GSA 2021
Virtual conference

6th–8th Oct

GSA
Genetics Society of
AustralAsia Inc.

SYMPOSIA TOPICS
Conservation & Ecological Genetics | Functional Genomics in Rare Disease | Mobile Genetic Elements | Earth Biogenome | Epigenetics

#GSAA21

Welcome to GSA2021!

Thank you for joining us online this year. The conference will be held on the platform Whova, which enables multisession live streaming. You will need to register to enter the platform using the access information sent to you via email. The platform can be joined using a computer or through the phone app (or both).

Please note: Speakers/Session Chairs should join though the supplied Zoom link for their session only.

We have an exciting program including three invited plenaries (see pg 4), ten sessions of submitted talks (across two concurrent streams, see pgs 5-7 and 11), a special plenary showcasing the work of this year's MJD White Medal recipient, Prof. Kathy Belov (see pg 11), and a GSA Award symposium showcasing all other 2021 individual award winners (see pg 11). The Thursday afternoon session (see pgs 8-10) will be held on Gather Town, and will include the poster session, ECR and undergraduate career development workshops, and opportunities to socialise casually by chatting with colleagues you encounter in the space or by engaging with the games arcade. We encourage you to explore Gather Town prior to the start of this session to maximise your experience (see page 8 for instructions). Come along and check it out!

We are also pleased to showcase the work of some of our **GSA Student Grant Scheme awardees** from 2019 and 2020 including Andrew Baldi, Megan Iminitoff, Johanna Jones, and Ruby Oberin. We thank the generous support of Illumina, The Ramaciotti Centre for Genomics, Point of Care Diagnostics and Brightside Scientific, which has made this scheme possible. **The 2021 Student Grant Scheme will open soon!**

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GSA Policies

GSA Conference Code of Conduct

We request that all GSA conference attendees and social media users follow these guidelines.

The organisers are committed to making this meeting productive, safe, and enjoyable for everyone, regardless of gender, sexual orientation, disability, physical appearance, body size, race, nationality or religion. We will not tolerate harassment of participants in any form. Please follow these guidelines:

- Behave professionally. Harassment and sexist, racist, or exclusionary comments or jokes are not appropriate. Harassment includes sustained disruption of talks or other events, inappropriate physical contact, sexual attention or innuendo, deliberate intimidation, stalking, and photography or recording of an individual without consent. It also includes offensive comments related to gender, sexual orientation, disability, physical appearance, body size, race or religion.
- All communication should be appropriate for a professional audience including people of many different backgrounds. Sexual language and imagery is not appropriate.
- Be kind to others. Do not insult or put down other attendees.

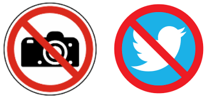
GSA Social Media Guidelines

GSA uses social media to communicate with members and conference attendees, and to communicate information about our meetings to the broader community. We encourage GSA members and conference attendees to contribute to scientific exchange by tweeting or otherwise sharing conference information on social media. We encourage all conference attendees to interact with GSA on social media by:

- Following GSA on Twitter: https://twitter.com/GeneticsAus
- Liking the GSA Facebook page: https://www.facebook.com/geneticsANZ/

