the environment.

You will hear from 9 outstanding plenary speakers, including the recipients of the prestigious 2023 Gruber Prize and the MJD White Medal, from Nobel Laureates and over 100 invited speakers and abstract authors presenting across 54 symposia addressing the 6 key theme areas.

Our commitment to diversity has resulted in presentations from researchers from 50 different countries and across a full range of gender and career stages.

Poster sessions are an integral element of the scientific program designed to showcase the latest research and to foster discussion and dialogue about work undertaken across the 6 theme areas, through presentations over the extended lunch periods and digital formats available to view on the Congress App.

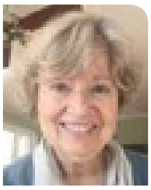
Sessions will be conducted in the following rooms, with each theme in a dedicated room for Symposia Sessions:

Plenary Sessions	Plenary Room 2 (Ground Floor)
Symposia Sessions	Level 2
Evolutionary Genetics	Room 203
Genetics & the Environment	Room 204
Genomics & Genomic Technologies	Room 210/211
Genetics & Human Health	Room 212/213
Molecular, Cellular & Developmental Genetics	Room 219
Agricultural & Plant Genetics	Room 220

The Scientific Program will be lead by the following outstanding Plenary speakers:

Professor Mark Blaxter

Wellcome Sanger Institute, UK



Professor Nancy Cox

Vanderbilt Brain Institute, USA

Professor Anne Ferguson-Smith

University of Cambridge, UK

Professor Neil Gemmell

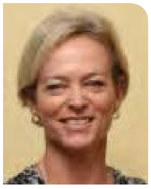
University of Otago, New Zealand

Professor Eddie Holmes

University of Sydney, Australia

Professor Ruth Lehmann

Whitehead Institute for Biomedical Research, USA



Professor Nicola Mulder

University of Cape Town, South Africa

Professor Detlef Weigel

Max Planck Institute for Biology, Germany

Professor Allan Jacobson

University of Massachusetts, USA

2023 Gruber Genetic Prize Recipient

Professor Lynne Maquat

University of Rochester, USA

2023 Gruber Genetic Prize Recipient

PROGRAM AT A GLANCE

SUNDAY 16 JULY 2023

0900-1700	**Optional Satellite Meeting - Biodiversity Genomics - A Global Perspective** *Melbourne Convention & Exhibition Centre* – **ROOM 219**
	PUBLIC PROGRAM
1600-1630	Celebrating Science & Faith *St Paul's Cathedral*
1200-1930	Registration Open **- FOYER**
1700-1745	**Congress tips for HDR Students and Early Career Researchers - MCEC - Hospitality Room 6 Upper Level**
1800-2100	**Opening Ceremony & Welcome Reception - PLENARY HALL 2**

MONDAY 17 JULY 2023

0730-1730	Registration Open - Foyer					
0830-0930	**Plenary Session 1 – PLENARY HALL 2**					
	Mark Blaxter - Wellcome Sanger Institute, UK New biology from new genomes: The Tree of Life project *Chair: Jenny Graves, Australia*					
0930-1000	Morning Tea and Poster Viewing – Exhibition Hall					
1000-1200	**SYMPOSIA SESSION A**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**A1:** Genomes & Biodiversity **ROOM 203**	**A2:** Microbes & Microbiomes **ROOM 204**	**A3:** Indigenous Genomics in the Precision Medicine Era **ROOM 210/211**	**A4:** Rare Disease Genetics & Biology **ROOM 212/213**	**A5:** Atlases for Cell & Developmental Biology **ROOM 219**	**A6:** Plant Ecological & Conservation Genetics **ROOM 220**
1200-1400	Lunch and Poster Session (odd number posters presented) – Exhibition					
1215-1345	Industry Lunch Sessions					
1400-1600	**SYMPOSIA SESSION B**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**B3:** Paleogenomics **ROOM 203**	**B2:** Population Genetics & Genomics **ROOM 204**	**B5:** Emerging Applications in 'Omics Technologies - Filling the Gaps **ROOM 210/211**	**B4:** Ethical, Legal & Social Issues in Genomic Medicine **ROOM 212/213**	**B6:** Cell Signalling & Regeneration **ROOM 219**	**B1:** Plant Biotechnology & Genome Editing **ROOM 220**
1600-1630	Afternoon Tea and Poster Viewing – Exhibition Hall					
1630-1730	**Plenary Session 2 – PLENARY HALL 2**					
	Nicola Mulder - University of Cape Town, South Africa Leveraging bioinformatics capacity to implement African genomics for health *Chair: Alex Brown Australia*					
	PUBLIC PROGRAM					
1800-1930	Women in Science – Unique journeys to different peaks *Melbourne Convention & Exhibition Centre* – **ROOM 210**					

TUESDAY 18 JULY 2023

0700-0815	Industry Breakfast Session					
0730-1730	Registration Open - **FOYER**					
0830-0930	**Plenary Session 3 – PLENARY HALL 2**					
	Ruth Lehmann, Whitehead Institute for Biomedical Research, USA 'Seeing' translation - in germ granules *Chair: Hongyan Wang, Singapore*					
0930-1000	Morning Tea and Poster Viewing **- EXHIBITION HALL**					
1000-1200	**SYMPOSIA SESSION C**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**C1:** Host/Pathogen Interactions **ROOM 203**	**C2:** Conservation Genetics **ROOM 204**	**C3:** Equity & Diversity in the Application of Human Genomics **ROOM 210/211**	**C4:** Disease Gene Identification & Functional Genomics Using Animal Models **ROOM 212/213**	**C5:** Gene Regulation & RNA Biology **ROOM 219**	**C6:** Plant Breeding & Food Security **ROOM 220**
1200-1400	Lunch and Poster Session (even number posters presented) – Exhibition					
1215-1345	Industry Lunch Sessions					
1400-1600	**SYMPOSIA SESSION D**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**D1:** Evolution & Development **ROOM 203**	**D2:** Ecological Epigenetics **ROOM 204**	**D3:** Bioinformatics & Computational Biology **ROOM 210/211**	**D4:** Genomic Therapies & Precision Medicine **ROOM 212/213**	**D5:** Neurogenetics of Behaviour **ROOM 219**	**D6:** Plant interactions with Other Organisms **ROOM 220**
1600-1630	Afternoon Tea and Poster Viewing – Exhibition Hall					
1630-1730	**Plenary Session 4 – PLENARY HALL 2**					
	Neil Gemmell, University of Otago, New Zealand Fishing for insights in sex determination, differentiation and reproductive biology *Chair: Peter Dearden, New Zealand*					
	PUBLIC PROGRAM					
1930	Oratorio - Origins of the Universe, of Life, of Species, of Humanity Melbourne Recital Centre					

PROGRAM AT A GLANCE

Continued

WEDNESDAY 19 JULY 2023

0700-0815	Industry Breakfast Session					
0730-1730	Registration Open **- FOYER**					
0830-0930	Plenary Session 5 – Gruber Genetics Prize 2023 Recipients **- PLENARY HALL 2**					
	Allan Jacobson, University of Massachusetts, USA NMD, translation termination, and readthrough therapy: consequences and suppression of genetic nonsense Lynne Macquat, University of Rochester, USA Nonsense-mediated mRNA decay in human health and disease *Chair: Allan Spradling, USA*					
0930-1000	Morning Tea and Poster Viewing **- EXHIBITION HALL**					
1000-1200	**SYMPOSIA SESSION E**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**E1:** Genetic Strategies to Control Pests & Disease Vectors **ROOM 203**	**E2:** Climate Change Genetics **ROOM 204**	**E3:** Tandem-Repeat Genomics Informing Polygenic Human Disorders & Traits **ROOM 210/211**	**E4:** Counselling, Communication & Consent in Human Genetics Contexts Across The Lifetime **ROOM 212/213**	**E5:** Cell & Organoid Models for Human Disease Mechanisms **ROOM 219**	**E6:** Agricultural & Horticultural Genetics **ROOM 220**
1200-1400	Poster Viewing – Exhibition (exhibition closes at 1430)					
	Afternoon Speciality Sessions					
1200-1530	Genetic Society of Australasia (GSA) Program – ROOM 210 GSA AGM GSA Award Presentations					
1300-1615	Human Genetics Society of Australasia (HGSA) Program – ROOM 212 HGSA Sutherland Lecture HGSA AGM HGSA Oration					
1630-1730	Meet the Editor – ROOM 203					
	PUBLIC PROGRAM					
1730-1830	Genetics vs Sport - Are super athletes born or made? Melbourne Conversations held at Melbourne Convention & Exhibition Centre - Room 210					
1830-1930	Future Forums: The genetic rescue of our fantastic beasts Melbourne Museum					

THURSDAY 20 JULY 2023

0700-0815	Industry Breakfast Session					
0730-1730	Registration Open **- FOYER**					
0830-0930	Plenary Session 6 **- PLENARY HALL 2**					
	Detlef Weigel - Max Planck Institute, Germany Paranoid Plants: Genetic Conflict in the Immune System *Chair: Suresh Balasubramanian, Australia*					
0930-1000	Morning Tea and Poster Viewing **- EXHIBITION HALL**					
1000-1200	**SYMPOSIA SESSION F**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**F1:** Evolutionary Genetics Theory **ROOM 203**	**F2:** Environmental Genomics **ROOM 204**	**F3:** Cell-free DNA Technologies: Challenges & Opportunities **ROOM 210/211**	**F4:** Identifying Functional Target Genes at GWAS Loci **ROOM 212/213**	**F5:** New Experimental Model Organisms for Genetics Research **ROOM 219**	**F6:** Plant Cell & Developmental Biology **ROOM 220**
1200-1400	Lunch and Poster Session (odd number posters presented) – Exhibition					
1215-1345	Industry Lunch Sessions					
1400-1600	**SYMPOSIA SESSION G**					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**G1:** Genetics & Epigenetics of Sex **ROOM 203**	**G2:** Invasion Genetics **ROOM 204**	**G3:** Accelerating Genomics **ROOM 210/211**	**G4:** Genetics of Complex Disease & Quantitative Traits **ROOM 212/213**	**G5:** Advanced Imaging in Cellular & Developmental Genetics **ROOM 219**	**G6:** Genetics & Genomics of Plant Evolution **ROOM 220**
1600-1630	Afternoon Tea and Poster Viewing **- EXHIBITION HALL**					
1630-1730	Plenary Session 7 **- PLENARY HALL 2**					
	Nancy Cox - Vanderbilt Brain Institute, USA How heritability of everyday laboratory values leads to big health disparities *Chair: Kathryn Burdon, Australia*					
	PUBLIC PROGRAM					
1800-1900	Population DNA Screening for Disease Risk Melbourne Convention & Exhibition Centre – Room 210					
	Optional Social Event					
1900-2100	Connect - The Lume Melbourne Convention & Exhibition Centre					

PROGRAM AT A GLANCE

Continued

FRIDAY 21 JULY 2023

0730-1730	Registration Open - **FOYER**					
0830-0930	Plenary Session 8 **– PLENARY HALL 2**					
	Anne Ferguson-Smith, University of Cambridge, UK The genetics of epigenetic variation *Chair: Marieke Oudelaar, Germany*					
0930-1000	Morning Tea and Poster Viewing – Exhibition Hall					
1000-1200	SYMPOSIA SESSION H					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Special Symposium**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**H1:** Systematics & Phylogeography **ROOM 203**	**H2:** The Genetics of Local Adaptation **ROOM 204**	**H3:** Genomics-driven Healthcare **ROOM 210/211**	**H4:** Early Career Researcher Showcase **ROOM 212/213**	**H5:** Epigenetic Mechanisms & Chromatin Biology **ROOM 219**	**H6:** From Genebanks to Fields: Leveraging Genomics Innovations for Characterising Genetic Diversity **ROOM 220**
1200-1330	Lunch and Poster Session (even number posters presented) **– EXHIBITION**					
1330-1530	SYMPOSIA SESSION I					
Theme	**Evolutionary Genetics**	**Genetics & the Environment**	**Genomics & Genomic Technologies**	**Genetics & Human Health**	**Molecular, Cellular & Developmental Genetics**	**Agricultural & Plant Genetics**
Symposia	**I1:** Molecular Evolution **ROOM 203**	**I2:** Genetics of Wildlife Disease & Responses to Infection **ROOM 204**	**I3:** Genetics & Genomics of Pandemic, Endemic & Emerging Infectious Organisms **ROOM 210/211**	**I4:** Pharmaco - genomics in Drug Discovery & Development **ROOM 212/213**	**I5:** Genetics & Biology of Ageing **ROOM 219**	**I6:** Plant Response to Environmental Change **ROOM 220**
1530-1600	Afternoon Tea **- FOYER**					
1600-1700	Plenary Session 9 **– PLENARY HALL 2**					
	Eddie Holmes, University of Sydney, Australia (GSA – MJD White Award Recipient) Redefining the virosphere *Chair: Peter Doherty, Australia*					
1700-1730	Congress Closing (including Award Presentations)					

This program is subject to change.

DAILY PROGRAM

SUNDAY 16 JULY 2023

0900-1700	Optional Satellite Meeting
Room 219	**Biodiversity Genomics - A Global Perspective** Melbourne Convention & Exhibition Centre

1700 - 1745	Optional Meeting
Hospitality Room 6 Upper Level	**Congress tips for HDR students and early career researchers**

1200-1930	Registration Open Melbourne Convention & Exhibition Centre Foyer
1800-2100 Plenary Room 2	Opening Ceremony & Welcome Reception Melbourne Convention & Exhibition Centre

MONDAY 17 JULY 2023

0700-1730	Registration Open Melbourne Convention & Exhibition Centre Foyer

0830-0930	Plenary Session 1
Plenary Room 2	**Mark Blaxter - Wellcome Sanger Institute, UK** New biology from new genomes: The Tree of Life project ***Chair: Jenny Graves, Australia*** *Session supported by BGI/MGI*
1000-1200	SYMPOSIA SESSIONS A
Room 203	A1: Genomes & Biodiversity (Evolutionary Genetics) *Session supported by Bioplatforms Australia*
Convenors	*Tammy Steeves, New Zealand & Claire Mérot, France*
1000-1030	**Claire Mérot, CNRS ECOBIO / Université de Rennes, France** The role of structural genomic variants in the evolution of biodiversity
1030-1100	**Carolina Pardo-Diaz, Universidad del Rosario, Colombia** Drivers of diversification in a neotropical biodiversity hotspot: lessons from spiders, birds, and butterflies
1100-1115	**Scott Edwards, Harvard University, USA** Pangenomes of North American Scrub-Jays (Aphelocoma) reveal abundant structural variation and rapid shifts in genome size
1115-1130	**Jonathan Sandoval Castillo, Flinders University, Australia** Genomic basis of body miniaturization in Southern pygmy perch (*Nannoperca australis*; Teleostei)
1130-1145	**Carolyn Hogg, University of Sydney, Australia** Integrating genomics, conservation, and Indigenous knowledge to protect a unique marsupial
1145-1200	**Philipp Schiffer, University of Cologne, Germany** Biodiversity genomics of asexual and anhydrobiotic nematodes in extreme environments

This program is subject to change.

