



This preliminary program is subject to change and is current at 6 July 2023

SUNDAY 16 JULY 2023

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

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
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0830-0930	Plenary Session 1 -
Plenary Room 2	Mark Blaxter - Wellcome Sanger Institute, UK New biology from new genomes: The Tree of Life project <i>Chair: Jenny Graves, Australia</i>

1000-1200	Symposia Sessions A
Room 203	A1: Genomes & Biodiversity (Evolutionary Genetics)
Convenors	<i>Tammy Steeves, New Zealand & Claire Mérot, France</i>
1000-1030	Claire Mérot, CNRS ECOBIO / Université de Rennie, France The role of structural genomic variants in the evolution of biodiversity
1030-1100	Carolina Pardo-Díaz, 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 (<i>Aphelocoma</i>) 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 (<i>Nannoperca australis</i> ; 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	<i>Belinda Ferrari, Australia & Claudia Coleine, Italy</i>
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)
Convenors	<i>Phillip Wilcox, New Zealand & Azure Hermes, Australia</i>
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 kiwai 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)
Convenors	<i>Stephen Robertson, New Zealand & Evan Eichler, USA</i>
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	<i>Christine Wells, Australia & Leonie Quinn, Australia</i>
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 (Agriculture & Plant Genetics)
Convenors	<i>Daniel Ortiz-Barrientos, Australia & Victoria Sork, USA</i>
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 <i>Arabidopsis</i> 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

1400-1600	Symposia Sessions B
Room 203	B1: Paleogenomics (Evolutionary Genetics)
Convenors	<i>Lisa Matisoo-Smith, New Zealand</i>
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	<i>Sally Potter, Australia & Maren Wellenreuther, New Zealand</i>
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 <i>Recipient of the GSA Smith-White Travel Award</i> 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)
Convenors	<i>Ruby Lin, Australia & Mirana Ramialison, Australia</i>
1400-1430	Mirana Ramialison, 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 <i>in silico</i> 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	<i>Ainsley Newson, Australia & Erisa Sabakaki Mwaka, Uganda</i>
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, University of Arizona, 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)
Convenors	<i>Peter Currie, Australia & Yoshiko Takahashi, Japan</i>
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 <i>Drosophila</i> 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 (Agriculture & Plant Genetics)
Convenors	<i>Peter Waterhouse, Australia & Kan Wang, USA</i>
1400-1430	Kan Wang, Iowa State University, USA A quick and simplified maize transformation and genome editing protocol using <i>Agrobacterium</i> 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 <i>Nicotiana benthamiana</i> : 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 <i>Medicago truncatula</i>



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

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
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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	<i>Michelle Wille, Australia & Anjana Karawita, Australia</i>
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 <i>Plasmodium falciparum</i> var DBL α 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	<i>Catherine Grueber, Australia & Rebecca Jordan, Australia</i>
1000-1030	Uma Ramakrishnan, National Centre for Biological Sciences, India How genetics can inform tiger conservation
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, <i>Bettongia lesueur</i>
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 Presentation tbc Mathew Lott, The Australian Museum Research Institute, Australia Genomic insights into the contemporary and historical population dynamics of the koala <i>Phascolarctos Cinerus</i>