Guidelines for presenters

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

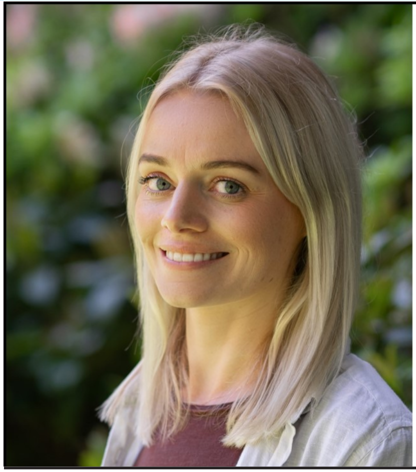


Guidelines for social media users

- Please respect the wishes of the presenter. If they do not want their presentation to be shared on social media, then please do not share it.
- Please do not take photographs of presenters slides without requesting permission. If you take a photograph of the speaker please ask their permission before sharing it.
- Unpublished results, i.e. those presented on a slide without a reference, **should not be shared.** This is critical in order to encourage presentation of unpublished data without risking it being shared widely out of context.
- If you are not sure of the presenter's wishes (e.g. if you missed the start of the talk), take a precautionary approach and don't share.
- Taking photographs and sharing of posters without the express permission of the presenter is not acceptable. Do not share if the presenter isn't there.
- We encourage the use of social media to ask questions, or provide comments and feedback, but this should be done in a constructive manner. Be polite on social media, as you would be in person. Rude and derogatory comments, and personal attacks, are inappropriate.
- We encourage attendees to promote the work of speakers, share quotes, share links to relevant papers etc., as appropriate. Please take time to respect the context of statements made at the conference, to avoid misrepresentation or misattribution.
- Credit presenters for their work by including their name and/or twitter handle in your tweets.
- Include the conference hashtag in your related tweets to allow others to easily follow the meeting. Feel free to also tag the GSA account @GeneticsAus.

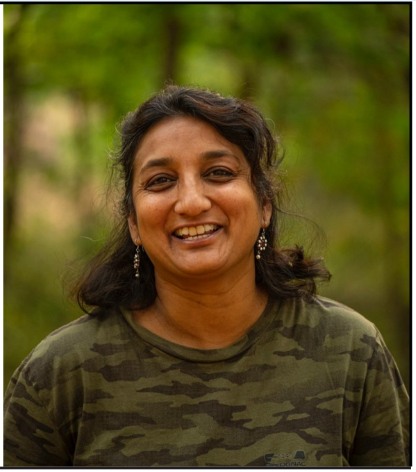
Participants asked to stop any inappropriate behaviour are expected to comply immediately. Attendees violating these rules may be asked to leave the event at the sole discretion of the organisers without a refund of any charge. Any participant who wishes to report a violation of this policy is asked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

Plenaries



Dr Jemma Geoghegan is an evolutionary virologist with a research interest in emerging infectious disease. Her research focuses on determining the fundamental patterns and processes of viral evolution, ecology and emergence. She is a Rutherford Discovery Fellow, a Senior Lecturer in Microbiology at the University of Otago and an Associate Scientist at the Institute of Environmental Science and Research. She is the recipient of the 2017 GSA Alan Wilton Award for her outstanding contributions as an early career scientist.

Professor Mark Dawson is a clinician-scientist and the Associate Director of Research Translation at the Peter MacCallum Cancer Centre. His research interest is studying epigenetic regulation in normal development and cancer. His research has helped identify several first-in-class epigenetic therapies resulting in various clinical trials across the world. He is a Professor at the University of Melbourne, the Sir Edward Dunlop Fellow for the Cancer Council of Victoria and a HHMI International Scholar. He has been elected to the Australian Academy of Science, the Australian Academy of Health and Medical Sciences and is an EMBO member. He is the recipient of the McCulloch & Till Award from the International Society of Experimental Haematology, the Jacques Miller Medal from the Australian Academy of Science and the 2020 Prime Minister’s Prize as Life Scientist of the year.



Professor Uma Ramakrishnan is a molecular ecologist. She has spent the last five years trying to understand the conservation genetics of Indian tigers. Using primarily non-invasive samples, she and her team have tried hard to understand population connectivity and the fate of small and isolated populations. She is a Senior Fellow, DBT Wellcome Trust India Alliance. She won the Parker Gentry Conservation award (2016) and the Homi Bhabha award for Science Education (2020).