SUNDAY 16 JULY 2023

MONDAY 17 JULY 2023

Room 204	A2: Microbes & Microbiomes (Genetics & the Environment)
Convenors	*Belinda Ferrari, Australia & Claudia Coleine, Italy*
1000-1030	**Claudia Coleine, Tuscia University, Italy** Microbiomes from extreme environments: challenges to thrive in the most prohibitive conditions
1030-1100	**Alison Murray, Desert Research Institute, USA** Decoding microbiome genomes at the bottom of the world to uncover Antarctic natural products
1100-1115	**Lucas Huggins, University of Melbourne, Australia** Nanopore sequencing using the full length 16s rRNA gene is a promising veterinary diagnostic tool for the detection of blood-borne bacterial pathogens
1115-1130	**Andrew Wallace, Livestock Improvement Corporation, New Zealand** Large scale shotgun metagenomic sequencing study of the New Zealand dairy cow milk microbiome
1130-1145	**Rebecca Grimwood, University of Otago, New Zealand** Host specificity shapes fish viromes across lakes on an isolated remote island
1145-1200	**Gabriel Moreno-Hagelsieb, Wilfrid Laurier University, Canada** Fast delimitation of enterobacterales species

Room 210/211	A3: Indigenous Genomics in the Precision Medicine Era (Genomics & Genomic Technologies) *Session supported by the University of Melbourne*
Convenors	*Phillip Wilcox, New Zealand & Azure Hermes, Australia*
1000-1030	**Phillip Wilcox, University of Otago, New Zealand** Study designs for enhancing indigenous Māori participation in medical genomics: one size does not fit all
1030-1100	**Karen Miga, University of California, USA** Expanding studies of global genomic diversity with complete, telomere-to-telomere (T2T) assemblies
1100-1115	**Jaye Moors, Variant Bio, USA** Making genomic research results meaningful: lessons learned from community engagement
1115-1130	**Isabela Alvim, University of Melbourne, Australia** Addressing the claim for genomic studies in neglected populations: pharmacogenetics actionable genotypes in Andean and Amazonian native Americans
1130-1145	**Jordon Lima, University of Otago, New Zealand** Māu tēnā kīwai o te kete, māku tēnei: the equitable application of circulating tumour DNA to the Māori population in Aotearoa New Zealand
1145-1200	**Simone Cree, University of Otago, New Zealand** Investigating the genetic modulators of cardiac biomarkers among Pasifika

Room 212/213	A4: Rare Disease Genetics & Biology (Genetics & Human Health) *Session supported by Illumina*
Convenors	*Stephen Robertson, New Zealand & Evan Eichler, USA*
1000-1030	**Evan Eichler, University of Washington, USA** Long-read sequencing and assembly of patient genomes
1030-1100	**Heather Mefford, St Jude Children's Research Hospital, USA** The genetic landscape of rare pediatric epilepsies: from etiology to precision medicine
1100-1115	**Michael Silk, Centre for Population Genomics, Australia** Measuring constraint to missense variation in the context of three-dimensional protein structure
1115-1130	**Haloom Rafehi, Walter & Eliza Hall Institute of Medical Research, Australia** Genetic discovery and diagnosis of ataxia in an Australian hereditary ataxia cohort
1130-1145	**Shokouh Shahrokhi Sabzevar, Murdoch Children's Research Institute, Australia** Defining cell-type specific transcriptome signatures and pathways dysregulated in prefrontal cortex of individuals with Prader-Willi syndrome
1145-1200	**Clare van Eyk, University of Adelaide, Australia** Defining the genetic etiology of cerebral palsy: Systematic reanalysis of genomic data from the Australian Cerebral Palsy Biobank cohort

Room 219	**A5: Atlases for Cell & Developmental Biology (Molecular, Cellular & Developmental Genetics)**
Convenors	*Christine Wells, Australia & Leonie Quinn, Australia*
1000-1030	**Muzlifah Haniffa, Wellcome Sanger Institute, UK** (virtual presentation) Decoding the developing human immune system
1030-1100	**Nathan Palpant, University of Queensland, Australia** A conserved genome-wide epigenetic repressive signature underpins cell identity
1100-1115	**Carolyn de Graaf, Walter & Eliza Hall Institute of Medical Research, Australia** Comparison of gene expression and transcriptional regulation of haematopoietic cells across vertebrates
1115-1130	**Jovana Maksimovic, Peter McCallum Cancer Centre, Australia** Single-cell atlas of the paediatric airway
1130-1145	**Drew Neavin, Garvan Institute of Medical Research, Australia** Ancestry annotation from single-cell data identifies underrepresented ethnic groups in single-cell consortia
1145-1200	**Christine Wells, University of Melbourne, Australia** In silico modelling to improve stem cell sources of human myeloid cells
Room 220	**A6: Plant Ecological & Conservation Genetics (Agricultural & Plant Genetics)**
Convenors	*Daniel Ortiz-Barrientos, Australia & Victoria Sork, USA*
1000-1030	**Victoria Sork, University of California, USA** DNA methylation as a possible driver of phenotypic variation in oaks
1030-1100	**Yalong Guo, Chinese Academy of Science, China** Forces driving transposable element load variation during *Arabidopsis* range expansion
1100-1115	**Jason Bragg, Royal Botanic Garden Sydney, Australia** Adapted and adaptable plant populations for conservation
1115-1130	**Thais Ribeiro Pfeilsticker, University of Tasmania, Australia** Will hybridisation contribute to climate change adaptation in Australian eucalypts?
1130-1145	**Tara Hopley, Royal Botanic Gardens Victoria, Australia** A genomic perspective helps guide conservation of an endangered orchid from south-eastern Australia
1145-1200	**Colin Ahrens, Cesar Australia, Australia** Reality bites: on the misinterpretation of genetic offset models

1230-1330 Exhibition	**Poster Session (odd number posters presented)**

1400-1600	**SYMPOSIA SESSIONS B**
Room 203	**B1: Paleogenomics (Evolutionary Genetics)**
Convenors	*Lisa Matisoo-Smith, New Zealand & Michael Knapp, New Zealand*
1400-1430	**Maria Nieves-Colón, University of Minnesota, USA** (virtual presentation) Pilot ancient DNA study of a historic Afro-diasporic population in Peru
1430-1500	**Nicolas Rawlence, University of Otago, New Zealand** Palaeogenomic insights into prehistoric New Zealand from top to bottom
1500-1515	**Michael Knapp, University of Otago, New Zealand** From dwarfs to giants – the evolution of New Zealand's giant birds
1515-1530	**Pascale Lubbe, University of Otago, New Zealand** Responses of New Zealand birds to Pleistocene climate change
1530-1545	**Catherine Collins, University of Otago, New Zealand** Piecing together the settlement of the Pacific with Pacific rat genomics
1545-1600	**Anna Gosling, University of Otago, New Zealand** First ancient genome from Papua New Guinea

Room 204	B2: Population Genetics & Genomics (Genetics & the Environment)
Convenors	*Sally Potter, Australia & Maren Wellenreuther, New Zealand*
1400-1430	**Maren Wellenreuther, Plant & Food Research, New Zealand** Going beyond SNPs: structural variants as facilitators of eco-evolutionary change
1430-1500	**Josefa Gonzalez, Institute of Evolutionary Biology, Spain** Adaptation to natural and urban environments: a transposable element perspective
1500-1515	**Soleille Miller, University of New South Wales, Australia** ***Recipient of the GSA Smith-White Travel Award*** Genetic and phenotypic consequences of local losses of sexual reproduction in the wild
1515-1530	**Emily Roycroft, Australian National University, Australia** The genomic impact of island isolation in Australian mammals
1530-1545	**David Field, Macquarie University, Australia** The maintenance of alternative fitness peaks in the face of gene flow
1545-1600	**Lightning Presentations** **Anna Santure, Auckland University, New Zealand** Sex differences in the recombination landscape for a threatened passerine with high levels of sexual conflict **Beilei Bian, University of Queensland** Extensive antagonistic variants across the human genome **Minami Imamoto, Tokyo Institute of Technology, Japan** Did egg-eater lose the ecological competition? Strong population bottleneck in matumbi hunter the paedophage **Simon Baxter, University of Melbourne, Australia** The rapid spread of a recessive insecticide resistance mutation across Australia **Natalie Forsdick, Manaaki Whenua – Landcare Research, New Zealand** Conservation genomics of Kuaka Whenua Hou/Codfish Island diving petrel

Room 210/211	B3: Emerging Applications in 'Omics Technologies' - Filling the Gaps (Genomics & Genomic Technologies) *Session supported by Illumina*
Convenors	*Ruby Lin, Australia & Fernando Rossello, Australia*
1400-1430	**Dr Hieu Nim, Murdoch Children's Research Institute, Australia** VR-omics: exploration of spatial transcriptomes in 3D and in virtual reality
1430-1500	**Braden Tierney, Weill-Cornell Medical College, USA** A multi-omic perspective on the adaptation of life to humanity's greatest frontiers: the oceans and space
1500-1515	**Teresa Zhao, Murdoch Children's Research Institute, Australia** High throughput functional genomics – the next big hit
1515-1530	**Matthew Ritchie, Walter & Eliza Hall Institute of Medical Research, Australia** Benchmarking long-read RNA-sequencing analysis tools using *in silico* mixtures
1530-1545	**Liang Wu, BGI Research / BGI Shenzhen, China** Spatially-resolved transcriptomics analyses of solid tumors
1545-1600	**Sriharsa Pradhan, New England Biolabs Inc., USA** Genome wide integrative spatio-functional genomics using novel bifunctional nicking enzyme

Room 212/213	B4: Ethical, Legal & Social Issues in Genomic Medicine (Genetics & Human Health)
Convenors	*Ainsley Newson, Australia & Erisa Sabakaki Mwaka, Uganda*
1400-1430	**Erisa Sabakaki Mwaka, Makerere University, Uganda** Feedback of results of genetic and genomic research: How prepared is sub-Saharan Africa?
1430-1500	**Krystal Tsosie, Arizona State University, USA** Catch-22: perils, promises, and profit from indigenous peoples' DNA
1500-1515	**Fiona Lynch, University of Melbourne, Australia** Ethical, implementation and practical issues associated with automated genomic reanalysis: genomic workforce perspectives
1515-1530	**Vaishnavi Nathan, University of Queensland, Australia** Genetic counsellors' attitudes towards disability and prenatal testing: survey findings from the Australasian workforce
1530-1545	**Stephanie Best, Peter MacCallum Cancer Centre, Australia** Reflecting the complexity of implementing genomic medicine research
1545-1600	**Jane Tiller, Monash University, Australia** The Australian public's views regarding direct notification of at-risk relatives (with patient consent) by health professionals

Room 219	**B5: Cell Signalling & Regeneration (Molecular, Cellular & Developmental Genetics)** ***Session supported by Australian Regenerative Medicine Institute***
Convenors	*Peter Currie, Australia & Yoshiko Takahashi, Japan*
1400-1430	**Yoshiko Takahashi, Kyoto University, Japan** Gut peristaltic movements: studies with optogenetics and contractile organoids
1430-1500	**Eldad Tzahor, Weizmann Institute of Science, Israel** Advancing cardiac therapeutics
1500-1515	**Maja Adamska, Australian National University, Australia** Sponges' spectacular regeneration abilities: cells, genes and clues to the origin of animals
1515-1530	**Marek Mlodzik, Icahn School of Medicine at Mount Sinai, USA** Intraflagellar transport complex a (IFT-A) and Kinesin-2 are required for nuclear translocation of beta-catenin upon Wnt-signaling activation
1530-1545	**Lachlan Wallace, University of Melbourne, Australia** Netrins are involved in the epithelial wound response in *Drosophila* and Zebrafish
1545-1600	**Shanika Amarasinghe, Monash University, Australia** ResTORing bone growth - Investigating mTORC1 activation during perinatal catch-up growth of mouse limbs

Room 220	**B6: Plant Biotechnology & Genome Editing (Agricultural & Plant Genetics)**
Convenors	*Peter Waterhouse, Australia & Kan Wang, USA*
1400-1430	**Kan Wang, Iowa State University, USA** A quick and simplified maize transformation and genome editing protocol using Agrobacterium ternary vector system
1430-1500	**Jochen Kumlehn, Leibniz Institute of Plant Genetics and Crop Plant Research, Germany** Cas endonuclease technology in cereals: from site-directed mutagenesis towards more precise genome editing
1500-1515	**Sareena Sahab, Department of Energy, Environment and Climate Action, Australia** Transgene-free genome editing in canola
1515-1530	**Peter Waterhouse, Queensland University of Technology, Australia** Gene editing in *Nicotiana benthamiana*: transient silencing and homology-directed repair
1530-1545	**Jessica Hyles, CSIRO, Australia** A functional genomics platform to deliver adapted wheat
1545-1600	**Matthew Mayo-Smith, University of Auckland, New Zealand** Analysis of the inhibitor of growth (ING) genes in flowering and development in the model legume *Medicago truncatula*

1630- 1730	**Plenary Session 2**
Plenary Room 2	**Nicola Mulder, University of Cape Town, South Africa** Leveraging bioinformatics capacity to implement African genomics for health ***Chair: Alex Brown, Australia*** *Session supported by Illumina*

1800 – 1930	**Public Program**
Room 210	**Women in Science – Unique journeys to different peaks** **Professor Doctor Christiane Nüsslein-Volhard, Germany, Professor Anne Muigai, Kenya & Valda Vinson, USA** Melbourne Convention & Exhibition Centre

TUESDAY 18 JULY 2023

0700-1730	**Registration Open** **Melbourne Convention & Exhibition Centre Foyer**

0830-0930	**Plenary Session 3**
Plenary Room 2	**Ruth Lehmann, Whitehead Institute for Biomedical Research, USA** 'Seeing' translation - in germ granules ***Chair: Hongyan Wang, Singapore***

1000-1200	**SYMPOSIA SESSIONS C**
Room 203	**C1: Host/Pathogen Interactions (Evolutionary Genetics)**
Convenors	*Michelle Wille, Australia & Anjana Karawita, Australia*
1000-1030	**Lucie Etienne, Centre International de Recherche en Infectiologie, France** Genomic and functional diversification of the bat immune responses to viral infections
1030-1100	**Helena Westerdhal, Lund University, Sweden** The expressed MHC genetic diversity in songbirds matters in host-pathogen interactions
1100-1115	**Emily Remnant, University of Sydney, Australia** Virus specificity and spillover between host and parasite
1115-1130	**Mun Hua Tan, University of Melbourne, Australia** Conservation of *Plasmodium falciparum* var DBLα types through time and space in Africa
1130-1145	**Nynke Raven, Deakin University, Australia** Immune responses to biotic and abiotic factors in Tasmanian devils
1145-1200	**Anjana Karawita, CSIRO, Australia** Assembly and analysis of the native Australian ibis genomes to understand the species' competency to host infectious diseases
Room 204	**C2: Conservation Genetics (Genetics & the Environment)**
Convenors	*Catherine Grueber, Australia & Rebecca Jordan, Australia*
1000-1030	**Uma Ramakrishnan, National Centre for Biological Sciences, India** How genetics can inform tiger conversation
1030-1100	**Sally Aitken, University of British Columbia, Canada** How can genomic data inform conservation decision making for new climates? Lessons from widespread tree species
1100-1115	**Kym Ottewell, Department of Biodiversity, Conservation and Attractions, Australia** Genetic mixing in conservation translocations recovers diversity of a keystone threatened species, *Bettongia lesueur*
1115-1130	**Jana Wold, University of Canterbury, New Zealand** What's in the cryobank? An argument for a more holistic view of genome-wide diversity
1130-1145	**William Sherwin, University of New South Wales, Australia** Fragmentation by major dams and implications for the future viability of platypus populations
1145-1200	**Lightning Presentations** **Mathew Lott, The Australian Museum Research Institute, Australia** Genomic insights into the contemporary and historical population dynamics of the koala *Phascolarctos Cinerus* **Richard Frankham, Macquarie University, Australia** Large effects of different sized X or Z sex chromosomes on susceptibility to inbreeding depression for total fitness **Anna MacDonald, Australian Antarctic Division, Australia** Developing molecular tools to resolve uncertainties in seabird bycatch from longline fisheries **Joao Filipe, Department of Biodiversity, Conservation and Attractions, Australia** Signatures of natural selection in a foundation tree along Mediterranean climatic gradients

