XXIII^rd INTERNATIONAL CONGRESS OF GENETICS

GENETICS AND GENOMICS

Linking Life and Society

16-21 JULY **2023**
MELBOURNE CONVENTION & EXHIBITION CENTRE **AUSTRALIA**

This scientific program is subject to change and is current at 17 July 2023

SUNDAY 16 JULY 2023

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

1700 - 1745	Optional Session
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

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** (virtual presentation) 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 Rossell, Australia*
1400-1430	**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	**Gary Hime, University of Melbourne, Australia** The adult *Drosophila* salivary gland exhibits an unusual mode of cell division
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 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** (virtual presentation) 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 & Noam Shomron, Israel*
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 Bennett, 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	Light lunch served prior to the commencement of the session
1200-1315	**Annual General Meeting**
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, South Wharf** *(separate tickets must be purchased in advance with GSA)*

Room 212	Human Genetics Society of Australasia (HGSA) Program
1300-1345	Light lunch served prior to the commencement of the session
1300-1345	**HGSA Sutherland Lecture** **Zornitza Stark, Murdoch Children's Research Institute, Australia** Accelerating rare disease diagnosis
1345-1445	**HGSA Annual General Meeting**
1445-1450	**InGeNA** **Kathy Campbell**
1450-1500	**HGSA ASM 2024 & Information Session**
1500-1530	Afternoon Tea
1530-1615	**HGSA Oration Lecture** **James Pitt, Victorian Clinical Genetics Service, 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	**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
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 *dmrt*1 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 (Special Symposium)** ***Session 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 **Yvonne Adibguduge, Swinburne University of Technology, Australia** Exploring leaf epicuticular wax in japonica and indica rice for improved water improved water use efficiency

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: Pharmaco-genomics 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**