AEDT	Day 1, Wednesday, October 6th	
10:00	Welcome - Lee Ann Rollins	
10:15-10:45	**Plenary: Dr. Jemma Geoghegan,** Tracking COVID-19 in New Zealand using genomics; Chair, Lee Ann Rollins	
	Session A	Session B
10:45-12:30	Earth BioGenome; Chair - Kathy Belov	Mobile Genetic Elements; Chair - Sandy Richardson (co-organiser, Adam Ewing)
10:45	**Carolyn Hogg** - Bilby Genome Project: integrating genomics, conservation, and indigenous culture	**Ravindra Raut** - Comprehensive genome-wide analysis of transposable elements in rice (*Oryza sativa* L.)
11:00	**Emma Peel** - Size really does matter – influence of genome quality on complex gene family annotation	**Ahmad Luqman Abdul Fatah** - The interferon-stimulated gene protein HELZ2 inhibits human LINE-1 retrotransposition
11:15	**Kimberley Batley** - Whole genomes reveal multiple candidate genes and pathways involved in the immune response of dolphins to a highly infectious virus	**Shashank Chary** - The piRNA pathway: A flexible guardian against transposons
11:30	**Mike Gardner** - A sleepy genome	**David Adelson** - Horizontal Transfer of Transposons into Sea Snakes Affects Genome Structure
11:45	**Parwinder Kaur** - DNA Zoo Australia	**Julie Blommaert** - To B or not to B: Transposon dynamics, B-chromosomes and genome size variation in rotifers **/ Kooper Hunt** - Targeting transposable elements for analysis of DNA methylation in single cells **/ Joseph Mcconnell** - Read Simulation for Mobile Genetic Element Insertion Detection
12:00-12:30	**Mandira Katuwal Bhattarai** - Genome assemblies of invasive pest weevils using Minion and Illumina sequencers and their role in advancing biological control program **/ Hardip Patel** - Microchromosomes are building blocks of bird, reptile and mammal chromosomes **/ Upendra Bhattarai** - Insights into host manipulation by mind altering parasites through the whole genome, transcriptome, and bisulfite sequencing **/ Amy Locke -** Understanding the ecology and evolutionary history of *Caenorhabditis elegans* in Sydney and surrounds	
12:30-1:00	Break	
1:00-1:30	**Plenary: Prof. Uma Ramakrishnan,** How does genetic data inform tiger conservation?; Chair - Anna MacDonald	
1:30-3:15	Conservation and Ecological Genetics; Chair - Catherine Grueber (co-organiser, Anna MacDonald)	Functional Genomics in Rare Disease; Chair - Robert Bryson-Richardson (co-organiser, Coral Warr)
1:30	**Sean Buckley** - Long-term climatic stability drives accumulation and maintenance of divergent lineages in a temperate biodiversity hotspot	**Felipe Martelli** - Drosophila as a model to investigate and treat inborn errors of amino acid metabolism
1:45	**Duminda Dissanayake** - Sex reversal of alpine Eastern three-lined skink *Bassiana duperreyi* in South Eastern Australia	**Raman Sharma** - A patient inspired THOC2 variant mouse model for understanding the impact of altered TREX-mediated mRNA export in neurodevelopmental disabilities
2:00	**Elspeth McLennan** - Metapopulation management of a critically endangered marsupial in the age of genomics	**Vanessa Fear** - Rapid rare disease genetic variant interpretation with high efficiency CRISPR single nucleotide gene editing, iPSC disease modelling, and functional genomics