Room 210/211	**C3: Equity & Diversity in the Application of Human Genomics (Genomics & Genomic Technologies)** ***Session is supported by Illumina***
Convenors	*Alex Brown, Australia & Nadine Caron, Canada*
1000-1030	**Nadine Caron, University of British Columbia, Canada** Working towards equity in biobanking: an ongoing Canadian experience
1030-1100	**Ann McCartney, University of California Santa Cruz, USA** Equitable approaches to diversifying reference genomes
1100-1115	**Weerachai Jaratlerdsiri, University of Sydney, Australia** African indigenous genomics reveals lifestyle-relevant adaptation in human health
1115-1130	**Ira Deveson, Genomic Technologies Group, Australia** The landscape of genomic structural variation in Indigenous Australians
1130-1145	**Stephen Leslie, University of Melbourne, Australia** Indigenous Australian genomic variation reveals deep population structure
1145-1200	**Open Discussion**
Room 212/213	**C4: Disease Gene Identification & Functional Genomics Using Animal Models (Genetics & Human Health)** ***Session supported by Australian Functional Genomics Network***
Convenors	*Sally Dunwoodie, Australia & Hugo Bellen, USA*
1000-1030	**Hugo Bellen, Baylor College of Medicine, USA** Using *Drosophila* to help in the diagnosis of undiagnosed diseases
1030-1100	**Corinne Houart, Kings College London, UK** A *FoxG1* transformation tunes local decisions in neurons
1100-1115	**Justin Szot, Victor Chang Cardiac Research Institute, Australia** Congenital NAD deficiency disorder: causes and possible prevention
1115-1130	**Rudrarup Bhattacharjee, University of Adelaide, Australia** Genetic, molecular and mouse model investigations of broad neurodevelopmental impact of deleterious variants of the TREX mRNA export complex subunits
1130-1145	**Michael Hildebrand, University of Melbourne, Australia** Mutation of *cyclophillin-40* molecular chaperone causes persistent stuttering
1145-1200	**Rita Serrano, Monash University, Australia** Mitochondrial degeneration is the initial cellular pathology in *uba5* deficiency and indicates a role for ufmylation in mitochondrial homeostasis
Room 219	**C5: Gene Regulation & RNA Biology (Molecular, Cellular & Developmental Genetics)**
Convenors	*Thomas Preiss, Australia & Minna-Liisa Änkö , Finland*
1000-1030	**Minna-Liisa Änkö, Tampere University, Finland** RNA structures shape cellular functions
1030-1100	**Gracjan Michlewski, International Institute of Molecular and Cell Biology in Warsaw, Poland** Sequence specificity of RIG-I/IFN signaling
1100-1115	**Tim Moser, University of Otago, New Zealand** Ribosomal DNA heterogeneity is essential for female differentiation in zebrafish
1115-1130	**Felipe De Felippes, Queensland University of Technology, Australia** Read-through and silencing suppressor (RTSS) domain: a new element in plant terminators and its role in the regulation of gene expression
1130-1145	**Alexandre Cristino, Griffith Institute for Drug Discovery, Australia** The functional role of an introgressed neanderthal single nucleotide polymorphism within the schizophrenia-associated locus *microRNA-137*
1145-1200	**Paul Waters, University of New South Wales, Australia** Functional coherence of long non-coding RNAs that mediate X chromosome inactivation

Room 220	C6: Plant Breeding & Food Security (Agricultural & Plant Genetics) *Session supported by ARC Centre of Excellence for Plant Success in Nature & Agriculture*
Convenors	*Jessica Hyles, Australia & Inez H Slamet-Loedin, Philippines*
1000-1030	**Inez H. Slamet-Loedin, International Rice Research Institute, Philippines** Precision genetic technologies in rice for lasting positive impact in sustainable agriculture
1030-1100	**Jose Barrero Sanchez, CSIRO, Australia** GM crops for food security: the case of an insect-resistant cowpea in Nigeria
1100-1115	**Scott Boden, University of Adelaide, Australia** Harnessing the genetic variation of wild accessions to improve the performance of cultivated barley
1115-1130	**Josquin Tibbits, Department of Environment and Primary Industries, Australia** Taming genotype-by-environment interaction (GxE) for genomic prediction using cluster analysis – a case study in commercial barley breeding program
1130-1145	**Madeleine Post, AbacusBio Limited, New Zealand** Utilizing selection indexes to maximize benefits in plant breeding.
1145-1200	**Bettina Lado, Universdad de la República, Uruguay** Impact of breeding on wheat and barley genetic diversity

1230-1330 Exhibition	Poster Session (even number posters presented)

1400-1600	SYMPOSIA SESSIONS D
Room 203	D1: Evolution & Development (Evolutionary Genetics)
Convenors	*Peter Dearden, New Zealand & Christiane Nüsslein-Volhard, Germany*
1400-1430	**Christiane Nüsslein-Volhard, Max Planck Institute for Biology, Germany** Animal beauty: function and evolution of biological aesthetics
1430-1500	**Peter Currie, Australian Regenerative Medicine Institute, Australia** Evolution of muscle stem cell systems across the vertebrate phylogeny
1500-1515	**Camilla Whittington, University of Sydney, Australia** Evolution of the vertebrate placenta
1515-1530	**Donna Bond, University of Otago, New Zealand** Novel marsupial imprinting, germline epigenetic erasure and metabolic reprogramming in brushtail possum
1530-1545	**Oliver Griffith, Macquarie of University, Australia** Taming inflammation is key to the extension of pregnancy in mammals
1545-1600	**Eduardo Flores-Sandoval, Monash University, Australia** Auxin response minima mediated by a single B-Class AUXIN RESPONSE FACTOR is essential to maintain totipotency in liverworts
Room 204	D2: Ecological Epigenetics (Genetics & the Environment) *Session supported by Bioplatforms Australia*
Convenors	*Alyson Ashe, Australia & Kees van Oers, The Netherlands*
1400-1430	**Kees van Oers, Netherlands Institute of Ecology (NIDO-KNAW), The Netherlands** The origin and temporal stability of DNA methylation in wild vertebrates
1430-1500	**Andrea Liebl, University of South Dakota, USA** The effect of group size on epigenetic marks in the cooperatively breeding chestnut-crowned babbler
1500-1515	**Livia Gerber, CSIRO, Australia** How social variables affect the rate of ageing in a natural population of bottlenose dolphins
1515-1530	**Clare Holleley, CSIRO, Australia** An atlas of vertebrate chromatin accessibility - mapped through space and time
1530-1545	**Anna Miltiadous, Deakin University, Australia** From DNA to zebra finch: avian maternal corticosterone affects offspring global DNA methylation
1545-1600	**Coralina Collar Fernandez, Florey Institute of Neurosciences and Mental Health, Australia** Whole genome nanopore DNA analysis shows that chronic corticosterone supplementation in mice results in altered sperm DNA methylation and hydroxymethylation in exposed animals and their offspring

Room 210/211	D3: Bioinformatics & Computational Biology (Genomics & Genomic Technologies)
Convenors	*Quin Wills, UK & Denis Bauer, Australia*
1400-1430	**Quin Wills, Ochre Bio, UK** Humans as the model: "Organ ICUs" and the deep genomic phenotyping of living human organs
1430-1500	**Kim-Anh Le Cao, University of Melbourne, Australia** Multivariate integration of multi-omics data
1500-1515	**Mark Cowley, Children's Cancer Institute, Australia** The zero childhood cancer cloud: a digital ecosystem for national-scale precision medicine
1515-1530	**Nikeisha Caruana, University of Melbourne, Australia** RDMassSpec Explorer: An online platform for the interrogation of rare disease functional data
1530-1545	**Michael Hall, Peter Doherty Institute for Infection and Immunity, Australia** Drug resistance prediction with reference graphs
1545-1600	**Lightning Presentations** **Nozhat Hassan, University of Adelaide, Australia** The R2 retrotransposon discovery and activity prediction workflow **Adrian Salavaty, Children's Cancer Institute, Australia** Incrimp: A versatile computational model for the integrative analysis of multi-omics data **Gulrez Chahal, Murdoch Children's Research Institute, Australia** Caravan: prioritising pathogenic cardiac variants in the non-coding genome using boosting algorithm **Zhen Qiao, Garvan Institute of Medical Institute, Australia** Population-scale single-cell transcriptomics of clonal haematopoiesis **Rotem Aharon, Peter MacCallum Cancer Centre, Australia** cDNA and direct RNA long-read sequencing result in reads that are significantly different

Room 212/213	D4: Genomic Therapies & Precision Medicine (Genetics & Human Health)
Convenors	*Sue Fletcher, Australia & Lori Isom, USA*
1400-1430	**Noam Shomron, Tel Aviv University, Israel** AI aiding medical decisions
1430-1500	**Lori Isom, University of Michigan, USA** Dancing to a different tune: tango provides hope for Dravet syndrome
1500-1515	**Jayshen Arudkumar, University of Adelaide, Australia** Genome editing: bridging the gap for a stronger future in Duchenne muscular dystrophy (DMD)
1515-1530	**Anne Klein, CSIRO, Australia** *In silico* design of new capsids for AAV therapeutical applications
1530-1545	**Raman Sharma, University of Adelaide, Australia** Humanized preclinical mouse model of *TIMMDC1* deep intronic poison exon activating splice-variant causing a fatal childhood neurodegenerative dignatiisorder
1545-1600	**Amanda Spurdle, QIMR Berghofer Medical Research Institute, Australia** The ClinGen enigma *BRCA1/2* expert panel: a dynamic framework for evidence-based recommendations to improve classification criteria for variants in *BRCA1* and *BRCA2*

Room 219	D5: Neurogenetics of Behaviour (Molecular, Cellular & Developmental Genetics)
Convenors	*Barry Dickson, Australia & Elissa Hallem, USA*
1400-1430	**Elissa Hallem, University of California Los Angeles, USA** Neural mechanisms of skin penetration in a human-infective worm
1430-1500	**Claude Desplan, New York University, USA** The generation of neuronal diversity and its evolution
1500-1515	**Kenneth Blum, Ariel University, USA** Neurogenetic evidence in support of early identification of pre addiction using the genetic addiction risk severity (GARS) assessment
1515-1530	**Yong Q Zhang, Chinese Academy of Sciences, China** *CHD8* mutations increase gliogenesis to enlarge brain size in non-human primate
1530-1545	**Josie Gleeson, University of Melbourne, Australia** Nanopore direct RNA sequencing reveals insight into the transcriptome and epitranscriptome of human brain
1545-1600	**Tien Nguyen, Macquarie University, Australia** An investigation of visual lateralization in birds

Room 220	D6: Plant interactions with Other Organisms (Agricultural & Plant Genetics)
Convenors	*Michael Udvardi, Australia & Pamela Ronald, USA*
1400-1430	**Pamela Ronald, University of California Davis, USA** Genome editing of a rice CDP-DAG synthase confers broad-spectrum resistance
1430-1500	**Dugald Reid, La Trobe University, Australia** Zinc as second messenger in posttranslational control of environmental responses in plants
1500-1515	**Fatima Naim, Curtin University, Australia** Spatiotemporal analysis of tan spot in wheat using transcriptome and high-resolution elemental imaging
1515-1530	**Gerhad Braus, University of Goettingen, Germany** *Verticillium dahliae* VTA3 promotes *ELV1* virulence factor gene expression in xylem sap, but tames Mtf1-mediated late stages of fungus-plant interactions and microsclerotia formation
1530-1545	**Ashley Jones, Australian National University, Australia** Exploring post-transcriptional modifications during myrtle rust pathogen-plant interactions
1545-1600	**Mathew Lewsey, La Trobe University, Australia** Transcription factor dynamics in cross-regulation of plant hormone signaling pathways

1630-1730	Plenary Session 4
Plenary Room 2	**Neil Gemmell, University of Otago, New Zealand** Fishing for insights in sex determination, differentiation and reproductive biology ***Chair: Peter Dearden, New Zealand*** *Session supported by Bioplatforms Australia*

1930	Public Program
	Oratorio - Origins of the Universe, of Life, of Species, of Humanity Melbourne Recital Centre

WEDNESDAY 19 JULY 2023

0700-1730	**Registration Open** **Melbourne Convention & Exhibition Centre Foyer**

0830-0930	**Plenary Session 5**
Plenary Room 2	**Gruber Genetics 2023 Prize Recipients** **Allan Jacobson, University of Massachusetts, USA** NMD, translation termination, and readthrough therapy: consequences and suppression of genetic nonsense **Lynne Maquat, University of Rochester, USA** Nonsense-mediated mRNA decay in human health and disease ***Chair: Allan Spradling, USA***

1000-1200	**SYMPOSIA SESSIONS E**
Room 203	**E1: Genetic Strategies to Control Pests & Disease Vectors (Evolutionary Genetics)** ***Session supported by University of Melbourne***
Convenors	*Charles Robin, Australia & Jackson Champer, China*
1000-1030	**Kimberley Cooper, University of California San Diego, USA** Meiotic Cas9 expression mediates gene conversion in the male and female mouse germline
1030-1100	**Austin Burt, Imperial College London, UK** Prospects for genetic biocontrol
1100-1115	**Xuejiao Xu, Peking University, China** Design and construction of an improved homing suppression drive type with a higher genetic load
1115-1130	**Fatemeh Kargarfard, CSIRO, Australia** Identification of natural gene drives in rabbit populations
1130-1145	**Max Scott, North Carolina State University, USA** Male-only and split homing gene drive strains for genetic biocontrol of the global fruit crop pest *Drosophila suzuki*
1145-1200	**Luke Gierus, University of Adelaide, Australia** Leveraging a natural murine meiotic drive to suppress invasive populations
Room 204	**E2: Climate Change Genetics (Genetics & the Environment)**
Convenors	*Belinda van Heerwaarden, Australia & Vanessa Kellerman, Australia*
1000-1030	**Jon Bridle, University College London, UK** Understanding the potential for adaptation to novel climates: hidden genetic variation in plasticity increases fitness in novel ways at the ecological margin in senecio daisies
1030-1100	**Kay Hodgins, Monash University, Australia** Structural variants underlie rapid climate adaptation in a globally invasive species
1100-1115	**Rebecca Jordan, CSIRO, Australia** Can trees keep pace with climate change? Investigating rates of genomic change and adaptability in *Eucalyptus pauciflora*
1115-1130	**Paul Rymer, Western Sydney University, Australia** Quantifying adaptive capacity and vulnerability to novel environments
1130-1145	**Shannon Duffy, University of Western Australia, Australia** Genomic regions associated with coral larvae survival following acute heat stress
1145-1200	**Luciano Beheregaray, Flinders University, Australia** The adaptive capacity to climate change of Australian rainbowfishes