	<p>Richard Frankham, Macquarie University, Australia Large effects of different sized X or Z sex chromosomes on susceptibility to inbreeding depression for total fitness</p> <p>Anna MacDonald, Australian Antarctic Division, Australia Developing molecular tools to resolve uncertainties in seabird bycatch from longline fisheries</p> <p>Joao Filipe, Department of Biodiversity, Conservation and Attractions, Australia Signatures of natural selection in a foundation tree along Mediterranean climatic gradients</p>
Room 210/211	C3: Equity & Diversity in the Application of Human Genomics (Genomics & Genomic Technologies)
Convenors	<i>Alex Brown, Australia & Nadine Caron, Canada</i>
1000-1030	<p>Nadine Caron, University of British Columbia, Canada Working towards equity in biobanking: an ongoing Canadian experience</p>
1030-1100	<p>Ann McCartney, University of California Santa Cruz, USA Equitable approaches to diversifying reference genomes</p>
1100-1115	<p>Weerachai Jaratlerdsiri, University of Sydney, Australia African indigenous genomics reveals lifestyle-relevant adaptation in human health</p>
1115-1130	<p>Ira Deveson, Genomic Technologies Group, Australia The landscape of genomic structural variation in Indigenous Australians</p>
1130-1145	<p>Stephen Leslie, University of Melbourne, Australia Indigenous Australian genomic variation reveals deep population structure</p>
1145-1200	<p>Ashley Farlow, Australian National University, Australia Causes and consequences of population structure in Indigenous Australian genomes</p>
Room 212/213	C4: Disease Gene Identification & Functional Genomics Using Animal Models (Genetics & Human Health)
Convenors	<i>Sally Dunwoodie, Australia & Hugo Bellen, USA</i>
1000-1030	<p>Hugo Bellen, Baylor College of Medicine, USA Using <i>Drosophila</i> to help in the diagnosis of undiagnosed diseases</p>
1030-1100	<p>Corinne Houart, Kings College London, UK A <i>FoxG1</i> transformation tunes local decisions in neurons</p>
1100-1115	<p>Justin Szot, Victor Chang Cardiac Research Institute, Australia Congenital NAD deficiency disorder: causes and possible prevention</p>
1115-1130	<p>Hui Hu, Laboratory Department of Wuhan Central Hospital, China The mechanism of vascular endothelial dysfunction induced by ferroptosis mediated by <i>NARFL</i> knockout</p>
1130-1145	<p>Michael Hildebrand, University of Melbourne, Australia Mutation of <i>cyclophilin-40</i> molecular chaperone causes persistent stuttering</p>
1145-1200	<p>Rita Serrano, Monash University, Australia Mitochondrial degeneration is the initial cellular pathology in <i>uba5</i> deficiency and indicates a role for ufmylation in mitochondrial homeostasis</p>
Room 219	C5: Gene Regulation & RNA Biology (Molecular, Cellular & Developmental Genetics)
Convenors	<i>Thomas Preiss, Australia & Minna-Liisa Änkö, Finland</i>
1000-1030	<p>Minna-Liisa Änkö, Tampere University, Finland RNA structures shape cellular functions</p>
1030-1100	<p>Gracjan Michlewski, International Institute of Molecular and Cell Biology in Warsaw, Poland Sequence specificity of RIG-I/IFN signaling</p>
1100-1115	<p>Tim Moser, University of Otago, New Zealand Ribosomal DNA heterogeneity is essential for female differentiation in zebrafish</p>
1115-1130	<p>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</p>
1130-1145	<p>Alexandre Cristino, Griffith Institute for Drug Discovery, Australia The functional role of an introgressed neanderthal single nucleotide polymorphism within the schizophrenia-associated locus <i>microRNA-137</i></p>
1145-1200	<p>Paul Waters, University of New South Wales, Australia Functional coherence of long non-coding RNAs that mediate X chromosome inactivation</p>



Room 220	C6: Plant Breeding & Food Security (Agriculture & Plant Genetics)
Convenors	<i>Jessica Hyles, Australia & Inez H Slamet-Loedin, Philippines</i>
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	Nasser Kouadio Yao, Alliance Biodiversity International – CIAT, Kenya Market-led approach and perspective to plant breeding: insights and benefits for increased food and nutrition security
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, Universidad de la República, Uruguay Impact of breeding on wheat and barley genetic diversity

1400-1600	Symposia Sessions D
Room 203	D1: Evolution & Development (Evolutionary Genetics)
Convenors	<i>Peter Dearden, New Zealand & Christiane Nüsslein-Volhard, Germany</i>
1400-1430	Christiane Nüsslein-Volhard, Germany Animal beauty: function and evolution of biological aesthetics
1430-1500	Peter Currie, Monash University, Australia Evolution of muscle stem cell system 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 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)
Convenors	<i>Alyson Ashe, Australia & Kees van Oers, The Netherlands</i>
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	<i>Quin Wills, UK & Denis Bauer, Australia</i>
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	<i>Sue Fletcher, Australia & Lori Isom, USA</i>
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 <i>In silico</i> design of new capsids for AAV therapeutical applications
1530-1545	Raman Sharbioinforma, University of Adelaide, Australia Humanized preclinical mouse model of <i>TIMMDC1</i> 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 <i>BRCA1/2</i> expert panel: a dynamic framework for evidence-based recommendations to improve classification criteria for variants in <i>BRCA1</i> and <i>BRCA2</i>
Room 219	D5: Neurogenetics of Behaviour (Molecular, Cellular & Developmental Genetics)
Convenors	<i>Barry Dickson, Australia & Elissa Hallem, USA</i>
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 <i>CHD8</i> 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 (Agriculture & Plant Genetics)
Convenors	<i>Michael Udvardi, Australia & Pamela Ronald, USA</i>
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 <i>Verticillium dahliae</i> VTA3 promotes <i>ELV1</i> 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 Presentation title tbc <i>Chair: Peter Dearden, New Zealand</i>
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
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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)
Convenors	<i>Charles Robin, Australia & Jackson Champer, China</i>
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 <i>Drosophila suzuki</i>
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	<i>Belinda van Heerwaarden, Australia & Vanessa Kellerman, Australia</i>
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 <i>Eucalyptus pauciflora</i>
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	<i>Melanie Bahlo, Australia & Anthony Hannan, Australia</i>
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	<i>Lyndon Gallacher, Australia & Gemma Chandratillake, UK</i>
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 McInerney-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)
Convenors	<i>Andrew Sinclair, Australia & Hongyan Wang, Singapore</i>
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 <i>alpk3</i> -induced cardiomyopathy
1115-1130	Helen Abud, Monash Biomedicine Discovery Institute, Australia Role of <i>NRG1</i> 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-Clustering 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 (Agriculture & Plant Genetics)
Convenors	<i>Ian Godwin, Australia & Alison Van Eenennaam, USA</i>
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 Papatotopoulos, 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 Program (GSA)
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, Southwharf <i>(separate tickets must be purchased in advance with GSA)</i>