Long talks; short talks

AEDT	Session A	Session B
2:15	**Lara Urban** - Leveraging adaptive sampling of environmental DNA for monitoring the critically endangered kākāpō	**Cameron McKnight** - Using human pluripotent stem cell models of mitochondrial disease to identify candidate drug treatments
2:30-3:05	**Erin Hahn** - Fixed in time: characterising historical genomes from formalin-preserved museum specimens **/ Marissa Le Lec** - Assessment of genetic management options for the critically endangered kākāpō using a combined population and genome model **/ Luis Mijangos** - Fragmentation by large dams and implications for the future viability of small platypus populations / **Tom Schmidt -** Comparing heterozygosity across populations and studies: Best practices for genome-wide sequence data **/ Luke Silver** - A targeted approach to investigating immune genes of an iconic Australian marsupial / **Joshua Thia** - Population genomics reveals that Atlantic and Indo-Pacific wahoo (*Acanthocybium solandri*) are distinct genetic stocks and not a globally homogeneous population	**Travis Johnson** - A cis-regulatory-based pipeline for the identification of novel cardiac development and disease genes **/ Bianca Grosz** - Exploring the non-coding GJB1 c.-103C>T mutation causing CMTX1 **/ Linden Muellner-Wong** - Modelling mitochondrial disease variants of the ATAD3 gene cluster **/ Connie Jiang -** High-throughput assay provides functional evidence to assist with reclassification of VUS in KCNH2 **/ Dalia Mizikovsky -** Complex trait genetic data can parse cellular gene programs to predict the influence of genetic variation on phenotypes
3:05		**Andrew Sinclair, Co-Chair Australian Functional Genomics Network** - How to get funding from the Australian Functional Genomics Network

Long talks; short talks

AEDT	Day 2, Thursday, October 7th	
10:00-10:30	**Plenary, Professor Mark Dawson** - Epigenetic mechanisms of malignant clonal dominance and immune evasion; Chair - Camilla Whittington	
	Session A	Session B
10:30-12:00	Conservation and Ecological Genetics; Chair - Anna MacDonald (co-organiser, Catherine Grueber)	Developmental Genetics; Chair - Oliver Griffith
10:30	**Samuel Andrew** - Transcriptomic variation in the response of *Acacia* species to a heatwave shows clinal patterns	**Cuneyt Caglar** - Fast transcriptional activation of developmental signalling pathways during injury response and wound healing in syconoid calcareous sponges
10:45	**Gemma McLaughlin** - Molecular Methods to Manage Wasps in New Zealand	**Jiaheng Xie** - Dark-reared zebrafish as a vertebrate model for myopia studies
11:00	**Georgina Samaha** - Exploring the advantages and limitations of cross-species variant calling and genotyping approaches for conservation research: a case study in wild felids	**Wei Chen** - Defining the imidacloprid target in *Drosophila melanogaster*
11:15	**Oliver Stuart** - Genome structure and inheritance in Australia's most endangered insect, *Dryococelus australis* (Phasmatodea)	**Kellie Veen** - Investigating dedifferentiation regulators driving neuronal diversity and regeneration
11:30-12:00	**Josh Gilligan** - Steps towards implementing a Gene Drive for invasive wasp species / **Mengjia Lau** - Genetic stability of *Aedes aegypti* populations following invasion by wMel Wolbachia / **Veronique Paris** - Population genomics provides information on the urban ecology of a native Australian mosquito involved in disease transmission / **Boris Yagound -** Brain transcriptome analysis reveals gene expression differences associated with dispersal behaviour between range-front and range-core populations of invasive cane toads in Australia	**Aaron Krylov** - Characterising neural cell regeneration in the zebrafish retina / **Sun Yichen** - Neuroligin 2 Regulates F-Actin Dynamics in *Drosophila* Through Cofilin Signaling / **Tien Nguyen** - Genetic basis of lateralization in chick brain / **Georgia Cullen -** Division clusters: Evidence that honeybee oogenesis lacks germ stem cells
12:00-12:30	Break (Undergraduate Lunch with Plenary)	
12:30-2:00	Epigenetics and Chromatin Structure; Chair - Rakesh David	Genomics and Transcriptomics; Chair - Jack Scanlan
12:30	**Jenny Graves** - Chromosomal sex via epigenetic modification? Sex-specific splicing of Z and W-borne alleles of candidate sex determining gene Nr5a1 in the dragon lizard suggests control by sex chromosome conformation	**Johanna Jones** - Genetic variants associated with paediatric cataracts identified in an Australian cohort
12:45	**Sarah Whitely** - Novel JARID2 and KDM6B isoforms are spliced under sex reversal inducing temperatures in the dragon lizard, *Pogona vitticeps*	**Renzo Balboa** - Structural variation in diverse human populations
1:00	**Megan Iminitoff** - Investigating the epigenetic regulator SMCHD1 as a potential therapeutic target for the treatment of Prader-Willi Syndrome and Schaaf-Yang Syndrome	**Clancy Lawler** - Biasing sex ratios as a means of local population suppression: computational and empirical investigation of a non-homing gene drive
1:15	**Jia Zhou** - Genetic similarity enhances the strength of the relationship between gut bacteria and host DNA methylation	**Sarah Inwood** - Transcriptomic characterization of a declining biocontrol system reveals novel virus
1:30-2:00	**William Schierding** - Genetic Variation as a Long-Distance Modulator of RAD21 Expression in Humans / **Alyson Ashe** - SET-domain proteins in epigenetic inheritance: hidden depths / **Enakshi Sinniah** - Conserved epigenetic regulatory logic infers genes governing cell identity / **Jake Newland -** Glia and neurons in the fly brain use different epigenetic mechanisms of gene repression	**Andrew Baldi** - Iron supplementation and the intestinal microbiota – 16S and shotgun metagenomics in an iron intervention trial in Bangladesh / **Tim McInerney** - Deep histories of humans inferred from haplotype genealogies / **Navya Shukla** - Genetic diversity in chimpanzee transcriptomics does not represent wild populations / **Cadel Watson -** dedUCE: efficient identification of Ultraconserved Elements from multiple genomes