Room 210/211	**E3: Tandem-Repeat Genomics Informing Polygenic Human Disorders & Traits (Genomics & Genomic Technologies)**
Convenors	*Melanie Bahlo, Australia & Anthony Hannan, Australia*
1000-1030	**Melissa Gymrek, University of California San Diego, USA** Polymorphic short tandem repeats make widespread contributions to blood and serum traits
1030-1100	**Egor Dolzhenko, Pacific Biosciences, USA** Resolving the unsolved: Comprehensive assessment of tandem repeats at scale
1100-1115	**Harriett Dashnow, University of Utah, USA** Don't forget the repeats! The power of short tandem repeat calling algorithms to diagnose Mendelian disease
1115-1130	**Paul Lockhart, Murdoch Children's Research Institute, Australia** New tools for diagnosis and discovery of pathogenic repeat expansions
1130-1145	**Mark Bennet, Walter and Eliza Hall Institute of Medical Research, Australia** A novel complex repeat expansion associated with progressive myoclonic epilepsy
1145-1200	**Sridevi Sureshkumar, Monash University, Australia** Plants to humans: mechanisms of trinucleotide repeat expansions
Room 212/213	**E4: Counselling, Communication & Consent in Human Genetics Contexts Across the Lifetime (Genetics & Human Health)**
Convenors	*Lyndon Gallacher, Australia & Gemma Chandratillake, UK*
1000-1030	**Kirsten Boggs, Australian Genomics, Australia** Beyond traditional genetic counselling: from preconception to childhood
1030-1100	**Gemma Chandratillake, NHS East Genomics, UK** From cradle to grave; systemic adoption of genomics in a national health service
1100-1115	**Samantha Croy, Centre for Population Genomics, Australia** Developing genomics research participant information materials for Australian ancestry groups underrepresented in genomic research and datasets
1115-1130	**Lucas Mitchell, Garvan Medical Research Institute, Australia** My research results: returning clinically actionable genomic findings to research participants
1130-1145	**Kathy Wu, St Vincent's Clinical Genomics, Australia** The psychosocial impact and health outcomes of genetics consultations and testing in Australia: a multicentre patient survey
1145-1200	**Aideen McInerny-Leo, University of Queensland, Australia** Evaluating a protocol for communicating melanoma personalised risk scores: A pilot study
Room 219	**E5: Cell & Organoid Models for Human Disease Mechanisms (Molecular, Cellular & Developmental Genetics)** ***Session supported by Australian Functional Genomics Network***
Convenors	*Andrew Sinclair, Australia & Hongyan Wang, Singapore*
1000-1030	**Hongyan Wang, Duke-NUS Medical School, Singapore** Golgi-dependent reactivation and regeneration of quiescent neural stem cells
1030-1100	**Alan Rubin, Walter and Eliza Hall Institute of Medical Research, Australia** Enabling clinical translation of high-throughput mutagenesis data
1100-1115	**James McNamara, Murdoch Children's Research Institute, Australia** Human pluripotent stem cell models reveal the mechanism of *alpk3*-induced cardiomyopathy
1115-1130	**Helen Abud, Monash Biomedicine Discovery Institute, Australia** Role of *NRG1* in mediating plasticity of stem cells during intestinal regeneration
1130-1145	**Stefka Tasheva, University of Adelaide, Australia** Impaired synaptic connectivity and disrupted cell adhesion interactions in in vitro models of PCDH19-*C*lustering Epilepsy
1145-1200	**Vanessa Fear, Telethon Kids Institute, Australia** High efficiency CRISPR homology directed repair, cardiac disease modelling and functional genomics: a pipeline for congenital heart disease genetic variant analysis

Room 220	**E6: Agricultural & Horticultural Genetics (Agricultural & Plant Genetics)**
Convenors	*Ian Godwin, Australia & Alison Van Eenennaam, USA*
1000-1030	**Alison Van Eenennaam, University of California, USA** Genetic improvement of the sheep's back
1030-1100	**Jacqueline Batley, University of Western Australia, Australia** Using pan genomics to identify disease resistance genes in brassica species
1100-1115	**Zhixi Tian, Institute of Genetics and Developmental Biology / Chinese Academy of Sciences, China** Soybean Pan-genome and Pan-3D-genome
1115-1130	**Weibo Xie, Huazhong Agricultural University, China** The post-GWAS era of crops: from genetic variants to function
1130-1145	**Rebecca Clarke, AgResearch, New Zealand** Determining structural variation in the sheep genome utilising HD-SNP chip data
1145-1200	**Vasileios Papasotiropoulos, University of Patras, Greece** Whole genome resequencing of selected strawberry genotypes and expression of key genes influencing aroma and flavor

Room 210	**Genetic Society of Australasia (GSA) Program**
1200-1315	**Annual General Meeting** (light lunch served at 1200)
1315-1345	**Catcheside Prize Presentation** (virtual presentation) **Sarah Whitely, University of Canberra, Australia** Gene-environment interactions in thermally sensitive sex determination systems
1345-1415	**Alan Wilton Award Presentation** **Charles Foster, University of New South Wales, Australia** Does convergent gene recruitment underpin convergent evolution of pregnancy and the placenta?
1415-1445	**GSA Education Presentation** **Masha Smallhorn, Flinders University, Australia** Flipped approach transforms the genetics classroom leading to improved engagement and learning outcomes
1445-1515	**Ross Crozier Award Presentation** **Bastien Llamas, University of Adelaide, Australia** Conducting respectful and sustainable paleogenomic research: examples from Australia and Indonesia
1515-1530	**Announcement of other GSA Awardees and Closing**
1800	**GSA Social Event – Melbourne Public, Southwharf** *(separate tickets must be purchased in advance with GSA)*

Room 212	**Human Genetics Society of Australasia (HGSA) Program**
1300-1345	**HGSA Sutherland Lecture** (light lunch served at 1245) **Zornitza Stark, Murdoch Children's Research Institute, Australia** Accelerating rare disease diagnosis
1345-1445	**HGSA Annual General Meeting**
1445-1450	**InGeNA** **Kathy Campbell**
1445-1500	**HGSA ASM 2024 & Information Session**
1500-1530	Afternoon Tea
1530-1615	**HGSA Oration Lecture** **James Pitt, University of Melbourne, Australia** Puzzles in biochemical genetics

Room 203	**Meet the Editor**
1630-1730	**Valda Vinson, Executive Editor, SCIENCE**

	Public Program
1730- 1830 **Room 210**	**Genetics vs Sport - Are super athletes born or made?** Melbourne Conversations held at Melbourne Convention & Exhibition Centre
1830-1930	**Future Forums: The genetic rescue of our fantastic beasts** Melbourne Museum

THURSDAY 20 JULY 2023

0700-1730	**Registration Open** **Melbourne Convention & Exhibition Centre Foyer**

0830-0930	**Plenary Session 6**
Plenary Room 2	**Detlef Weigel, Max Planck Institute, Germany** Paranoid plants: Genetic conflict in the immune system ***Chair: Suresh Balasubramanian, Australia***

1000-1200	**SYMPOSIA SESSIONS F**
Room 203	**F1: Evolutionary Genetics Theory (Evolutionary Genetics)**
Convenors	*Hamish Spencer, New Zealand & Anna Santure, New Zealand*
1000-1030	**Ailene MacPherson, Simon Fraser University, Canada** Eco-evolutionary implications of allele surfing
1030-1100	**Tim Connallon, Monash University, Australia** Effects of population size change on the genetics of adaptation
1100-1115	**Nicholas O'Brien, University of Queensland, Australia** The evolutionary systems genetics of adaptation
1115-1130	**Luis Mijangos, University of Canberra, Australia** Unexpected genetic resilience of small populations is produced by selection against deleterious alleles of linked genes
1130-1145	**Mark Tanaka, University of New South Wales, Australia** How can large asexual populations go extinct?
1145-1200	**Ekta Ekta, Monash University, Australia** The relative contribution of mito-nuclear interactions to male reproductive success at different temperatures
Room 204	**F2: Environmental Genomics (Genetics & the Environment)**
Convenors	*Elise Furlan, Australia & Toshifumi Minamoto, Japan*
1000-1030	**Toshifumi Minamoto, Kobe University, Japan** Environmental DNA analysis of macroorganisms: recent trends and future prospects in Japan and worldwide
1030-1100	**Matthew Barnes, Texas Tech University, USA** Understanding communities out of thin air: progress using airborne environmental DNA to study terrestrial plants and animals
1100-1115	**Gert-Jan Jeunen, University of Otago, New Zealand** Molecular time-capsules – reconstructing Antarctica's marine ecosystem using historical and contemporary eDNA from marine sponge specimens.
1115-1130	**Bruce Deagle, CSIRO, Australia** Using DNA metabarcoding to better understand marine trophic interactions: case studies and future directions
1130-1145	**Linda Neaves, Australian National University, Australia** Using genomic tools to understand trophic interactions and enhance conservation and restoration in sanctuaries
1145-1200	**Tahlia Perry, University of Adelaide, Australia** Combining genomics with citizen science produces continent-scale information on an iconic egg-laying mammal: lessons from EchidnaCSI
Room 210/211	**F3: T Cell-free DNA Technologies: Challenges & Opportunities (Genomics & Genomic Technologies)**
Convenors	*Ignatia Van den Veyver, USA & Cristin Print, New Zealand*
1000-1030	**Ignatia Van den Veyver, Baylor College of Medicine, USA** New developments in prenatal cfDNA screening for chromosomal and single-gene disorders, and in cell-based non-invasive prenatal testing
1030-1100	**Sarah-Jane Dawson, Peter MacCallum Cancer Centre, Australia** Circulating tumour DNA: Concepts, challenges and future opportunities
1100-1115	**Bernard Pope, University of Melbourne, Australia** Ultra-sensitive detection of circulating tumour DNA enriches for patients with higher risk disease in clinically localised prostate cancer
1115-1130	**Zimeng Ye, University of Melbourne, Australia** CSF cell-free DNA liquid biopsy for detecting somatic mosaicism in brain
1130-1145	**Russell Diefenbach, Macquarie University, Australia** Sensitive detection of methylated circulating tumor DNA in melanoma patients using a custom next generation sequencing panel
1145-1200	**Katrina Scarff, Victorian Clinical Genetics Services, Australia** Cytogenetic and pregnancy outcomes for women with an increased risk trisomy 14 or trisomy 15 cfDNA screening result

Room 212/213	**F4: Identifying Functional Target Genes at GWAS Loci (Genetics & Human Health)**
Convenors	*Jonathon Beesley, Australia & Maya Ghoussaini, UK*
1000-1030	**Anna Gloyn, Stanford University, USA** Unravelling mechanisms for islet-cell dysfunction in diabetes using multi-omic data
1030-1100	**Maya Ghoussaini, Regeneron Pharmaceuticals, UK** Open targets genetics: an atlas of GWAS-associated loci to systematically guide causal gene assignment and target prioritization
1100-1115	**Jonathan Beesley, QIMR Berghofer Medical Research Institute, Australia** Multiple phenotypic screens identify novel breast cancer susceptibility genes
1115-1130	**Hamish King, Walter and Eliza Hall Institute of Medical Research, Australia** Integrated single-cell genomics to predict cellular etiology of autoimmune risk loci
1130-1145	**Jubao Duan, University of Chicago, USA** Chromatin accessibility mapping in hiPSC informs functional GWAS risk variants and target genes for neuropsychiatric disorders and Alzheimer's disease
1145-1200	**Yan Guo, Xi'an Jiaotong University, China** The enhancer variants at 2P14 can regulate *Spred2* and *Acrtr2* to protect against rheumatoid arthritis
Room 219	**F5: New Experimental Model Organisms for Genetics Research (Molecular, Cellular & Developmental Genetics)**
Convenors	*Maja Adamska, Australia & Ralf Sommer, Germany*
1000-1030	**Ralf Sommer, Max Planck Institute for Biology, Germany** Novel mechanisms of transgenerational inheritance: lessons from unbiased forward genetics in a novel nematode model system
1030-1100	**Avnika Ruparelia, University of Melbourne, Australia** Does skeletal muscle stop ageing physiologically?
1100-1115	**Trent Newman, University of Melbourne, Australia** *PRKACB*: a new imprinted gene in a marsupial
1115-1130	**Stephen Frankenberg, University of Melbourne, Australia** Pluripotency in marsupial stem cells and embryos
1130-1145	**Gary Hime, University of Melbourne, Australia** The adult *Drosophila* salivary gland exhibits an unusual mode of cell division
1145-1200	**Amanda Austin, University of Otago, New Zealand** Mechanisms of segmentation in the honeybee
Room 220	**F6: Plant Cell & Developmental Biology (Agricultural & Plant Genetics)**
Convenors	*Marcus Heisler, Australia & Cristina Ferrandiz, Spain*
1000-1030	**Cristina Ferrandiz, Instituto de Biología Molecular y Celular de Plantas / CSIC-UPV, Spain** Time to stop: the end of reproduction in annual plants
1030-1100	**Utpal Nath, Indian Institute of Science Bengaluru, India** Active suppression of leaflet emergence as a mechanism of simple leaf development
1100-1115	**Tom Fisher, Monash University, Australia** PIN-FORMED supports meristem formation in *Marchantia polymorpha*
1115-1130	**Joanna Putterill, University of Auckland, New Zealand** Three duplicated *Medicago soc1* genes and their key roles in growth and flowering
1130-1145	**John Golz, University of Melbourne, Australia** Groucho/TUP1-like co-repressors Leunig and Leunig homolog redundantly control apical cell identity in *Arabidopsis* embryos through physical interactions with WOX transcription factors
1145-1200	**Marta Peirats-Llobet, La Trobe University, Australia** Barley spatial transcriptomics, unravelling germination one spot at a time

1230-1330 Exhibition	**Poster Session (odd number posters presented)**

1400-1600	SYMPOSIA SESSIONS G
Room 203	**G1: Genetics & Epigenetics of Sex (Evolutionary Genetics)**
Convenors	*Arthur Georges, Australia & Qi Zhou, China*
1400-1430	**Qi Zhou, Zhejiang University, China** The rise of genomic diversity of animal sex chromosomes
1430-1500	**Asato Kuroiwa, Hokkaido University, Japan** Turnover of mammal sex chromosomes in the SRY-deficient species, amami spiny rat
1500-1515	**Changwei Shao, Yellow Sea Fisheries Research Institute / Chinese Academy of Fishery Sciences, China** Epigenetic regulation of sex determination and differentiation in fish: the interaction between genes and the environment
1515-1530	**Francesc Piferrer, Institut de Ciencies del Mar (ICM-CSIC), Spain** Types, causes and consequences of sex reversal in natural populations
1530-1545	**Craig Smith, Monash University, Australia** The power of two: how does *dmrt1* gene dosage regulate avian gonadal sex determination?
1545-1600	**Florian Devloo-Delva, CSIRO, Australia** Are sharks caught in an X/Y sex chromosome trap? Evolutionary stability of the sex-chromosome systems of 21 shark and ray species through sex-linked markers
Room 204	**G2: Invasion Genetics (Genetics & the Environment)**
Convenors	*Katarina Stuart, Australia & Katrina Dlugosch, USA*
1400-1430	**Katrina Dlugosch, University of Arizona, USA** Ecological and evolutionary contributions to species invasions
1430-1500	**Cristina Vieira, Claude Bernard Lyon 1 University, France** Transposable elements and the success of invasive species
1500-1515	**Leslie Hutchins, University of California Berkeley, USA** Arthropods are kin: operationalizing indigenous data sovereignty to respectfully utilize genomic data from indigenous lands
1515-1530	**Kristen Fernandes, University of Otago, New Zealand** Expanding the applicability of eDNA metabarcoding through data reuse: insights for landscape-scale ecology and invasive species monitoring
1530-1545	**Manpreet Dhami, Manaaki Whenua – Landcare Research, New Zealand** Predicting biological invasions in the age of genomics
1545-1600	**Harrison Eyck, University of New South Wales, Australia** Opening a can of worms: The secrets of a cryptic invader
Room 210/211	**G3: Accelerating Genomics (Genomics & Genomic Technologies)**
Convenors	*Marco Herold, Australia & Elizabeth Worthey, USA*
1400-1430	**Elizabeth Worthey, University of Alabama, USA** Application of 'omics in rare diseases: from MDx to precision medicine
1430-1500	**Irina Voineagu, University of New South Wales, Australia** Functional characterisation of active enhancers in human astrocytes using CRISPRi screening
1500-1515	**Susan Tousi, Illumina Inc., USA** Enabling the genome era
1515-1530	**Callum MacPhillamy, University of Adelaide, Australia** Cross-species prediction of enhancers with machine learning
1530-1545	**Hasindu Gamaarachchi, Garvan Institute of Medical Research, Australia** An ecosystem for scalable and computationally efficient nanopore data processing
1545-1600	**Lara Parata, University of Western Australia, Australia** How low can you go? Using low-coverage draft genomes to inform high-quality reference genome projects