Room 212	Human Genetics Society of Australasia Program (HGSA)
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
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	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
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0830-0930	Plenary Session 6
Plenary Room 2	Detlef Weigel, Max Planck Institute, Germany Paranoid plants: Genetic conflict in the immune system <i>Chair: Suresh Balasubramanian, Australia</i>

1000-1200	Symposia Sessions F
Room 203	F1: Evolutionary Genetics Theory (Evolutionary Genetics)
Convenors	<i>Hamish Spencer, New Zealand & Anna Santure, New Zealand</i>
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	<i>Elise Furlan, Australia & Toshifumi Minamoto, Japan</i>
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	<i>Ignatia Van den Veyver, USA & Cristin Print, New Zealand</i>
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	<i>Jonathon Beesley, Australia & Maya Ghousaini, UK</i>
1000-1030	Anna Gloyn, Stanford University, USA Unravelling mechanisms for islet-cell dysfunction in diabetes using multi-omic data
1030-1100	Maya Ghousaini, 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 <i>Spred2</i> and <i>Acrtr2</i> to protect against rheumatoid arthritis
Room 219	F5: New Experimental Model Organisms for Genetics Research (Molecular, Cellular & Developmental Genetics)
Convenors	<i>Maja Adamska, Australia & Ralf Sommer, Germany</i>
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 <i>PRKACB</i> : 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 <i>Drosophila</i> 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 (Agriculture & Plant Genetics)
Convenors	<i>Marcus Heisler, Australia & Cristina Ferrandiz, Spain</i>
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 <i>Marchantia polymorpha</i>
1115-1130	Joanna Putterill, University of Auckland, New Zealand Three duplicated <i>Medicago soc1</i> 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 <i>Arabidopsis</i> 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



1400-1600	Symposia Sessions G
Room 203	G1: Genetics & Epigenetics of Sex (Evolutionary Genetics)
Convenors	<i>Arthur Georges, Australia & Qi Zhou, China</i>
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 Ciències 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 <i>dmrt1</i> 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	<i>Katarina Stuart, Australia & Katrina Dlugosch, USA</i>
1400-1430	Katrina Dlugosch, University of Arizona, USA Ecological and evolutionary contributions to species invasions
1430-1500	Cristina Vieira, 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	<i>Marco Herold, Australia & Elizabeth Worthey, USA</i>
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 Tosi, 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	<i>Sarah Medland, Australia & David Evans, Australia</i>
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	<i>Jennifer Stow, Australia & Denise Montell, USA</i>
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 HP1 α 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 + Bxb1 integrase for genome editing applications
Room 220	G6: Genetics & Genomics of Plant Evolution (Agriculture & Plant Genetics)
Convenors	<i>John Bowman, Australia & Junko Kyojuka, Japan</i>
1400-1430	Junko Kyojuka, Tohoku 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 <i>Marchantia polymorpha</i>
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

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
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0830-0930	Plenary Session 8
Plenary Room 2	Anne Ferguson-Smith, University of Cambridge, UK The genetics of epigenetic variation Chair: Marieke Oudelaar, Germany

1000-1200	Symposia Sessions H
Room 203	H1: Systematics & Phylogeography (Evolutionary Genetics)
Convenors	<i>Craig Moritz, Australia & Sonal Singhal, USA</i>
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	<i>Collin Ahrens, Australia & Rose Andrew, Australia</i>
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 Columbia, 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 <i>Senecio lautus</i>
Room 210/211	H3: Genomics-driven Healthcare (Genomics & Genomic Technologies)
Convenors	<i>Richard Gibbs, USA & Sean Grimmond, Australia</i>
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 Researchers Showcase (Special Symposium)
Convenors	<i>Leonie Quinn, Australia & Damian Dowling, Australia</i>
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	Benjamin 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 (<i>Helicoverpa armigera</i>)
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	<i>Marnie Blewitt, Australia & Anne Ferguson-Smith, UK</i>
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 (Agriculture & Plant Genetics)
Convenors	<i>Sally Norton, Australia & Vania Azevedo, Peru</i>
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



1330-1530	Symposia Sessions I
Room 203	I1: Molecular Evolution (Evolutionary Genetics)
Convenors	<i>Simon Ho, Australia & Sandra Alvarez-Carretero, UK</i>
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	<i>Beata Ujvari, Australia & Lee Rollins, Australia</i>
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 (<i>hepatocystis</i> 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 <i>Sylvilagus hepaciviruses</i> 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	<i>Eddie Holmes, Australia & Rebeca Carballar-Lejarazu, USA</i>
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 <i>Plasmodium falciparum</i>
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 Irrc15 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	<i>Sonia Shah, Australia & Chiara Fabbri, UK</i>
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	<i>Linda Partridge, UK & Andrew Pask, Australia</i>
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 (Agriculture & Plant Genetics)	
Convenors	<i>Megan Shelden, Australia & Jian-Kang Zhu, China</i>		
1330-1400	Jian-Kang Zhu, Southern University of Science and Technology, China 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 <i>Chair: Peter Doherty, Australia</i>		
1700-1730	Congress Close & Award Presentation		