Long talks; short talks

Don’t miss the Gather Town event on Thursday afternoon! (2:00-4:00 pm AEDT) In addition to our Poster Session, it contains career development mini-workshops for ECRs, a career panel discussion for undergraduates, the opportunity to socialise with other attendees via video link in a wide range of public and semi-private spaces, and a virtual games arcade!

Gather Town Instructions:

When you enter Gather, you will have the opportunity to complete a brief tutorial to learn about platform features. The arrow keys will allow you to move across the space and engage with other attendees and poster presenters, and enter career workshop spaces and the games arcade. Gather requires a computer with mic and camera, a web browser and headphones are recommended (not required). A full guide to the Gather platform can be found here: https://tinyurl.com/9d99x76h

2:00-4:00	**Thursday, 7th October, Gather Town Session**
2:00-2:30	**Poster presenters in attendance at posters.** *Poster Hall.*
2:30-2:45	**ECR Career Workshop: How to network effectively.** Presenter: Dr. Carolyn Hogg. *West Meeting Room (blue).*
2:50-3:05	**ECR Career Workshop: How to get a job at an applied research organisation.** Presenter: Dr. Tom Walsh, CSIRO. *East Meeting Room (green).*
3:10-3:25	**ECR Career Workshop: How to get your first fellowship.** Presenter: Prof. Coral Warr, La Trobe University. *West Meeting Room (blue).*
3:30-3:45	**ECR Career Workshop: How to ace a job interview.** Presenter: Prof. Arthur Georges, University of Canberra. *East Meeting Room (green).*
3:15-4:00	**Undergraduate Career Panel.** Panel Chair: Dr. Emily Wong, Victor Chang Institute. Panellists: Cuneyt Caglar, Emily Roycroft, Yi-Kai Tea. *Undergraduate Lounge.*

ECR Career Mini-Workshops: If you want to attend a workshop, head ‘south’ in Gather Town to access the East and West Meeting Rooms (near the Games Arcade). Workshops have a limited number of chairs (25 per session), and are offered on a first-come, first-served basis. However, they will be recorded so if you can’t get a seat and want to watch them later, we’ll provide links on Friday to Google Drive. Enjoy!