Room 212/213	G4: Genetics of Complex Disease & Quantitative Traits (Genetics & Human Health)
Convenors	*Sarah Medland, Australia & David Evans, Australia*
1400-1430	**Benjamin Neale, Massachusetts General Hospital, USA** Human genetics at scale
1430-1500	**David Evans, University of Queensland, Australia** Using Mendelian randomization to investigate potential causal relationships in large-scale observational epidemiological studies
1500-1515	**Victoria Jackson, Walter and Eliza Hall Institute of Medical Research, Australia** AI-Phenotyping allows spatial examination of the genetic drivers of retinal thickness
1515-1530	**Clara Albiñana, Aarhus University, Denmark** Multi-PGS enhances polygenic prediction - weighting 937 polygenic scores
1530-1545	**Daniel Chin, University of Leicester, UK** Improved genomic coverage and sample size for fine-mapping and gene discovery for idiopathic pulmonary fibrosis
1545-1600	**Jian Zeng, University of Queensland, Australia** Leveraging functional genomic annotations and genome coverage to improve polygenic prediction of complex traits within and between ancestries

Room 219	G5: Advanced Imaging in Cellular & Developmental Genetics (Molecular, Cellular & Developmental Genetics)
Convenors	*Jennifer Stow, Australia & Denise Montell, USA*
1400-1430	**Donna Whelan, La Trobe University, Australia** Super-resolution mapping of resection and recombination complexes at broken replication forks
1430-1500	**Denise Montell, University of California, USA** Live imaging of controlled cellular cannibalism to enhance CAR-M cancer therapy
1500-1515	**Jieqiong Lou, University of Melbourne, Australia** Histone FRET microscopy reveals that genome architecture is differentially regulated by a HP1α monomer to dimer transition
1515-1530	**Jennifer Zenker, Monash University, Australia** Microtubules direct early embryonic cell fate decisions by differential RNA localisation and translation
1530-1545	**Gavin Chapman, Victor Chang Cardiac Research Institute, Australia** Automated embryo phenotyping reveals congenital anomalies in a mouse model of WBP11 haploinsufficiency
1545-1600	**Jesse Kennedy, University of Adelaide, Australia** Progress towards highly efficient, programmable, and specific whole gene insertion via dual-peg prime editing + BxbI integrase for genome editing applications

Room 220	G6: Genetics & Genomics of Plant Evolution (Agricultural & Plant Genetics)
Convenors	*John Bowman, Australia & Junko Kyozuka, Japan*
1400-1430	**Junko Kyozuka, Tohuku University, Japan** Step-by-step evolution of strigolactone function as a phytohormone
1430-1500	**Kevin Davies, Plant and Food Research, New Zealand** The evolution of flavonoid biosynthesis
1500-1515	**Facundo Romani, University of Cambridge, UK** Systematic analysis of transcription factor promoter activity in the liverwort *Marchantia polymorpha*
1515-1530	**Zoe Broad, University of Queensland, Australia** Gene network divergence drives adaptive trait evolution in an Australian wildflower
1530-1545	**Jonathan Levins, Monash University, Australia** bHLH subclass II, a key regulator in the ancestral function of spore wall deposition in land plants
1545-1600	**Kasey Pham, University of Florida, USA** Functional or fluke? Genome-wide identification of introgressed genes in naturally occurring eucalyptus hybrids

1630- 1730	Plenary Session 7
Plenary Room 2	**Nancy Cox, Vanderbilt Brain Institute, USA** How heritability of everyday laboratory values leads to big health disparities ***Chair: Kathryn Burdon, Australia*** *Session supported by Amazon Web Services*

1730-1830	Public Program
Room 210	**Population DNA Screening for Disease Risk** Melbourne Convention & Exhibition Centre

1900-2100	Congress Social Event
	LUME: "Connection" Venue: Melbourne Convention & Exhibition Centre

FRIDAY 21 JULY 2023

0700-1730	**Registration Open** **Melbourne Convention & Exhibition Centre Foyer**

0830-0930	**Plenary Session 8**
Plenary Room 2	**Anne Ferguson-Smith, University of Cambridge, UK** The genetics of epigenetic variation ***Chair: Marieke Oudelaar, Germany*** *Session supported by the British High Commission*

1000-1200	**SYMPOSIA SESSIONS H**
Room 203	**H1: Systematics & Phylogeography (Evolutionary Genetics)**
Convenors	*Craig Moritz, Australia & Sonal Singhal, USA*
1000-1030	**Sonal Singhal, California State University, USA** The demography of speciation: a case study from Sphenomorphine skinks
1030-1100	**Daniel Cadena, Universidad de los Andes, Columbia** Mountains, genetics and the origin of a tropical biodiversity hotspot
1100-1115	**Alexander Myburg, University of Pretoria, South Africa** Species, pan-genome and population level analysis of the iconic eucalypts of Australia
1115-1130	**Sally Potter, Macquarie University, Australia** The role of extensive chromosomal rearrangements in speciation of rock-wallabies
1130-1145	**Bai-Wei Lo, Max Planck Institute Molecular Genetics, Germany** Genomic analyses revealed complex gene flow history among bowhead and right whales
1145-1200	**Rose Andrew, University of New England, Australia** Composition and timing of introgression in woodland eucalypts
Room 204	**H2: The Genetics of Local Adaptation (Genetics & the Environment)**
Convenors	*Collin Ahrens, Australia & Rose Andrew, Australia*
1000-1030	**Tanja Pyhäjärvi, University of Helsinki, Finland** Mystery of local adaptation in Scots pine: now you see it, now you don't
1030-1100	**Marco Todesco, University of British Colombia, Canada** Now you see me, now you don't: adaptive colour variation in wild sunflowers
1100-1115	**Melissa Ilardo, University of Utah, USA** Adaptations to diving in the Haenyeo divers of Jeju, Korea
1115-1130	**Katie Gates, Flinders University, Australia** Environmental selection, rather than neutral processes, best explain regional patterns of diversity in a tropical rainforest fish
1130-1145	**Katarina Stuart, University of Auckland, New Zealand** A whole genome perspective on genetic variation and rapid adaptation
1145-1200	**Candice Bywater, University of Queensland, Australia** The genetic basis of adaptation in *Senecio lautus*
Room 210/211	**H3: Genomics-driven Healthcare (Genomics & Genomic Technologies)** ***Session is supported by Bioplatforms Australia***
Convenors	*Richard Gibbs, USA & Sean Grimmond, Australia*
1000-1030	**Richard Gibbs, Baylor College of Medicine, USA** Clan genomics in the clinic
1030-1100	**David Thomas, Garvan Institute of Medical Research, Australia** Precision oncology: a paradigm shift in cancer management
1100-1115	**Katherine Howell, Murdoch Children's Research Institute, Australia** Shifting the paradigm of genetic diagnosis: an international multi-centre pilot study of rapid genome sequencing in infantile epilepsy
1115-1130	**Hamish Scott, Centre for Cancer Biology, Australia** Maximizing diagnostic yield of genomic autopsies in pregnancy loss and perinatal death
1130-1145	**Simon Bodek, Austin Health Clinical Genetics Service, Australia** Experience of the first adult-focused undiagnosed disease program in Australia (AHA-UDP)
1145-1200	**John Christodoulou, Murdoch Children's Research Institute, Australia** The Australian genomic health alliance mitochondrial flagship: a national program delivering mitochondrial diagnoses

Room 212/213	H4: Early Career Researcher Showcase *Supported by University of Melbourne*
Convenors	*Leonie Quinn, Australia & Damian Dowling, Australia*
1000-1015	**Mariano Hernandez, University of Tasmania, Australia** Insights into the evolution of genes responsible for the synthesis of cuticular wax compounds in eucalypts
1015-1030	**Fei Yang, University of Queensland, Australia** Dynamic transcriptomic changes in endometrial tissue and its association with endometriosis and related infertility
1030-1045	**Benjamín Duran-Vinet, University of Otago, New Zealand** CRISPR-based detection for marine biomonitoring: deep learning modelling as a novel tool for smart CRISPR RNA designs
1045-1100	**Carol Li, Peking University, China** Harnessing Wolbachia cytoplasmic incompatibility alleles for confined gene drive
1100-1115	**Andreas Bachler, Australian National University, Australia** Unraveling a dynamic genome: the first pan-genome assessment of the global mega-pest, cotton bollworm (*Helicoverpa armigera*)
1115-1130	**Georgia Cullen, University of Otago, New Zealand** Predetermining the germline: how larval development supports the reproductive needs of the adult honeybee queen
1130-1145	**Avneet Kaur, University of Queensland, Australia** The genetic architecture of adaptive evolution in contrasting environments
1145-1200	**Zelia Soo, 23strands, Australia** Identification of endometriosis gene lists: an example of revolutionising women's health using genomics
Room 219	H5: Epigenetic Mechanisms & Chromatin Biology (Molecular, Cellular & Developmental Genetics)
Convenors	*Marnie Blewitt, Australia & Anne Ferguson-Smith, UK*
1000-1030	**Ryan Lister, University of Western Australia, Australia** Learning to forget: erasing somatic epigenetic memory in human cell reprogramming
1030-1100	**Marieke Oudelaar, Max Planck Institute for Multidisciplinary Sciences, Germany** Regulation of gene expression in the three-dimensional genome
1100-1115	**Alyson Ashe, University of Sydney, Australia** Set-domain proteins in epigenetic inheritance: hidden depths
1115-1130	**Cassandra Glanfield, University of Otago, New Zealand** Understanding active DNA demethylation specificity and transcriptional consequences in stem cells
1130-1145	**Patrick Western, Hudson Institute of Medical Research, Australia** PRC2 establishes H3K27me3 at developmental genes in growing oocytes and regulates offspring development
1145-1200	**Tie-Lin Yang, Xi'an Jiaotong University, China** Dynamic rearrangement of chromatin loops and epigenomic features during adipocytes commitment
Room 220	H6: From Genebanks to Fields: Leveraging Genomics Innovations for Characterising Genetic Diversity (Agricultural & Plant Genetics)
Convenors	*Sally Norton, Australia & Vania Azevedo, Peru*
1000-1030	**Vania Azevedo, International Potato Centre, Peru** Genetic and genomic diversity for conservation and use of genetic resources at the international potato center genebank
1030-1100	**Carolina Sansaloni, International Maize and Wheat Improvement Center, Mexico** Genomic for genebanks: unlocking the genetic diversity of the CIMMYT wheat collection
1100-1115	**Gabriel Keeble-Gagnere, Agriculture Victoria, Australia** From gene banks to varieties: unlocking the potential of plant genetic resources for breeding
1115-1130	**Maurizio Rossetto, Royal Botanic Garden Sydney, Australia** Establishing genomic 'knowledge infrastructure' to support restoration and management strategies
1130-1145	**Kerrie Forrest, Agriculture Victoria, Australia** Maximizing the value of genetic and genomic datasets with Pretzel to accelerate crop research and breeding
1145-1200	**Lightning Presentations** **Vito Butardo, Swinburne University of Technology, Australia** Philippine rice diversity panel: a local genetic platform for novel gene discovery **Shimna Sudheesh, Agriculture Victoria, Australia** Integrating past, present and future genomic and genetic resources in field pea through pretzel **Richard Campbell, Diversity Arrays Technology, Australia** Universal Test Bench – an extensible testing platform for genomic prediction algorithms, with non-linear predictor feature selection

1230-1315 Exhibition	**Poster Session (even number posters presented)**

1330-1530	**SYMPOSIA SESSIONS I**
Room 203	**I1: Molecular Evolution (Evolutionary Genetics)**
Convenors	*Simon Ho, Australia & Sandra Alvarez-Carretero, UK*
1330-1400	**Sandra Álvarez-Carretero, University of Bristol, UK** Bayesian phylogenomic dating: reproducibility and accessibility challenges
1400-1430	**Dahiana Arcila, Scripps Institution of Oceanography, USA** Decoding the diversity of fishes
1430-1445	**Kavitha Uthanumallian, University of Melbourne, Australia** Genome-wide patterns of selection-drift variation strongly associate with organismal traits across the green plant lineage (Viridiplantae)
1445-1500	**Steven Cooper, University of Adelaide, Australia** Evolution of sensory systems in the dark biosphere: the dynamic evolution of chemosensory genes in subterranean water beetles
1500-1515	**Gabrielle Genty, Flinders University, Australia** Into the blue: evolutionary adaptations associated with the diversification of baleen whales
1515-1530	**Tatsuki Nagasawa, Tokyo Institute of Technology, Japan** Molecular evolution of the OMP genes after the whole genome duplication in teleost fish
Room 204	**I2: Genetics of Wildlife Disease & Responses to Infection (Genetics & the Environment)**
Convenors	*Beata Ujvari, Australia & Lee Rollins, Australia*
1330-1400	**Michelle Wille, University of Sydney, Australia** Evolutionary ecology and genetics of avian influenza virus in wild bird hosts
1400-1430	**Hannah Siddle, University of Queensland – QAAFI, Australia** The evolution of immune escape in an emerging transmissible cancer in the Tasmanian devil
1430-1445	**Paige Haffener, University of Utah, USA** Genetic variation, phylogenetics and host-specificity in malaria-like parasites (hepatocystis spp.) infecting wild non-human primates
1445-1500	**Adam Miller, Deakin University, Australia** Whole genome resequencing reveals signatures of rapid selection in a virus-affected commercial fishery
1500-1515	**Beata Ujvari, Deakin University, Australia** Telomeres, the loop tying cancer to organismal life -histories
1515-1530	**Lightning Presentations** **Maria Jenckel, CSIRO, Australia** Meta-transcriptomic identification of novel *Sylvilagus hepaciviruses* via pathogen profiling in North American Lagomorphs **Kimberley Batley, University of Sydney, Australia** Less is more: MHC gene copy number variation linked to anti-DFTD immune responses of Tasmanian devils **Heather McDonald-Haynes, University of Sydney, Australia** Establishing whole-genome CRISPR-Cas9 knockout screen feasibility in Tasmanian devil facial tumour cells **Grace Day, Deakin University, Australia** Deep dive into dolphin immune genes **Tian Du, University of Sydney, Australia** Uncovering convergent mechanisms for venom action through whole genome CRISPR screening
Room 210/211	**I3: Genetics & Genomics of Pandemic, Endemic & Emerging Infectious Organisms (Genomics & Genomic Technologies)**
Convenors	*Eddie Holmes, Australia & Rebeca Carballar-Lejarazu, USA*
1330-1400	**Yukinori Okada, University of Tokyo, Japan** Statistical genetics elucidates host genetics of COVID-19
1400-1430	**Rebeca Carballar-Lejarazú, University of California Irvine, USA** Mosquito population modification and the malaria eradication agenda
1430-1445	**Matthew Adeleke, University of Kwazulu-Natal, South Africa** Computational identification of transmission block vaccine candidate based on fused antigens of pre- and post-fertilization gametocytes against *Plasmodium falciparum*
1445-1500	**Carol Lee, CSIRO, Australia** Data-driven analysis of pathogen genomes
1500-1515	**Kirsty McCann, Deakin University, Australia** Malaria parasite transmission and drug resistance in Cambodia
1515-1530	**Matthew Waller, University of Sydney, Australia** Fibroblast-expressed lrrc15 is a receptor for SARS-COV-2 spike and controls antiviral and antifibrotic transcriptional programs