Please note that we will have 18 undergraduate attendees who have been selected to attend GSA2021. These individuals’ avatars will be wearing purple mortarboards, so please do not choose this option if you are not an undergraduate! If you see undergraduates in Gather, please engage with them so that they can get the experience of attending a conference.

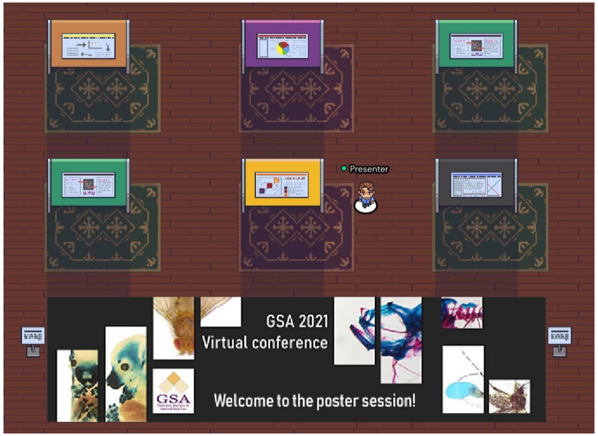
Undergraduate Award Winners

Kiana Asgari
Liam Bourke
Hamish Carter
Honglin Kevin Chen
Al-Aabid Chowdhury
Grace Day
Agnes Dear
Janath Fernando
Katrina Filshie
Catherine Gatt
Morgan Gilbert
Sienna Graham
Ethan Kok
Adam Morris
Madeline Thornton
Alex van der Weerden
Kevin Winardi
Z-Yie Yap

Gather Town Poster Viewing Instructions

In Gather Town, participants will explore a 2D world with 8-bit graphics, walking by moving their avatar with keyboard arrow keys. The posters will be pre-loaded and organised in a grid similar to an in-person conference. To interact with a poster, conference attendees will walk up to the poster and press the 'x' key to enter a full screen viewing.

When poster presenter avatars are in the private space near their poster, all other conference attendee avatars in that space will be able to see and hear the presenter through webcams/microphones. Those avatars in a private space near a poster will only be interacting with people in that space and not the neighbouring spaces. This promotes conversation with the presenters without interrupting conversation going on at other posters and provides an immersive virtual experience.



2:00-4:00	Poster Session - Meet on Gather Town
	1. **Maja Adamska**, Xavier Bailly, Stéphanie Bertrand, Agnès Boutet, JP Chambon, Bénédicte Charrier, Patrick Cormier, Salvatore D'Aniello, Sébastien Darras, Haley Flom, Eve Gazave, Raphaël Lami, Julia Morales, Stefano Piraino, Nicolas Rabet, Bernd Schierwater, Simon Sprecher, Stefano Tiozzo, David Wahnoun. DIGITALMARINE: Hybrid educational and research training on the use of marine models in life sciences. 2. **Simon Baxter**, Greg Baker, Carlos Caceres-Barrios, Amanda Choo, Peter Crisp, Beth Fung, Kym Perry, Kevin Powis, Chris Ward. Sequencing interspecific hybrid genomes to identify major mutations. 3. **Alexandra Boyling,** Anthony Cutrupi, Garth A. Nicholson, Gonzalo Perez-Siles, Marina L. Kennerson, Investigating the pathomechanism of the intergenic structural variation causing CMTX3 neuropathy 4. **Georgina Bramwell**, Emi S. Ab Rahim, Aaron G. Schultz, Antoine M. Dujon, Kim Weston, Brett A. Ingram, Sam Jahangard, Frédéric Thomas, Beata Ujvari, Craig D.H. Sherman. Hatchery-imposed selection does not impact the genetic diversity of farmed blue mussels. 5. **Richard Burke**, Kyle Lyon, Lauren Kirn and Bichao Zhang. Post-translational regulation of copper transport by the ubiquitin proteasomal system. 6. **Alexander L. Carleton**, Dorothy Chan, Juan Manuel Botto, Geoffrey J. Faulkner, and Sandra R. Richardson. L1-Cre: a reporter system to circumvent engineered LINE-1 silencing. 7. **Renee Chu**, Alexander L. Carleton, and Sandra R. Richardson. LINE-1 activity in primordial germ cell specification. 8. **Toby Kovacs.** Molecular phylogenetics of the "cave cockroach" family Nocticolidae 9. **ZM Liu**, WW Lu, YK Lee, HT Li, W Chen. Gene-trait matching and transcriptome analysis reveal putative genes involved in *Bifidobacterium* spp. biofilm formation.

2:00-4:00	**Poster Session - Meet on Gather Town**
	10. Kelsie A. Lopez, **Callum S. McDiarmid**, Simon C. Griffith, Irby J. Lovette and Daniel M. Hooper. Evaluating evidence of mitonuclear incompatibilities with the sex chromosomes in an avian hybrid zone. 11. Qais Al Rawahi, Helen Senn, **Jose Luis Mijangos**, Mehar S Khatkar, Mohammed A. AL Abri, Mansoor H. AlJahdhami, Jennifer Kaden, Katherine Brittain, Jaime Gongora. Rescued back from extinction in the wild: past, present and future of the genetics of the Arabian oryx in Oman. 12. **Melissa von Moger**, Sally Potter, Mark Eldridge, Craig Moritz. Current population structure of *Petrogale penicillata* following the 2019/20 Australian bush fires. 13. **Tiffanie M. Nelson**, Catherine Bromhead, Melissa Burke, Simon Gladman, Johan Gustafsson, Mark Gray, Dominique Gorse, Christina Hall, Justin Lee, Steven Manos, Igor Makunin, Gareth Price, Audrey Stott, Michael Thang, Nigel Ward, Jeffrey H. Christiansen, Andrew Lonie. Robust public computational services supporting Genome Assembly and Annotation for Australian Researchers. 14. **Chai-Ann Ng**, Rizwan Ullah, Jessica Farr, Adam P. Hill, Krystian A. Kozek, Loren R. Vanags, Devyn Mitchell, Brett M. Kroncke and Jamie I. Vandenberg. Deciphering VUS in KCNH2 using functional phenotyping assays 15. **Peter Prentis**, Ray Norton and Lauren Ashwood. Genomic, structural and functional evidence indicate that the sea anemone 8 toxin family does not represent an extension of the ShK fold. 16. Alexander J. F. Verry, Lachie Scarsbrook, **Nicolas J. Rawlence**. Ancient mitogenomes reveal individualistic responses of Aotearoa New Zealand fauna to the last Ice Age. 17. **Lachlan Wallace**, Enoch Wong, Vishal Chaturvedi, Patricia Jusuf and Michael J. Murray. Netrins are involved in the epithelial wound response in Drosophila and Zebrafish. 18. **Fionna Zhu**, Georgia Malloy and Michael J. Murray. Discs Large is a novel regulator of the Enteroblast Mesenchymal-to-Epithelial Transition in the adult Drosophila midgut.