Room 212/213	**I4: Pharmacogenomics in Drug Discovery & Development (Genetics & Human Health)**
Convenors	*Sonia Shah, Australia & Chiara Fabbri, UK*
1330-1400	**Chiara Fabbri, University of Bologna, Italy** Pharmacogenomics in depression: moving from cytochrome genes to the whole genome in big data
1400-1430	**William Reay, University of Newcastle, Australia** Genetics to enhance target identification and enable precision medicine in common, chronic disorders
1430-1445	**Aya Taki, University of Melbourne, Australia** Genomic-guided discovery of an orphan target of an anthelmintic by thermal proteome profiling
1445-1500	**Constance Li, National Cancer Centre, Singapore** Pairing patient-derived cell lines with source tissue data to improve predictive biomarker development in head & neck cancer
1500-1515	**Toshinori Endo, Hokkaido University, Japan** A new approach to drug repurposing with two-stage prediction, machine learning, and unsupervised clustering of gene expression
1515-1530	**Paul Lacaze, Monash University, Australia** Aspirin for primary prevention of cardiovascular events in relation to lipoprotein(a) genotypes
Room 219	**I5: Genetics & Biology of Ageing (Molecular, Cellular & Developmental Genetics)**
Convenors	*Linda Partridge, UK & Andrew Pask, Australia*
1330-1400	**Linda Partridge, University College London, UK** Targeting the nutrient-sensing network for healthier ageing
1400-1430	**Mark Febbraio, Monash University, Australia** Role of organ-cross talk in aging: Importance of extracellular vesicles
1430-1500	**Matthew Piper, Monash University, Australia** The role of GCN2 in sustaining lifespan under amino acid deprivation
1500-1515	**Thiruma Arumugam, La Trobe University, Australia** The impact of intermittent fasting on the epigenetic signatures
1515-1530	**Vanessa Higham, Monash University, Australia** Mother's curse and mitonuclear genetic effects on lifespan are consistent across diets with variable amino acid constitution
Room 220	**I6: Plant Response to Environmental Change (Agricultural & Plant Genetics)**
Convenors	*Megan Shelden, Australia & Jian-Kang Zhu, China*
1330-1400	**Jian-Kang Zhu, Southern University of Science and Technology, China** (virtual presentation) Balancing plant growth and stress resistance through coordinated genetic engineering and chemical intervention
1400-1430	**Frances Sussmilch, University of Tasmania, Australia** An open or shut case? Investigating the evolution of molecular mechanisms underpinning stomatal movements in land plants
1430-1445	**Samarth Kulshrestha, The New Zealand Institute for Plant and Food Research, New Zealand** Do hornworts have a stress-induced flavonoid pathway?
1445-1500	**Amanda Johnson, Queensland University of Technology, Australia** Functional characterisation of flowering genes to improve breeding time in tree crops
1500-1515	**Samuel Andrew, CSIRO, Australia** Transcriptomic temperature stress responses can help describe the adaptive strategies of non-model species
1515-1530	**Ramanathan Sowdhamini, National Centre for Biological Sciences, India** Computational studies of plant stress management

1600- 1700	**Plenary Session 9**
Plenary Room 2	**Eddie Holmes, University of Sydney, Australia** **(GSA – MJD White Award Recipient)** Redefining the virosphere ***Chair: Peter Doherty, Australia*** *Session supported by CSL*
1700-1730	**Congress Close & Award Presentation**

INVITED SPEAKERS

An outstanding selection of invited speakers will lead the Symposia discussions. Each symposium offers two invited speakers and oral presentations from abstract authors.

FIRST NAME	LAST NAME	ORGANISATION	COUNTRY
Sally	Aitken	University of British Columbia	Canada
Sandra	Álvarez-Carretero	University of Bristol	UK
Minna-Liisa	Änkö	Tampere University	Finland
Dahiana	Arcila	Scripps Institution of Oceanography	USA
Vania	Azevedo	International Potato Centre	Peru
Matthew	Barnes	Texas Tech University	USA
Jose	Barrero Sanchez	CSIRO	Australia
Jacqueline	Batley	University of Western Australia	Australia
Hugo	Bellen	Baylor College of Medicine	USA
Kirsten	Boggs	Australian Genomics	Australia
Jon	Bridle	University College London	UK
Austin	Burt	Imperial College London	UK
Daniel	Cadena	Universidad de los Andes	Colombia
Rebeca	Carballar-Lejarazú	University of California Irvine	USA
Nadine	Caron	University of British Columbia	Canada
Gemma	Chandratillake	NHS East Genomics	UK
Claudia	Coleine	Tuscia University	Italy
Tim	Connallon	Monash University	Australia
Kimberly	Cooper	University of California San Diego	USA
Peter	Currie	Australian Regnerative Medicine Institute	Australia
Kevin	Davies	Plant & Food Research	New Zealand
Sarah-Jane	Dawson	Peter MacCallum Cancer Centre	Australia
Claude	Desplan	New York University	USA
Katrina	Dlugosch	University of Arizona	USA
Egor	Dolzhenko	Pacific Biosciences	USA
Evan	Eichler	University of Washington	USA
Lucie	Etienne	CIRI, Centre International de Recherche en Infectiologie	France
David	Evans	University of Queensland	Australia
Chiara	Fabbri	University of Bologna	Italy
Mark	Febbraio	Monash University	Australia
Cristina	Ferrandiz	Instituto de Biologia Molecular y Celular de Plantas	Spain
Maya	Ghoussaini	Regeneron Pharmaceuticals	UK
Richard	Gibbs	Baylor College of Medicine	USA
Anna	Gloyn	Stanford University	USA
Josefa	Gonzalez	Institute of Evolutionary Biology	Spain
Yalong	Guo	Chinese Academy of Sciences	China
Melissa	Gymrek	University of California San Diego	USA
Elissa	Hallem	Univerisity of California Los Angeles	USA
Muzlifah	Haniffa	Wellcome Sanger Institute	UK
Kathryn	Hodgins	Monash University	Australia
Corinne	Houart	King's College London	UK
Lori	Isom	University of Michigan	USA
Jochen	Kumlehn	Leibniz Institute of Plant Genetics and Crop Plant Research	Germany
Asato	Kuroiwa	Hokkaido University	Japan
Junko	Kyozuka	Tohuku University	Japan
Kim-Anh	Le Cao	University of Melbourne	Australia
Andrea	Liebl	University of South Dakota	USA
Ryan	Lister	The University of Western Australia	Australia
Ailene	MacPherson	Simon Fraser University	Canada
Ann	McCartney	University of California Santa Cruz	USA

Heather	Mefford	St. Jude Children's Research Hospital	USA
Claire	Mérot	CNRS ECOBIO / Université de Rennes	France
Gracjan	Michlewski	International Institute of Molecular and Cell Biology in Warsaw	Poland
Karen	Miga	University of California	USA
Toshifumi	Minamoto	Kobe University	Japan
Denise	Montell	University of California	USA
Alison	Murray	Desert Research Institute	USA
Erisa Sabakaki	Mwaka	Makerere University	Uganda
Utpal	Nath	Indian Institute of Science, Bengaluru	India
Benjamin	Neale	Massachusetts General Hospital	USA
Maria	Nieves-Colón	University of Minnesota	USA
Christiane	Nusslein-Volhard	Max Planck Institute for Biology	Germany
Yukinori	Okada	The University of Tokyo	Japan
Marieke	Oudelaar	Max Planck Institute for Multidisciplinary Sciences	Germany
Nathan	Palpant	University of Queensland	Australia
Carolina	Pardo-Diaz	Universidad del Rosario	Colombia
Linda	Partridge	University College London	UK
Tanja	Pyhäjärvi	University of Helsinki	Finland
Uma	Ramakrishnan	National Centre for Biological Sciences	India
Mirana	Ramialison	Murdoch Children's Research Institute	Australia
Nicolas	Rawlence	University of Otago	New Zealand
William	Reay	The University of Newcastle	Australia
Dugald	Reid	La Trobe University	Australia
Pamela	Ronald	University of California, Davis	USA
Alan	Rubin	Walter and Eliza Hall Institute of Medical Research	Australia
Avnika	Ruparelia	University of Melbourne	Australia
Carolina	Sansaloni	International Maize and Wheat Improvement Center	Mexico
Noam	Shomron	Tel Aviv University	Israel
Hannah	Siddle	The University of Queensland	Australia
Sonal	Singhal	California State University	USA
Inez H.	Slamet-Loedin	International Rice Research Institute	Philippines
Ralf	Sommer	Max Planck Institute for Biology	Germany
Victoria	Sork	University of California Los Angeles	USA
Frances	Sussmilch	University of Tasmania	Australia
Yoshiko	Takahashi	Kyoto University	Japan
David	Thomas	Garvan Institute of Medical Research	Australia
Braden	Tierney	Weill-Cornell Medical College	USA
Marco	Todesco	University of British Colombia	Canada
Krystal	Tsosie	Arizona State University	USA
Eldad	Tzahor	Weizmann Institute of Science	Israel
Ignatia	Van den Veyver	Baylor College of Medicine	USA
Alison L.	Van Eenennaam	University of California	USA
Kees	van Oers	Netherlands Institute of Ecology	Netherlands
Cristina	Vieira	Claude Bernard Lyon 1 University	France
Irina	Voineagu	University of New South Wales	Australia
Honyan	Wang	Duke-NUS Medical School	Singapore
Kan	Wang	Iowa State Unviersity	USA
Maren	Wellenreuther	Plant & Food Research	New Zealand
Helena	Westerdahl	Lund University	Sweden
Donna	Whelan	La Trobe University	Australia
Phillip	Wilcox	University of Otago	New Zealand
Michelle	Wille	The University of Sydney	Australia
Quin	Wills	Ochre Bio	UK
Elizabeth	Worthey	University of Alabama	USA
Qi	Zhou	Zhejiang University	China
Jian-Kang	Zhu	Southern University of Science & Technology	China

POSTER SESSIONS

Posters will be on display for the entire Congress with dedicated sessions held over the extended lunch breaks on Monday, Tuesday, Thursday and Friday. Authors will be at their posters from 1230-1330hrs during these sessions and from 1230-1315 on Friday to discuss their work.

Odd poster numbers are allocated to sessions on Monday and Thursday, Even poster numbers allocated to Tuesday and Friday.

Below is a list of posters in order of theme. You can view an alphabetical list by presenter on the Congress App and view a digital version of the presentation and the abstract.

First name	Last name	Organisation	Country	Presentation title	Poster board No.
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Natalia	Akulenko	National Research Center Kurchatov Institute	Russia	GERMLINE SPECIFIC PARALOG OF UBIQUITOUSLY EXPRESSED RIBOSOME ASSOCIATED NAC CHAPERONE OF DROSOPHILA MELANOGASTER	002
Ushani	Atapattu	University of Melbourne	Australia	GENETIC CHARACTERISATION OF TWO NOVEL SPECIES OF CANINE FILARIAL PARASITES CAUSING INFECTIONS IN HUMANS IN SRI LANKA	001
Soumitra	Bhide	University of Melbourne	Australia	DRIVING SYNTHETIC INVERSIONS WITH TEMPERATURE SENSITIVITY	003
John	Bowman	Monash University	Australia	WHITHER THE SEX CHROMOSOME: THE FATE OF SEX CHROMOSOMES DURING THE EVOLUTION OF MONOICY FROM DIOICY IN LIVERWORTS	004
Olivia	Boyd	Imperial College London	UK	USING SINGLE-NUCLEOTIDE POLYMORPHISMS TO ESTIMATE CONCORDANCE OF TRANSMISSION PAIRS FROM HOUSEHOLDS VS. NON-HOUSEHOLD CONTACTS IN AN ON-GOING PANDEMIC OUTBREAK	005
Georgina	Bramwell	Deakin University	Australia	THE EFFECT OF MITOCHONDRIAL RECOMBINATION ON FERTILIZATION SUCCESS IN BLUE MUSSELS	006
Benjamin	Camm	University of Melbourne	Australia	MODELLING GENE DRIVE LOCALISATION THROUGH GENETIC VARIATION	007
Ebony	Cave	University of Leicester	UK	SNP VARIANT ANALYSIS OF MULTIPLE HELICOBACTER PYLORI SUBPOPULATIONS REVEALS DIFFERENT EVOLUTIONARY HISTORIES.	008
Yao-ban	Chan	University of Melbourne	Australia	THE EFFECT OF COPY NUMBER HEMIPLASY ON GENE FAMILY EVOLUTION	009
J King	Chang	University of New South Wales	Australia	ANNOTATION OF THE EASTERN THREE-LINED SKINK	010
Kelton	Cheung	University of New South Wales	Australia	DO REPEAT REGIONS INFLATE THE ESTIMATION OF NUMTS?	011
Alexander	Cole	Centenary Institute	Australia	DESIGN AND VALIDATION OF A NOVEL MAMMALIAN DIRECTED EVOLUTION SYSTEM	012
Anne-Cecile	Colin	Western Sydney University	Australia	EVOLUTION OF LIFE-HISTORY TRAITS RELATED TO ARIDITY PROVIDED ADAPTATION TO DROUGHT IN EUCALYPTS	013
James	Damayo	University of Sydney	Australia	VIRUS DERIVED SIRNA PROFILES REVEAL REPLICATING VIRUSES IN VARROA DESTRUCTOR	014
Jackson	Dann	University of Adelaide	Australia	PSEUDOGENISATION OF NKX3.2 IN MONOTREMES IS ASSOCIATED WITH ALTERED GASTRIC DEVELOPMENT AND MORPHOLOGY	015
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Erin	Delargy	University of Otago	New Zealand	IT'S TIME TO GROW UP: VALIDATION OF THE TIMER-GENE SEGMENTATION HYPOTHESIS IN THE HONEYBEE	018
Christopher	Denes	University of Sydney	Australia	AN ENHANCED CRISPRA SYSTEM GENERATED USING A NOVEL MAMMALIAN DIRECTED EVOLUTION PLATFORM	019
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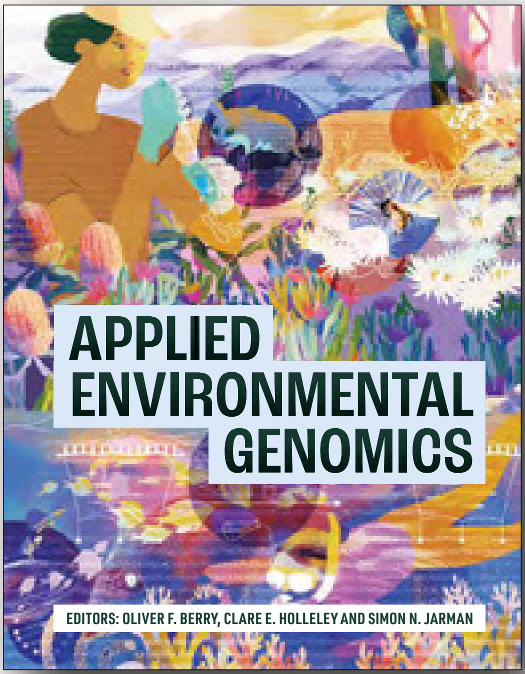

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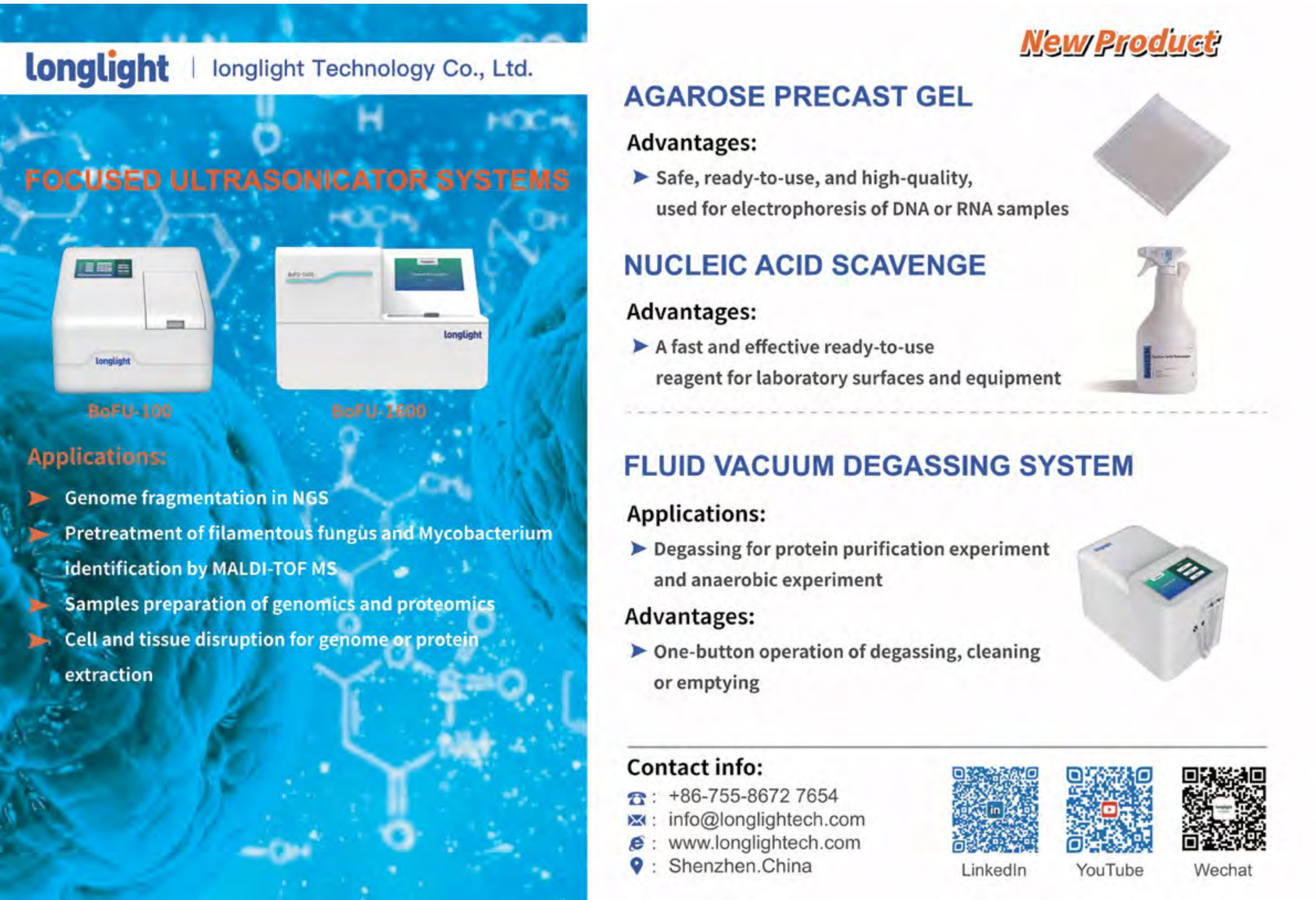
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SATELLITE MEETINGS

Satellite meetings held in advance of the Congress are detailed below. Bookings are required in advance. More information on each event and booking details can be found on the website **www.icg2023.com.au**

SATURDAY 15 JULY 0930-1600 Room 213 - MCEC	**GENOMICS UPDATE: NEW TECHNOLOGIES AND CLINICAL CASES**
Sunday 16 July 0900-1700 Room 219 -MCEC	**BIODIVERSITY GENOMICS - A GLOBAL PERSPECTIVE**

ADDITIONAL MEETING

THURSDAY 20 JULY 1215-1300 Room 203	**INTERNATIONAL GENETIC FEDERATION MEETING**

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SOCIAL EVENTS

To complement the outstanding scientific program, the social program provides you with the ideal relaxing environment to meet with colleague and to enhance your experience whilst in Melbourne.

Advance bookings are required so please contact the Congress Office to secure your tickets:

Opening Ceremony & Welcome Reception

Sunday 16 July 1800-2100hrs MCEC - Plenary Hall 2

Cost: Tickets are included for full registrations. Additional tickets may be purchased for $88 inc GST.

The Opening Ceremony will take you on a journey, intertwining glimpses of great moments of discovery in genetics and the history of this Congress, with its beginnings in 1899 before the re-discovery of Mendel's principles of inheritance. There will be fabulous imagery and music ranging the sounds of the didgeridoo to a performance from a star of the stage, Nigel Huckle. There will be a formal welcome and vignettes that point to some of the highlights of the 2023 Congress.

At the Reception that follows you can meet your peers from around the world while enjoying canapes and drinks. Do not miss your opportunity to attend this wonderful event that has been created for your enjoyment!

Opening Ceremony Credits:

Producer & Creative Concept: Philip Batterham
Molecular Animations: Drew Berry
Art Work: Map Creative
Welcome to Country: Ian Hunter
Performance: Nigel Huckle

Congress Social Evening - Connection

Thursday 20 July 1900-2100 Lume Gallery – MCEC Ground Floor

Cost: $130 per person inc GST.

Join us for an exclusive viewing of **"Connection"** a breathtaking celebration of First People's art, music and culture. Featuring over 550 artworks from more than 110 visual and music artists, this showcase is the largest experience of First People's Art ever gathered and fuses the world's oldest culture with the most cutting-edge technology.

This immersive gallery space with projections four stories high is a multisensory experience presenting an incredible display of Australia's most celebrated established and emerging First Nations artists through the lenses of Land, Water and Sky Country.

In collaboration with our Major Partner Illumina, and in celebration of their 25 years of innovation, a private viewing has been arranged with drinks and canapes showcasing Australian native and locally grown ingredients will be served for your enjoyment. And as you leave, a great opportunity to purchase some beautiful gifts or mementos. A night and experience that you will never forget.

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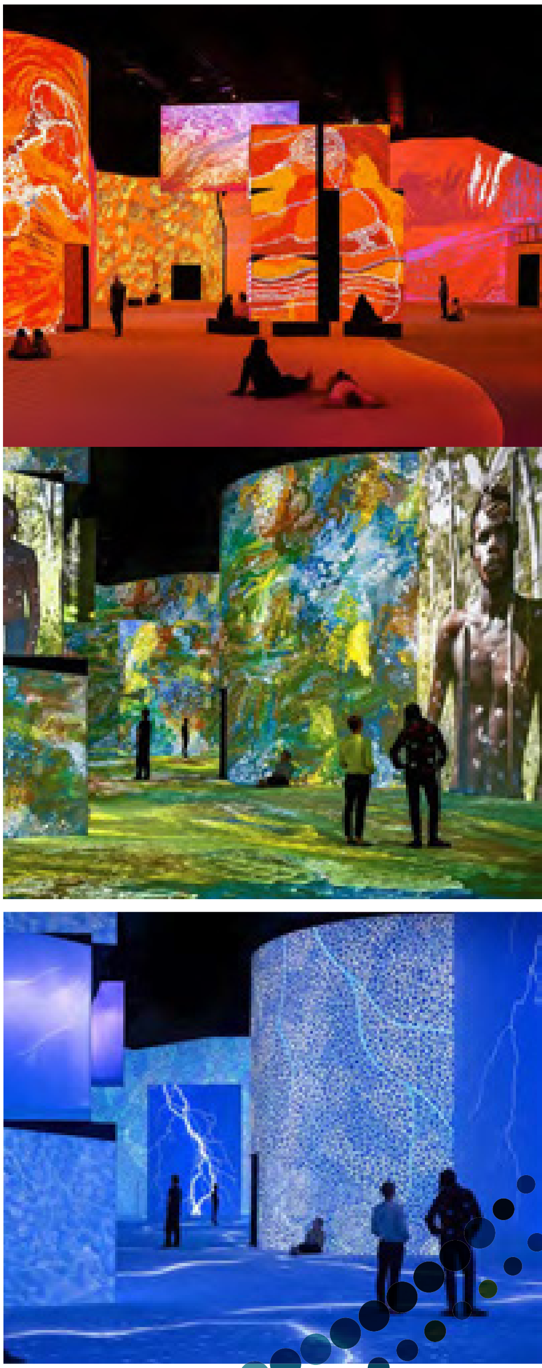


GENERAL INFORMATION

Venue

Melbourne Convention & Exhibition Centre (MCEC)
1 Convention Centre Place South Wharf
www.mcec.com.au

MCEC has onsite carparking available via the Normandy Street entrance or at the adjacent DFO. Please refer to the website for parking rates and early bird savings.

The MCEC is readily accessible by public transport with tram and nearby train access.

Airport Arrival

On arrival at Melbourne Airport, there are taxis and Ubers available. A Skybus coach service is also available and tickets can be purchased in advance or at the time. For more information contact www.skybus.com.au

App

Be sure to download the App in advance to take advantage of the most current information available – the scientific program, the social events, the public program, information about our partners and exhibitors, connect with colleagues and receive push notifications throughout the week. You will be sent an email with the download and log in details. Your personalised password to access the App will be printed on the reverse side of your name badge.

Catering

Morning and afternoon tea and lunch will be served in the Exhibition from Monday-Friday allowing you the chance to enjoy refreshments, meet with exhibitors and view the poster gallery.

The exception in on Wednesday. Morning tea will be served however lunch is not as the Exhibition is closing at 1430, allowing you the opportunity to participate in additional sessions or take some time out to discover what Melbourne has to offer. Lunch is available to purchase from the MCEC Goldfields Café.

For those attending the GSA and HGSA Programs, a light lunch will be served .

The lunch menus offer selections inclusive of vegetarian, vegan and gluten free options. A dedicated dietary buffet will be offer for those who have advised us of in advance of dietary requirements other than these.

Cloakroom

The Information Desk at the entrance to the MCEC can securely store coats and bags and there will be coat racks available outside the Symposia Rooms on Level Two for your convenience.

Congress Office

The Congress team will be onsite to assist you and are located at the Registration Desk. However you can contact us outside of these times by email icg2023@wsm.com.au and telephone +61 3 96456311.

Dining Out

Melbourne has a myriad of restaurants on offer across a range of cuisines reflective of Melbourne's multi-cultural community.

Right on the doorstep of the MCEC, in South Wharf is a range of restaurants for you to enjoy and by simply showing your Congress lanyard, a 10% discount is offered. Visit the website to view the options: https://mcec.com.au/experience-melbourne/south-wharf

Discover Melbourne

Melbourne truly is a city of contrasts – there are laneways, museums, galleries and foodie precincts to be explored. And if you are arriving early or staying a day or two longer, explore a little further and discover the winery regions of the Yarra Valley or Mornington Peninsula, the rugged coastline of the Great Ocean Road, visit the much-loved fairy penguins at Phillip Island or our native animals at Healesville and take in the beauty of the Dandenong Ranges. There is so much to see and do.

Visit the City of Melbourne Tour Desk in the Exhibition to assist with any recommendations or suggestions.

Exhibition

Visit the Congress Exhibition located on the Ground Floor, to learn about the latest products and services available for genetics and genomic research. A great meeting place to connect with our valued partners and exhibitors, to enjoy refreshments, grab a coffee or take seat and catch up with colleagues.

The exhibition will be open the following hours:

Monday/Tuesday/Thursday	0800-1730hrs
Wednesday	0800-1430hrs
Friday	0800-1330hrs

Family Room

The Family Room (Courtyard Room 2) is an area where you can bring young children and watch a live feed of the plenary and select sessions throughout the week in comfort for you and/or carers.

The MCEC also has a Parents Room. Please contact the Customer Service Team at the MCEC Information Desk for directions.

Inclusion & Diversity

The Congress is committed to a culture of inclusion, diversity and equity. We welcome and encourage participation by geneticists regardless of gender, gender expression, sexual orientation, ethnicity, nationality, disability, religion, age or geographic location.

Our commitment to diversity has resulted in presentations from researchers from 50 different countries and across a full range of gender and career stages.

The Congress offers a safe, respectful and inclusive environment for all participants and we thank you in advance for supporting this throughout the Congress.

Should you have any concerns during the Congress, please see our team at the Registration Desk for assistance.

Meet the Speakers Lounge

Within the Exhibition area is a dedicated Meet the Speakers Lounge where we encourage Plenary and Invited speakers to spend some time to meet with delegates following their presentations.

Networking Lounge

Within the Exhibition is a Networking Lounge where you can relax, check your emails or use it as a meeting point with your colleagues.

Poster Gallery

If you are presenting a poster, the Gallery in the Exhibition will be open from 8am on Monday 17 July to display your poster on your designated poster board. Velcro will be available on your board.

Posters will be on display for the entire Congress with dedicated sessions held over the extended lunch breaks on Monday, Tuesday, Thursday and Friday. Authors will be at their posters from 1230-1330hrs and from 1230-1315 on Friday to discuss their work.

Odd poster numbers are allocated to sessions on Monday and Thursday, even poster numbers are board numbers allocated to Tuesday and Friday poster sessions.

A detailed poster listing is included within this handbook and also available on the Congress App.

Prayer Rooms

Prayer rooms are available at the MCEC. Please contact the Customer Service Team at the MCEC Information Desk for directions.

Registration

The Registration Desk will be open the following times to enable you to collect your name badge on arrival which must be worn at all times to gain access to the Congress Sessions, Social Events and Exhibition. The Registration team are available to provide any assistance throughout the Congress.