AEDT	Day 3, Friday, October 8th	
10:00-10:30	**MJD White Medal Recipient, Prof. Kathy Belov** - Reflecting on twenty years of genetics in Australia: from autorads to cloud compute; Chair, Lee Ann Rollins	
10:30-12:00	Session A	Session B
	Epigenetics and Chromatin Structure; Chair - Rakesh David	Ecological and Evolutionary Genetics; Chair - Eddy Dowle
10:30	**Ruby Oberin** - Altered epigenetic programming of oocytes modulates offspring growth and accelerates bone development	**Meghan Castelli** - Transcriptional architecture of the embryonic brain-gonad axis in a temperature sex-reversing reptile
10:45	**Pei Qin Ng** - Arabidopsis TRM5 Encodes a Nuclear-localised Bifunctional tRNA Guanine and Inosine-N1-methyltransferase that is Important for Growth	**Katarina Stuart** - A genetic perspective on rapid adaptation in the globally invasive European starling (*Sturnus vulgaris*)
11:00	**Di Pan** - Histone modification dynamics during sponge regeneration	**Rodger Yan** - Investigation of Calcareous Sponge Microbiome Reveals Unique Microbial Composition in Sycon capricorn
11:15	**Teruhito Ishihara** - Can paternal H3K4me3 transmission in sperm affect imprinting status of paternally-expressed genes after fertilisation?	**Thu Nguyen** - Disruption of duplicated yellow genes in *Bactrocera tryoni* modifies pigmentation colouration and impacts behaviour
11:30-12:00	**Xiuwen Zhang** - Abnormal splicing of nr5a1, a candidate sex determining gene in the dragon lizard *Pogona vitticeps* involves interaction between nucleotide acid conformation and RNA binding proteins / **Susan Wagner** - Unique sox9 and amh expression profiles in genetic sex determination in the lizard *Pogona vitticeps* / **Sigrid Petautschnig** - Polycomb-dependent epigenetic programming in the oocyte modulates brain development and behaviour in offspring	**Stephanie Liang** - The determinants of population structure in a lizard with bimodal reproduction / **Astra Heywood** - Building a New Zealand *Apis mellifera* Representative Genome Graph / **Soleille Miller** - Fine-Scale Population Structure and Consequences of Asexual Reproduction in the Facultative Parthenogen, *Megacrania batesii* / **Sonu Yadav** - Plasma and scat metabolomics of the dingo and a comparison with domestic dog
12:00-12:30	Break	
12:30-2:15	GSA Awards Symposium; Chair - Lee Ann Rollins	
12:30	**Ross Crozier Medal Recipient, Camilla Whittington** - Genomics and evolution of vertebrate pregnancy	
12:45	**Alan Wilton Award Recipient, Seth Cheetham** - Single-molecule simultaneous profiling of DNA methylation and DNA-protein interactions with Nanopore-DamID.	
1:00	**D.G. Catcheside Prize recipient, Emily Roycroft** - Museum genomics unlocks a historical record of extinction in Australia.	
1:15	**Spencer Smith-White Travel Award recipient, Stephanie Chen** - Genomics of speciation and introgression: insights from waratah (*Telopea* spp.) as a model clade	
1:30	**Spencer Smith-White Travel Award recipient, Nynke Raven** - EcoImmunology of an endangered marsupial, the Tasmanian devil (*Sarcophilus harrisii*)	
1:45	**Award for Excellence in Education recipient, Phillip Wilcox** - (Re)Claiming spaces: indigenisation of genetics education in Aotearoa/New Zealand	
2:00	**Student Presentation Awards and Conference Closing**	

Long talks; short talks

Acknowledgements

We thank the following people for their contributions to this year's conference:

GSA2021 Organising Committee
Lee Ann Rollins, GSA President
Camilla Whittington, GSA Vice-President
Stephanie Chen
Livia Gerber
Soleille Miller
Katarina Stuart
Yi-Kai Tea
Boris Yagound

Student Presentation Awards Committee
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Undergraduate Student Liaisons
Maja Adamska
Parwinder Kaur

Career Workshop Presenters
Carolyn Hogg
Tom Walsh
Coral Warr
Arthur Georges
Emily Wong
Cuneyt Caglar
Emily Roycroft
Yi-Kai Tea

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Robert Bryson-Richardson*
Rakesh David*
Eddy Dowle
Adam Ewing*
Oliver Griffith
Catherine Grueber*
Anna MacDonald*
Sandy Richardson*
Jack Scanlan
Coral Warr*

Future Conferences

In 2022 GSA will be combined with ComBio:
https://www.combio.org.au/combio2022/

In 2023 GSA will be combined with the International Congress of Genetics. Stay tuned for more information!