Sunday	1200-1900hrs
Monday - Friday	0700-1730hrs

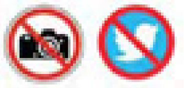
Social Media Guidelines

At ICG 2023 social media will be used during the Congress to share exciting moments in the program with the global community. We encourage you to contribute to the scientific exchange by tweeting/re-tweeting or sharing on other social media platforms. We encourage all Congress attendees to interact with the Congress on social media. Please follow us

- **Twitter (if you aren't already):** @Genetics2023 #icg2023
- **Facebook:** https://www.facebook.com/Genetics2023

GUIDELINES FOR SPEAKERS

- If you have a twitter handle, include this on your title slide or on your poster, so that others can tag and credit you.
- We encourage Congress delegates to share information about the meeting on social media, but speakers can ask for their work not to be shared. Please take the time to let the audience know your wishes.
- If you do not wish to have any of your presentation shared via Twitter, Facebook, blogs, or other social networks, please make this clear before and during your presentation.
- While data that is presented without a reference (i.e. Unpublished) should not be shared via social media, if you wish to emphasise this, you might wish to place these symbols on your slides:



GUIDELINES FOR SOCIAL MEDIA USERS

- Please respect the wishes of the presenter. If they indicate that they do not want their presentation to be shared on social media, then please do not share it.
- If you are not sure of the presenter's wishes (e.g. if you missed the start of the talk), take a precautionary approach and don't share.
- Taking photographs and sharing of posters without the express permission of the presenter is not acceptable. Do not share if the presenter isn't there.
- We encourage the use of social media to ask questions, or provide comments and feedback, but this should be done in a constructive manner. Be polite on social media, as you would be in person. Rude and derogatory comments, and personal attacks, are inappropriate.
- We encourage attendees to promote the work of presenters, share quotes, share links to relevant papers etc., as appropriate. Please take time to respect the context of statements made at the Congress, to avoid misrepresentation or misattribution.
- Credit presenters for their work by including their name and/or twitter handle in your tweets.
- Include the Congress hashtag #icg2023 in your related tweets to allow others to easily follow the meeting. Feel free to also tag the Congress account @Genetics2023.

Participants asked to stop any inappropriate behaviour are asked to comply immediately. Attendees violating these rules may be asked to leave the event at the sole discretion of the organisers without a refund of any charge. Any participant who wishes to report a violation of this policy is asked to speak, in confidence, at the Congress Registration Desk.

Speakers Preparation Room

The Speakers Preparation Room (Room 206) will be open the following times to enable speakers to upload their presentation in advance:

Sunday	1330-1730hrs
Monday, Tuesday & Thursday	0800-1630hrs
Wednesday & Friday	0800-1400hrs

Sustainability Measures

The Congress recognises the importance of environmental sustainability and is committed to minimising the environmental footprint of the Congress by undertaking a range of practices including:

- Conducting the Congress at the world leading 6 star green rated MCEC with their commitment to the UN Sustainable Development Goals and focusing on the following measures:
    - Sustainability Management Team and 5 year strategy
    - Food waste
    - Reducing its CO2 emissions
    - Adopting Food Growth practices
    - Sustainable Design of the Venue
    - Waste Diversion Program
    - Energy Management
    - Harvesting Captured Rainwater
- Conducting meetings of the Local Organising Committee and Scientific Program Committee online to avoid the impact of travel
- Marketing the Congress using digital and electronic mediums rather than print collateral
- Communicating with Congress stakeholders electronically rather than in print and focusing on the website as the central point for the most current information about the Congress
- Avoiding the use of any single use plastics such as drink bottles
- Using digital signage where possible to reduce the amount of wasted print material
- Selecting menus that feature locally sourced fresh produce and ensuring any unused food and beverages are donated to an approved charity
- Encouraging exhibitors to use recycled materials in their displays within the Congress exhibition
- Working with third party suppliers who support the sustainability approach of the Congress in the provision of their services/products.

We encourage our participants to support our sustainability approach to ensure collectively we have a greatly reduced impact on our environment.

WIFI

There is dedicated wifi for your use throughout the Congress. The password to the Congress service will be printed on the reverse side of your name badge.

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PUBLIC PROGRAM EVENTS

On Monday -Thursday evenings a series of events have been curated to enhance your Congress experience and to engage with our local community.

Bookings are required in advance. More information on each event and booking details can be found on the website **www.icg2023.com.au**

MONDAY 17 JULY 1800-1930 Room 210 - MCEC	**WOMEN IN SCIENCE: UNIQUE JOURNEYS TO DIFFERENT PEAKS** Discussion featuring Professor Doctor Christiane Nüsslein-Volhard, (Germany) Nobel Laureate, Professor Anne Muigai (Kenya) and Valda Vinson, (USA) Editor of Science
TUESDAY 18 JULY 1930 Melbourne Recital Centre	**Origins – of the Universe, of life, of Species, of Humanity** The world premiere of the new musical work, *Origins – of the Universe, of life, of Species, of Humanity* was written to be part of the Congress social program, using beautiful language and images of cosmology, molecular biology, evolution, ecology and anthropology. It highlights many all-Australian examples (fossilizing stromatolites, sexually selecting lyrebirds, speciating rock wallabies, extinct thylacines). It will be performed by a 100-voice choir, a 60-piece orchestra and four well known soloists, with visuals by award winning animator/videographer, Drew Berry. The beautiful Melbourne Recital Centre is our city's premiere music venue and is in walking distance from the MCEC. It is likely to be a sell-out, so book your tickets now.
WEDNESDAY 19 JULY 1730-1830 Room 210 - MCEC	**GENETICS VS SPORT – ARE SUPER ATHLETES BORN OR MADE?** Join us as our panel of experts takes on the nature vs nurture debate in sport. Panelists include Professor Kathryn North a global leader in research on human genetics, the Director of the Murdoch Childrens Research Institute and leads the national body Australian Genomics; Darcy Moore, an extraordinarily talented and widely respected AFL footballer, Captain of the Collingwood Football Club. The discussion will be moderated by Tracey Holmes, one of Australia's very best sports journalists. This forum is part of the City of Melbourne Conversation Series.
WEDNESDAY 19 JULY 1830-1930 Melbourne Museum	**FUTURE FORUMS – THE GENETIC RESCUE OF OUR FANTASTIC BEASTS** Hear from experts leading ground-breaking advancements in genetics to save critically endangered species from extinction. Join the conversation to explore cutting-edge research into genetics and genomics, and learn how these innovations can preserve genetic diversity, restore populations of endangered animals and protect the precious biodiversity of our planet. See the Fantastic Beasts exhibition before the conversation and we encourage you to arrive earlier and view all the Museum has to offer.
THURSDAY 20 JULY 1800-1900hrs Room 210 - MCEC	**POPULATION DNA SCREENING FOR DISEASE RISK IS COMING – WHAT YOU NEED TO KNOW** DNA screening for risk of disease that can be prevented or treated (like some cancers or heart disease) is being offered to 10,000 Australians (18-40yo) though the DNA Screen pilot study. This testing could save lives, but there are many ethical and societal issues to consider. Are Australians ready for this kind of testing? Would you take the test? What are the benefits? What are the drawbacks? How does this compare to international approaches? Join this exciting event to learn about cutting-edge research, informing the future of population DNA screening. Join the expert panel Associate Professor Paul Lacaze (Monash University), Dr Jane Tiller (Monash University) and Professor Nancy Cox (Vanderbilt University) for the discussion hosted of by ABC Radio presenter, Natasha Mitchell.

The Public Events Program is supported by

Australian Genomics

LA TROBE UNIVERSITY

THE UNIVERSITY OF MELBOURNE

INDUSTRY SESSIONS

Industry hosted breakfast and lunch events will be held throughout the Congress. Advance bookings are required and spaces are limited so please see the Registration Desk if you require any assistance.

BREAKFAST SESSIONS

TUESDAY 18 JULY 0700-0800hrs Room 208 – Level 2	**THE NEW FACE OF FABRY DISEASE: UPDATED AUSTRALIAN GUIDELINES AND LONG TERM DATA** Hosted by: Amicus Therapeutics
WEDNESDAY 19 JULY 0700-0800hrs Room 208 – Level 2	**ENHANCING THE UNDERSTANDING OF DISEASE GENOMES THROUGH OPTICAL GENOME MAPPING AND, INTRODUCING VIA - A COMPLETE GENOMIC DATA ANALYSIS PLATFORM FOR CLINICAL RESEARCH** Hosted by: bionano
THURSDAY 20 JULY 0700-0800hrs Room 208 – Level 2	**MISSED CONNECTIONS: WHY GENOMICS AND DIGITAL HEALTH AREN'T GETTING ALONG** Hosted by: Melbourne Genomics Health Alliance

LUNCH SESSIONS

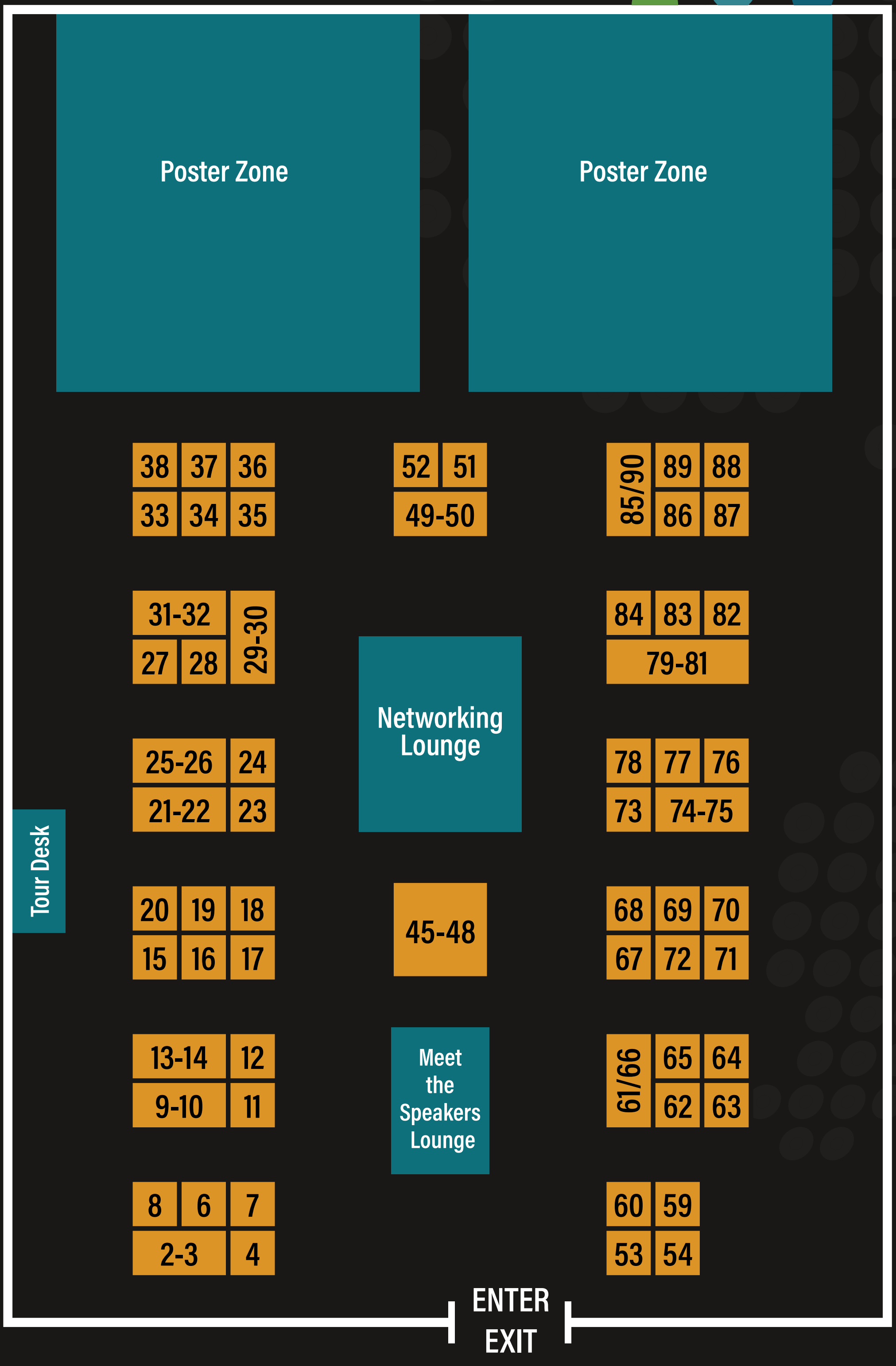
MONDAY 17 JULY 1215-1330hrs Eureka Room - Ground Floor	**ILLUMINA INNOVATION SYMPOSIUM: NAVIGATING THE FUTURE OF GENOMICS AND MULTIOMICS** Hosted by: illumina®
MONDAY 17 JULY 1215-1330hrs Hospitality Room 6& 7 - Upper Level	**UNLOCK THE POWER OF GENOMICS WITH AWS** Hosted by: aws
MONDAY 17 JULY 1230-1345hrs Room 208 - Level 2	**RECENT ADVANCES IN ACHONDROPLASIA** Hosted by: BIOMARIN®
TUESDAY 18 JULY 1215-1330hrs Eureka Room - Ground Floor	**GENOMICS FOR ALL: ADDRESSING DISPARITIES IN ACCESS AND DIVERSITY FOR BETTER HEALTH OUTCOMES** Hosted by: illumina®
TUESDAY 18 JULY 1215-1330hrs Room 208 – Level 2	**LATTICE IMAGING TECHNOLOGIES WITH ZEISS LATTICE LIGHTSHEET 7** Hosted by: ZEISS
TUESDAY 18 JULY 1215-1330hrs Hospitality Room 6& 7 - Upper Level	**OXFORD NANOPORE TECHNOLOGIES: RESEARCHERS LEADING THE WAY** Hosted by: Oxford NANOPORE Technologies™
THURSDAY 20 JULY 1215-1330hrs Room 208 – Level 2	**CAPACITY BUILDING - MOVING BEYOND FORMAL GENOMICS EDUCATION AND TRAINING** Hosted by: wellcome connecting science
THURSDAY 20 JULY 1215-1330hrs Hospitality 6 – Upper Level	**Next Generation Newborn Screening from Idea to Implementation** Hosted by: Agilent Trusted Answers

EXHIBITION

The exhibition is located on the Ground Floor and will be open the following hours:

Monday/Tuesday/Thursday	0800-1730hrs
Wednesday	0800-1430hrs
Friday	0800-1330hrs

Exhibitor Floorplan



Exhibitor list

STAND No.	ORGANISATION
85,90	Agilent Technologies Australia
59	AGTA
24	Alexion Pharmaceuticals
78	Amazon Web Services
53	Amicus Therapeutics
23	AstraZeneca
27	Australian BioCommons
36	Australian Functional Genomics Network
25,26	Australian Genome Research Facility
87	Azenta Singapore
15	Beckman Coulter Life Sciences
49,50	BGI Australia
2,3	Biomarin Pharmaceutical
72	Biomolecular Horizons 2024
65	Biomolecular Resource Facility (BRF)
8	Bionano Genomics
12	Celemics Inc.
67	Charles River Laboratories Australia
16	Daicel Arbor Biosciences
4	Decode Science
11	DUG Technology (Australia)
74,75	Eppendorf South Pacific
86	Fulgent Genetics
70	Garvan Sequencing Platform
33	Genetic Society of America
71	Genetic Technologies
54	Genetics Society of AustralAsia
18	GeneWorks
51	GenieUs Genomics
7	Histopath
64	Human Genetics Society of Australasia

STAND No.	ORGANISATION
45,46,47,48	Illumina
73	Integrated DNA Technologies (IDT)
88	Invitae
60	Lifebit
6	Longlight Technology
83	Macrogen
76	Millennium Science
17	MIMOTOPES
61,66	New England Biolabs
19	NOVOGENE (HK)
29,30	Oxford Nanopore Technologies
79,80,81	PacBio
20	PakAir Cargo
34	Pawsey Supercomputing Research Centre
21,22	PerkinElmer
52	QIAGEN
28	Ramaciotti Centre for Genomics UNSW
35	Roche Diagnostics
89	Sanofi Genzyme
62	SCC Soft Computer
82	Somalogic
68	Sonic Genetics
84	Summer Internship for Indigenous Peoples in Genomics (SING)
31,32	Tecan
9,10	Thermo Fisher Scientific
63	Trendbio
13,14	Twist BioScience
37	Vector Builder
77	Yourgene Health
38	ZEISS

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CONGRESS OF GENETICS

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